

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 21:22:03 ; Search time 2028.86 Seconds

(without alignments), 88.020 Million cell updates/sec

Title: US-09-016-464-8

Perfect score: 29

Sequence: 1 GCGCGCGTGGCGGCTGTGTGTGGCGCGG 29

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba1:*

2: gb_ba2:*

3: gb_ba3:*

4: gb_in1:*

5: gb_in2:*

6: gb_in3:*

7: gb_om:*

8: gb_ov:*

9: gb_pat1:*

10: gb_pat2:*

11: gb_ph:*

12: gb_p11:*

13: gb_p12:*

14: gb_p13:*

15: gb_p14:*

16: em_ba1:*

17: em_ba2:*

18: em_fun:*

19: em_htgo_hum:*

20: em_htgo_inv:*

21: em_htgo_rod:*

22: em_htg_hum1:*

23: em_htg_hum2:*

24: em_htg_hum3:*

25: em_htg_hum4:*

26: em_htg_hum5:*

27: em_htg_hum6:*

28: em_htg_hum7:*

29: em_htg_hum8:*

30: em_htg_inv1:*

31: em_htg_inv2:*

32: em_htg_other:*

33: em_htg_rod:*

34: em_hum1:*

35: em_hum2:*

36: em_hum3:*

37: em_hum4:*

38: em_hum5:*

39: em_hum6:*

40: em_hum7:*

41: em_in:*

42: em_om:*

43: em_or:*

44: em_ov:*

45: em_pat:*

46: em_ph:*

47: em_p1:*

48: em_ro:*

49: em_sts:*

50: em_sy:*

51: em_un:*

52: em_v1:*

53: gb_sts1:*

54: gb_sts2:*

55: gb_sts3:*

56: gb_sy:*

57: gb_un:*

58: gb_v1:*

59: gb_v12:*

60: gb_htg1:*

61: gb_htg2:*

62: gb_htg3:*

63: gb_htg4:*

64: gb_htg5:*

65: gb_htg6:*

66: gb_htg7:*

67: gb_htg8:*

68: gb_htg9:*

69: gb_htg10:*

70: gb_htg11:*

71: gb_htg12:*

72: gb_htg13:*

73: gb_htg14:*

74: gb_htg15:*

75: gb_htg16:*

76: gb_htg17:*

77: gb_htg18:*

78: gb_htg19:*

79: gb_htg20:*

80: gb_htg21:*

81: gb_htg22:*

82: gb_htg23:*

83: gb_htg24:*

84: gb_htg25:*

85: gb_p1:*

86: gb_p2:*

87: gb_p3:*

88: gb_p4:*

89: gb_p5:*

90: gb_p6:*

91: gb_p7:*

92: gb_p8:*

93: gb_p9:*

94: gb_p10:*

95: gb_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	29	100.0	1733	92	HSR2BREC	X68487 H. sapiens m
2	29	100.0	125099	86	AC006251	AC006251 Homo sapi
3	29	100.0	182134	83	HS121M24	AL354046 Homo sapi
4	21.6	74.5	1991	5	AF261947	AF261947 Crithidia
5	21.6	74.5	3000	93	HSU77129	U77129 Human SP51/
6	21.6	74.5	165178	69	AC025355	AC025355 Homo sapi
7	21.6	74.5	170595	83	CNS01DRR	AL118556 Homo sapi
8	21	72.4	3164	3	RCU46071	U46071 Rhodobacter
9	21	72.4	3274	6	STU31177	U31177 Leishmania
10	21	72.4	148362	74	AC069300	AC069300 Oryza sat
11	20.2	69.7	5962	2	MBS100PER	Y13228 Mycobacteri

12	20.2	69.7	36526	2	MSGY42	AD000005 Mycobacte
13	20.2	69.7	36804	3	MYCY210	Z84395 Mycobacteri
14	20.2	69.7	36850	3	MTCY369	Z80226 Mycobacteri
15	20.2	69.7	34841.1	2	AP003007	AP003007 Mesorhizo
16	20	69.0	13245	1	AE001977	AE001977 Deinococc
17	20	69.0	13245	1	AB017641	AB017641 Micromono
18	20	69.0	43780	73	AC068017	AC068017 Homo sapi
19	20	69.0	103610	64	AC015780	AC015780 Homo sapi
20	20	69.0	121619	75	AC073502	AC073502 Homo sapi
21	20	69.0	122430	62	AC010496	AC010496 Homo sapi
22	20	69.0	182399	63	AC013260	AC013260 Homo sapi
23	20	69.0	184000	64	AC016595	AC016595 Homo sapi
24	20	69.0	184169	70	AC026349	AC026349 Homo sapi
25	20	69.0	187358	66	AC019118	AC019118 Homo sapi
26	20	69.0	206782	69	AC024150	AC024150 Homo sapi
27	20	69.0	209060	65	AC019005	AC019005 Homo sapi
28	19.6	67.6	226	13	AY020280	AY020280 Oryza sat
29	19.6	67.6	239	7	AB010595	AB010595 Globiceph
30	19.6	67.6	164076	74	AC069429	AC069429 Homo sapi
31	19.4	66.9	224	13	AY022464	AY022464 Oryza sat
32	19.4	66.9	2310	3	AF089835	AF089835 Caulobact
33	19.4	66.9	2354	3	RRRP	Y09072 R.sphaeroid
34	19.4	66.9	2450	14	CH1586	Y11586 C.reinhardt
35	19.4	66.9	3005	2	HV095375	U95375 Ha1oferax v
36	19.4	66.9	3447	2	AF040268	AF040268 Caulobact
37	19.4	66.9	5011	59	HSICP11	D10658 Herpes simp
38	19.4	66.9	9117	3	PSEMETH	L29642 Pseudomonas
39	19.4	66.9	9980	1	AE004915	AE004915 Pseudomon
40	19.4	66.9	10561	1	AE002462	AE002462 Neisseria
41	19.4	66.9	10561	1	AE002465	AE002465 Neisseria
42	19.4	66.9	10575	1	AE001976	AE001976 Deinococc
43	19.4	66.9	10763	9	AR008973	AR008973 Sequence
44	19.4	66.9	10763	9	AR075314	AR075314 Sequence
45	19.4	66.9	11418	3	SCR15	AL132856 Streptomy

ALIGNMENTS

RESULT 1						
LOCUS	HSAB2BREC	1733 bp	mRNA	PRI	31-MAR-1995	
DEFINITION	H.sapiens mRNA for A2b adenosine receptor.					
ACCESSION	X68487.1 GI:400453					
VERSION	X68487.1 GI:400453					
KEYWORDS	A2b-adenosine receptor; adenosine receptor; transmembrane protein.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;					
AUTHORS	Primates; Catarrhini; Homiidae; Homo.					
JOURNAL	1 (bases 1 to 1732)					
TITLE	Jacobson, M.A.					
REFERENCE	Direct Submission					
AUTHORS	Submitted (16-SEP-1992) M.A. Jacobson, Merck Research Laboratories,					
JOURNAL	WP44-B126, West Point PA 19486, USA					
REFERENCE	2 (bases 1 to 1732)					
AUTHORS	Salvatore, C.A., Luneau, C.J., Johnson, R.G. and Jacobson, M.					
JOURNAL	Genomics					
FEATURES	In press					
SOURCE	Location/Qualifiers					
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	/tissue_type="brain"					
	/map="p12"					
	333..1331					
	/codon_start=1					
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	/protein_id="CAA48505.1"					
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	/translation="MLETODALYVALLEVALAASVAGNVILCAAVGTANTLPPTNY					

CDS

/codon_start=1
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BASE COUNT

352 a 479 c 485 g 417 t

Query Match

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 GGCGCCGTCGCCGCTTGTGGCGCG 29

Db

47 GGCGCCGTCGCCGCTTGTGGCGCG 19

RESULT 2						
LOCUS	AC006251/c					
DEFINITION	Homo sapiens chromosome 17, clone hprk.692_E_18, complete sequence.					
ACCESSION	AC006251					
VERSION	AC006251.3 GI:4309945					
KEYWORDS	HTG.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
JOURNAL	1 (bases 1 to 125099)					
TITLE	Birren, B., Linton, L., Nusbaum, C. and Lander, E.					
REFERENCE	2 (bases 1 to 125099)					
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,					
JOURNAL	Baker, J., Baldwin, J., Barina, N., Beckert, R., Benn, J., Brown, A.,					
TITLE	Castle, A., Cerny, J., Colangelo, M., Collins, S., Collumore, A.,					
REFERENCE	Cooke, P., Dearrellano, K., Depayre, E., Devon, K., Dewar, K.,					
AUTHORS	Donelan, L., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R.,					
JOURNAL	Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heatford, A.,					
TITLE	Herten, L., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A.,					
REFERENCE	Lehoczy, J., MacDonald, P., Marquis, N., McEwan, P., McGurk, A.,					
AUTHORS	McKernan, K., Meldrum, J., Molla, M., Morris, W., Morrow, J.,					
JOURNAL	Myhalackcy, J., Naylor, J., Nilloff, M., O'Connor, T., O'Donnell, P.,					
TITLE	Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A.,					
REFERENCE	Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C.,					
AUTHORS	Subramanian, A., Testfaye, S., Torturella-Miller, I., Vassiliev, H.,					
JOURNAL	Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.					
TITLE	Direct Submission					
JOURNAL	Submitted (23-DEC-1998) Whitehead Institute/MIT Center for Genome					
REFERENCE	Research, 320 Charles Street, Cambridge, MA 02141, USA					
AUTHORS	3 (bases 1 to 125099)					

TITLE

Submitted (27-FEB-1999) Whitehead Institute/MIT Center for Genome

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 1, 1999 this sequence version replaced gi:4309878.
 All repeats were identified using RepeatMasker: Smlt, A.F.A. &
 Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Only the first 12509 base pairs of this clone are being submitted.
The remainder overlaps accession number AC002553 (WICGR project
1251).

FEATURES

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source
    Location/Qualifiers
        1. 125099
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            /db_xref="taxon:9606"
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            /clone_1lb="RPCL-11 human BAC library"
            /map="17"
            /chromosome="17"
            complement(209..390)
            /rpt_family="MIR"
repeat_region
    504..650
            /rpt_family="MER3"
            complement(663..1541)
            /rpt_family="L1PA10"
repeat_region
    1682..1985
            /rpt_family="AluSx"
            complement(2061..2122)
            /rpt_family="MIR"
repeat_region
    2242..2432
            /rpt_family="MER6"
            /rpt_family="AluSg"
            2494..2538
            /rpt_family="TTTA)n"
            2666..2888
            /rpt_family="L1MEC"
            3024..3306
            /rpt_family="AluSg"
            3307..3334
            /rpt_family="TTAA)n"
            complement(3701..3867)
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    complement(3868..4181)
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repeat_region
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            complement(4490..4602)
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            4653..4684
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            5485..5547
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            7565..7754
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            complement(7755..7866)
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            /rpt_family="L1MEC"
            complement(8652..8914)
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            9084..9299
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            complement(16401..16682)
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            21050..21208
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            complement(22314..22609)
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            22918..23084
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            23797..23941
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            23942..24243
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Best Local Similarity 100.0%: Pred. No. 0.38;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGCCGTCGCCGCTTGTGTCGCCGCG 29
    |||
DB 56967 GGGCCGTCGCCGCTTGTGTCGCCGCG 56939

RESULT 3
HS12JM24/C
LOCUS      HS12JM24
DEFINITION Homo sapiens chromosome 17 clone PAC RPCI-1 12JM24 map 17p11.2, ***
SEQUENCING IN PROGRESS ***, 12 ordered pieces.
ACCESSION  AL354046
VERSION     AL354046.4 GI:9213339
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo;
             1 (bases 1 to 182134)
             Ramser,J., Langer,I., Steffens,C., Kiehn,M., Helmann,K.,
             Junker,E., Moll,F., Schuelzchen,S., Radloff,U., Francis,F.,
             Seranski,P., Pousteke,A., Reinhardt,R. and Lehrach,H.
             Unpublished
             2 (bases 1 to 182134)
             MORGENR.
             Direct Submission
             Submitted (28-APR-2000) MORGENR, Abt. Lehrach, Max Planck Institut
             fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany
             On Jul 15, 2000 this sequence version replaced g1:8248729.
             Clone received from the Resource Centre of the Human Genome Project
             at the Max-Planck-Institute for Molecular Genetics
             contig 01      1. 6193
             contig 02      6294. 24520
             contig 03      24621. 66502
             contig 04      66603. 72984
             contig 05      73085. 74370
             contig 06      74471. 79306
             contig 07      79407. 83185
             contig 08      83286. 96797
             contig 09      96898. 104173
             contig 10      104274. 134971
             contig 11      135072. 136924
             contig 12      137025. 182134.
             * NOTE: This is a 'working draft' sequence. It currently
             * consists of 12 contigs. Gaps between the contigs
             * are represented as runs of N. The order of the pieces
             * is believed to be correct as given, however the sizes
             * of the gaps between them are based on estimates that have
             * provided by the submittor.
             * This sequence will be replaced
             * by the finished sequence as soon as it is available and
             * the accession number will be preserved.
             1
             6194 6293: gap of 100 bp
             6294 24520: contig of 18227 bp in length
             24521 24620: gap of 100 bp
             24621 66502: contig of 41882 bp in length
             66503 66602: gap of 100 bp
             66603 72984: contig of 6382 bp in length
             72985 73084: gap of 100 bp
             73085 74370: contig of 1286 bp in length
             74371 74470: gap of 100 bp
             74471 79306: contig of 4836 bp in length
             79307 79406: gap of 100 bp
             79407 83185: contig of 3779 bp in length
             83186 83285: gap of 100 bp
             83286 96797: contig of 13512 bp in length
             96798 96897: gap of 100 bp

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FEATURES
SOURCE
    1. 182134
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       /clone="PAC RPCI-1 12JM24"
       /clone_lib="RPC11.3-5 Human PAC library, originating
       institute: Roswell Park Cancer Institute, creator: Piefer
       de Jong, P. Ioannou"
       /note="region between markers D17S842-D17S953"
       1
       /note="sp6_end:PAC RPCI-1 12JM24"
       182134
       misc_feature
       182134
       /note="T7_end:PAC RPCI-1 12JM24"
BASE COUNT  47159 a 39947 c 41252 g 52653 t 1113 others
ORIGIN
Query Match      100.0%: Score 29; DB 83; Length 182134;
Best Local Similarity 100.0%: Pred. No. 0.32;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGCCGTCGCCGCTTGTGTCGCCGCG 29
    |||
DB 148361 GGGCCGTCGCCGCTTGTGTCGCCGCG 148333

RESULT 4
AF261947/c
LOCUS      AF261947
DEFINITION Crithidia fasciculata nucleoside transporter 2 gene, complete cds.
ACCESSION  AF261947
VERSION     AF261947.1 GI:10764227
KEYWORDS
SOURCE      Crithidia fasciculata.
             Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.
             1 (bases 1 to 1991)
             Liu,W., Ntuba,D., Carter,N.S., Landfear,S.M. and Ullman,B.
             Isolation and Functional Characterization of the CfNT1 and CfNT2
             nucleoside transporter Genes from Crithidia fasciculata
             Unpublished
             2 (bases 1 to 1991)
             Liu,W., Ntuba,D., Carter,N.S., Landfear,S.M. and Ullman,B.
             Direct Submission
             Submitted (28-APR-2000) Biochemistry and Molecular Biology, Oregon
             Health Science University, 3181 SW Sam Jackson Rd., Portland, OR
             97201, USA
FEATURES
SOURCE
    1. 1991
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       <150. >1658
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       150. 1658
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       ASATYSAPDELITRYVYATGDPDAVAETPEPFMNANTFYNGATYVLOVLEPSTPEP
       MKRIPLSVRLVFGAGIPAEELLIIIVPAATIKSCHALAIYINVACVGGSKALCS
       CTNALVGFPTKFMNGQMGVLTVALMSIIQILKSMGTSFHDILTMKRTYFGIC
       GIDLPATFELAILRFNPFAOKYIAEYRAGARNQNNNESTLEETAPSMNEPAADID

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BASE COUNT 390 a 623 c 542 g 436 t
 ORIGIN
 LPAVDDKERALNEEGDEVRATVSEEFHVKRGAVLJATGADAKNVLDQONTTSTSE
 QLLRASAAVFKRVPMVCAVLITFTSLTTPGVGFLLSTTSGMTMYIVLFLNAGD
 FLSRMVLMFRPLRSPKVPVAGVILGRLILIPFVLCVRRINGEALPYVLTLLGLTN
 GYFGCMACHCRRTTLRYAGRSLSAAMLSGISMGLCFGSNLSAIIITLTH"

Query Match 74.5%; Score 21.6; DB 5; Length 1991;
 Best Local Similarity 85.7%; Pred. No. 6.1e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GCGCCGTGCGCGCTTGTGGCGCGG 29
 Db 568 GCGCCGTGCGCGACTGTGATGCGCGG 541

RESULT 5
 LOCUS HSU77129 3000 bp mRNA PRI 03-MAR-1997
 DEFINITION Human SPS1/STE20 homolog KHS1 mRNA, complete cds.
 ACCESSION U77129
 VERSION U77129.1 GI:1857330
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 3000)
 AUTHORS Tung, R.M. and Blenis, J.
 TITLE A Novel Human SPS1/STE20 Homologue, KHS, activates Jun N-terminal
 Kinase
 JOURNAL Oncogene 14 (1997) In press
 REFERENCE 2 (bases 1 to 3000)
 AUTHORS Tung, R.M. and Blenis, J.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-1996) Cell Biology, Harvard Medical School, 240
 Longwood Ave, Boston, MA 02115, USA
 FEATURES
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 location/Qualifiers
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BASE COUNT 936 a 632 c 688 g 744 t
 ORIGIN

Query Match 74.5%; Score 21.6; DB 93; Length 3000;
 Best Local Similarity 85.7%; Pred. No. 5.2e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 GCGCCGTGCGCGCTTGTGGCGCGG 29

Db 119 GCGCCGTGCGCGCTGATGCGCGCGG 146

RESULT 6
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 DEFINITION AC025355 165178 bp DNA HTG 24-MAR-2000
 AC025355 Homo sapiens chromosome 1 clone RP11-184B9 map 1, WORKING DRAFT
 SEQUENCE 15 unordered pieces.
 ACCESSION AC025355
 VERSION AC025355.2 GI:7321629
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 165178)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 JOURNAL Homo sapiens chromosome 1, clone RP11-184B9
 REFERENCE 2 (bases 1 to 165178)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bede, F.,
 Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,
 Campopiano, A., Castle, A., Choepel, J., Colangelo, M., Collins, S.,
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 Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
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 Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
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 O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Plerre, N.,
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 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange, R., Stojanovic, N., Subramanian, A., Talamas, J.,
 Testaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
 JOURNAL
 COMMENT
 Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 24, 2000 this sequence version replaced gi:7210077.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu
 Project Information
 Center project name: L7605
 Center clone name: 184_B_9
 Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Assembly: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 154713 bases at least Q40
 Consensus quality: 159968 bases at least Q30
 Consensus quality: 161968 bases at least Q20
 Insert size: 168000; agarose-fp
 Insert size: 163778; sum-of-contigs
 Quality coverage: 4.3 in Q20 bases; agarose-fp
 Quality coverage: 4.4 in Q20 bases; sum-of-contigs
 NOTE: This is a 'working draft' sequence. It currently
 consists of 15 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as

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* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1
1130 1229: contig of 1129 bp in length
1230 3291: contig of 2062 bp in length
3292 3391: gap of 100 bp
3392 5121: contig of 1730 bp in length
5122 5221: gap of 100 bp
5222 7868: contig of 2647 bp in length
7869 7968: gap of 100 bp
12113 12212: contig of 4144 bp in length
12213 20037: contig of 7825 bp in length
20038 20137: gap of 100 bp
20138 32475: contig of 12338 bp in length
32476 32575: gap of 100 bp
32576 44815: contig of 12240 bp in length
44816 44915: gap of 100 bp
44916 58669: contig of 13754 bp in length
58670 58769: gap of 100 bp
58770 70148: contig of 11379 bp in length
70149 70248: gap of 100 bp
70249 84403: contig of 14155 bp in length
84504 100391: contig of 15888 bp in length
100392 100491: gap of 100 bp
100492 119209: contig of 18718 bp in length
119210 119309: gap of 100 bp
119310 136663: contig of 17354 bp in length
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3392. 5121
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5222. 7868
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7969. 12112
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70249. 84403
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84504. 100391
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vector_side:left"
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/misc_feature /note="assembly_fragment"
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BASE COUNT 51486 a 31508 c 31360 g 49420 t 1404 others
ORIGIN

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Query Match 74.5%; Score 21.6; DB 69; Length 165178;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 2 GCGCGTGGCGGCTGTGCTGCGCGCG 29
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DB 38592 GCGCGTGGCGGCTGTGCTGCGCGCG 38619

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RESULT 7
CONS1DRR/c
LOCUS
DEFINITION
Homo sapiens chromosome 14 clone R-406H23, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
ACCESSION
AL118556
AL118556.3 GI:11875941
KEYWORDS
HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 170595)
Genoscope.
Direct Submission
Submitted (14-DEC-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
On Dec 17, 2000 this sequence version replaced gi:8346742.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: Segref@genoscope.cns.fr

```

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . even if efforts are made to eliminate these contaminating sequences. The following BAC sequence is oriented from the T7 to the SP6 end.

Upstream BAC (overlapping the T7 end) : R-247L20

----- Summary Statistics

Assembly program: Phrap; version 2.0

Quality coverage: 5.27x in Q20 bases; sum-of-contigs

Overall quality chart :

```

Range : bases
0 :
1 - 9 : 6
10 - 19 : 93
20 - 29 : 143
30 - 39 : 651
40 - 49 : 4251
50 - 59 : 7077
60 - 69 : 13795
70 - 79 : 31684
80 - 89 : 57664
90 - 99 : 55231

```

Percentage of bases with a quality value >= 40 : 99 %.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

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     STS               74827..74956
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                        identified using the e-PCR software (G. Schuler)"
     STS               87967..88139
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                        identified using the e-PCR software (G. Schuler)"
BASE COUNT            54525 a 32478 c 31585 g 52007 t
ORIGIN
Query Match          74.5%; Score 21.6; DB 83; Length 170595;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 GCGCGGTGCGGCTGTGTGGCGGCG 29
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Db 127891 GCGCGGTGCGGCTGTGTGGCGGCG 127864

RESULT 8
LOCUS      RCU46071      3164 bp      DNA      BCF      05-JUN-1996
DEFINITION Rhodobacter capsulatus cytochrome c biogenesis (cych) gene,
ACCESSION  U46071
VERSION     U46071.1 GI:1353871
KEYWORDS   .
SOURCE      Rhodobacter capsulatus strain=MT1131.
ORGANISM    Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
            Rhodobacter.
REFERENCE   1 (bases 1 to 3164)
AUTHORS    Lang,S.E., Jenney,F.E. and Daldal,F.
TITLE      Rhodobacter capsulatus cych: A bipartite gene that affects
            differentially the biogenesis of various c-type cytochromes
            unpublished
JOURNAL     2 (bases 1 to 3164)
AUTHORS    Lang,S.E., Jenney,F.E. and Daldal,F.
TITLE      Direct Submission
JOURNAL     Submitted (17-JAN-1996) Fwz1 Daldal, Biology, University of
            Pennsylvania, 204 Mudd Bldg, Philadelphia, PA 19104-6018, USA
FEATURES             Location/Qualifiers
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ORIGIN
Query Match          72.4%; Score 21; DB 3; Length 3164;
Best Local Similarity 82.8%; Pred. No. 8.1e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GCGCGGTGCGGCTGTGTGGCGGCG 29
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Db 1121 GCGCGGTGCGGCTGTGTGGCGGCG 1149

RESULT 9
LOCUS      STU31177/c      3274 bp      DNA      INV      11-JUL-1997
DEFINITION Leishmania tarentolae glutamate dehydrogenase precursor (GDH) gene,
ACCESSION  U31177
VERSION     U31177.1 GI:945092
KEYWORDS   .
SOURCE      Leishmania tarentolae.
ORGANISM    Leishmania tarentolae.
            Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae;
            Leishmania; Lizard Leishmania.
REFERENCE   1 (bases 1 to 3274)
AUTHORS    Brineaud,F., Striebeck,R., Frech,G.C., Freedland,S., Turk,C.,
            Byrne,E.M. and Simpson,L.
TITLE      Mitochondrial glutamate dehydrogenase from Leishmania tarentolae is
            a guide RNA-binding protein
JOURNAL     Mol. Cell. Biol. 17 (7), 3915-3923 (1997)
MEDLINE     97342629
REFERENCE   2 (bases 1 to 3274)
AUTHORS    Simpson,L.
TITLE      Direct Submission

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LPELSYPNGVGVAALTLRAIHKLPIKARITFREGE"  
5308..5535  
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5308..5535  
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/transl_table=11  
/protein_id="CA73680.1"  
/db_xref="GI:2113874"  
/db_xref="SWISS-PROT:O06050"  
/translation="MAVGVSPGELRELITDEELAEURLRESKEELFNLRFQMATGOLNNN  
RLRLTVROELIARIYTVSARTPTGSGGDMARW"  
5545..5955  
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5545..5955  
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/transl_table=11  
/protein_id="CA73681.1"  
/db_xref="GI:2113875"  
/db_xref="SWISS-PROT:O06051"  
/translation="MAEAKTGAKAAPRVAKAARPAKKAAPDAEIGAANAAVYKGP  
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SVAGIDRVSLSMETRPLSATKRRRLVEILEKAKP"  
5955..6400  
BASE COUNT 1245 a 1860 c 1996 g 861 t  
ORIGIN  
Query Match 69.7%; Score 20.2; DB 2; Length 5962;  
Best Local Similarity 88.0%; Pred. No. 1.2e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 CGCGTCCGCGTCTTGCTGGCGGCG 28  
|||||  
Db 983 CGCGTCCGCGTTCATGCGTCCGCG 959  
|||||
```

RESULT 12
MSG42 36526 bp DNA BCT 03-DEC-1996
LOCUS Mycobacterium tuberculosis sequence from clone y42.
DEFINITION AD000005
ACCESSION AD000005.1 GI:1702973
VERSION
KEYWORDS
SOURCE Mycobacterium tuberculosis (clone: y42) ds-DNA.
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 36526)
Du L.
REFERENCE Direct Submission
AUTHORS Submitted (11-OCT-1996) L.Du, Genome Therapeutics Corporation, 100
JOURNAL Beaver Street, Maltham, MA, USA, 02154 du@crlc.com
COMMENT GSDB:S:1004721
FEATURES
source 1..36526
/organism="Mycobacterium tuberculosis"
/db_xref="taxon:1773"
/clone="y42"
BASE COUNT 6241 a 12283 c 11284 g 6718 t
ORIGIN
Query Match 69.7%; Score 20.2; DB 2; Length 36526;
Best Local Similarity 88.0%; Pred. No. 5.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 GCGTGGCCGCTTGTGGCGCGC 28
|||||
Db 19001 GCGTGGCCGCTTGTGGCGCGC 19025
RESULT 13
MTCY210 36804 bp DNA BCT 17-JUN-1998
LOCUS Mycobacterium tuberculosis H37Rv complete genome; segment 34/162.
DEFINITION 284395 AL123456
ACCESSION 284395.1 GI:3261698
VERSION
KEYWORDS
SOURCE Mycobacterium tuberculosis.
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium.
1 (bases 1 to 36804)
REFERENCE Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
AUTHORS Harris D., Gordon S.V., Eigmeier K., Gas S., Barry III C.E.,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R., Devlin K., Fellwell T., Gentles S.,
Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J.,
Moule S., Murphy L., Oliver S., Osborne J., Quail M.A.,
Ratandream M.A., Rogers J., Rutter S., Seeger K., Skelton S.,
Squares S., Squires R., Sultson J.E., Taylor K., Whitehead S. and
Barrell B.G.
TITLE Deciphering the biology of Mycobacterium tuberculosis from the
JOURNAL complete genome sequence
MEDLINE Nature 393 (6685), 537-544 (1998)
REMARK 98295987
Erratum: [[published erratum appears in Nature 1998 Nov
12;396(6707):1901]]
2 (bases 1 to 36804)
REFERENCE Direct Submission
AUTHORS Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
JOURNAL tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk

COMMENT
On Jun 27, 1998 this sequence version replaced gi:1806149.
Notes:
Details of M. tuberculosis sequencing at the Sanger Centre are
available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have
been renumbered from the original cosmid submissions but the old
gene designations are in brackets after the new gene numbers.
Gene prediction was based on a Hidden Markov Model of TB genes
implemented in TBParse (Krogh) supplemented with visual inspection
of positional base preference in codons, especially where there is
an increase in the observed/expected third position G + C.
CAUTION: In some cases we may not have predicted the correct
initiation codon. Where possible we choose an initiation codon
(atg, gtg, or ttg) which is preceded by an upstream ribosome
binding site sequence (optimally 5-13bp before the initiation
codon). If this cannot be identified we choose the most upstream
initiation codon.
FEATURES
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/strain="H37Rv"
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<1..35513
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/strain="H37Rv"
/db_xref="taxon:1773"
/clone="y210"
119..1309
/gene="tuf"
119..1309
/gene="tuf"
/note="RV0685, (MTCY210.02), len: 396, tuf, identical to
EFYU_MycTU_P31501 elongation factor tu (ef-tu) (396 aa),
score is 0.854; contains PS00017 ATP/GTP-binding site
motif A, PS00301 GTP-binding elongation factors signature"
/codon_start=1
/transl_table=11
/product="tuf"
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/db_xref="GI:1806151"
/db_xref="SWISS-PROT:P31501"
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GAILVVAATDGPMPQTRHVLARQVGYPIYLALNKADAVDEELILVEVEVEL
AAQERDDAPVYRVSALKALRGDAKVASVEELMAVDSEIPDPVRETRKPLMPVED
VFTTGRGTVTGVRERYINNEVEYVIGRPSRTTKTVYGVEMFRKLDDQAGDN
VGLLRGVKREDVERGVVTRPGTTPTPTEGGVYILSKDEGGRHTEFNNYRQFY
FRTPDVTGVVTLPEGTENVMPDNTNISVKLIQPVAMDEGLRFAIRREGGRVGAQRT
KIK"
173..196
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/note="PS00017 ATP/GTP-binding site motif A"
275..322
/gene="tuf"
/note="PS00301 GTP-binding elongation factors signature"
1447..2244
/gene="RV0686"
1447..2244
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/gene="RV0686"
/note="RV0686, (MTCY210.03), len: 265 aa, unknown,
hydrophobic N-terminus, TBPase score is 0.908"
/codon_start=1
/transl_table=11
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/protein_id="CA06472.1"
/db_xref="GI:1806152"
/db_xref="SPTREMBL:P95032"
/translation="MLARYIKQLVLGCGGVIFLVYVETFLGSLMSMFYVGL
ITTVADIVVALATVYGAKTAAKTAALRSCVLAATGTGSEGTRTINDPLVYVH
HISGVTIPFTEEDRVIVSVRLGULTRKLVLYLVNPTQOYLIDMESALVNGVLA
QFTVAEDKTYDLSGQTPLEIIQILKANNPPLNRWDINSNPLRQOVAAVVRRAA
ERQAPAAVPSAGSIAERLAELESIRASGAVNAEYESKRAQIIISEI"
2397..3224
gene

gene
 CDS
 complement(6368 . 6964)
 /gene="Rv0691c"
 /note="Rv0691c"
 /gene="Rv0691c" (MTCY210.08c), len: 198 aa, probable transcriptional regulator similar to eg STMCRP.1 Streptomyces glaucescens TCMR_STRA P39885 tetracenomycin c transcriptional repressor (226 aa), fasta score, opt: 178. E(): 8.5e-06, (27.9% identity in 201 aa overlap), score is 0.934; contains P500017 ATP/GTP-binding site motif A (P-loop) and probable helix-turn helix motif from aa 35-56"
 /codon_start=1

Query Match 69.7%; Score 20.2; DB 3; Length 36804;
 Best Local Similarity 88.0%; Pred. No. 5.5e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 16499 GCCGTGCCGCTCTTGGTGGCGGC 28
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 MTCY369/c 36850 bp DNA BCT 17-JUN-1998
 LOCUS MTCY369 36850 bp DNA BCT 17-JUN-1998
 DEFINITION Mycobacterium tuberculosis H37Rv complete genome; segment 36/162.
 ACCESSION Z80226 AL123456
 VERSION Z80226.1 GI:3261638
 KEYWORDS
 SOURCE
 ORGANISM Mycobacterium tuberculosis.
 Mycobacterium tuberculosis
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
 Mycobacterium.
 1 (bases 1 to 36850)
 Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C., Harris,D., Gordon,S.V., Eigleier,K., Gas,S., Barry III,C.E., Tekala,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T., Connor,R., Davies,R., Devlin,K., Fellwell,T., Gentles,S., Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J., Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A., Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S., Squares,S., Squires,R., Sulston,J.E., Taylor,K., Whitehead,S. and Barrell,B.G.
 Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
 Nature 393 (6685), 537-544 (1998)
 96295987
 Erratum: [[published erratum appears in Nature 1998 Nov 12;396(6707):190]]
 2 (bases 1 to 36850)
 Parkhill,J.
 Direct Submission
 Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
 On Jun 27, 1998 this sequence version replaced gi:2078438.

Notes:
 Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.
 (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers.

Gene prediction was based on a Hidden Markov Model of TB genes implemented in TParse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (aug, gty, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

FEATURES

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/strain="H37Rv"
/db_xref="taxon:1773"
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/db_xref="taxon:1773"
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/codon_start=1
/transl_table=11
/product="hypothetical protein Rv0756c"
/protein_id="CAB02399.1"
/db_xref="GI:1550634"
/db_xref="SPTREMBL:P71813"
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OGGILDLRTAEGMGAMORALPGCLADOLLAEDGLRIVLSDDGLADRLRGGVLLT
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PGRPARSSRSRSVRVDSE"
1356..2099
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1356..2099
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/note="rv0757, (MTCY369.02), len: 247, phop-like, similar to PHOP_BACSU P13792 alkaline phosphatase synthesis transcription regulatory protein (240 aa), fasta scores, opt: 594, E(): 2.3e-33, (41.0% identity in 234 aa overlap), also similar to MTCY31.31c (45.4% identity in 229 aa overlap), MTCY1062_16, MTU88959_1 Mycobacterium tuberculosis response regulator (257 aa, 46.7% identity in 225 aa overlap) etc."
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/protein_id="CAB02400.1"
/db_xref="GI:1550635"
/db_xref="SPTREMBL:P71814"
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SLQDIAGLTGGDDYVTRKPSLEEVARLVILRRAGKNGKPNRVLTPADILDE
ETHYWKAGORVSLSPREFTLRVFNAGVLSKPKILDIHWMRDPCGDVAVESYV
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2144..3601
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2144..3601
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gene
Mycobacterium tuberculosis sensor (509 aa), MTCY1062_17, etc."
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/db_xref="SPTREMBL:P71815"
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QVIGSALVAVPGVAGYAVVRSRLPLAEFQTAAGIDRDRVPMHPTREYGLR
SLANGSLAIOORAVASAESSEKARDESDNRROPITPASHELRTPLTIGFAFLR
OGAARDVGMILSRISSEASRMGLVDLILLARLDARHPELCRYDILALASDAHDA
RAMDPKRITLTLEVDGPGCTPRYLGDSESLRQVLRNLVANAIOHPESADYVAVNCTEG
DDALILEVADGFGMSQEDALRFERFTRADSRASGCTGLGISVLSLVANAGGAV
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/note="rv0759c, (MTCY369.04c), len: 110, some similarity to IPK1_BOVIN P16436 protein kinase c inhibitor 1 (Pkt-1) (125 aa), fasta scores, opt: 195, E(): 5.2e-08, (33.3% identity in 111 aa overlap); highly similar to YHRF_MYCLE P49774hypothetical 17.0 kd protein hlt-like (155 aa), fasta scores, opt: 766, E(): 0, (78.7% identity in 150 aa overlap); similar to hlt-like proteins, also similar to MTCY50.20, (32.2% identity in 118 aa overlap)"
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/transl_table=11
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/db_xref="SPTREMBL:P71816"
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RAALAOLA"
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/gene="rv0760c"
/complement(4015..4434)
/gene="rv0760c"
/note="rv0760c, (MTCY369.05), len: 139, unknown, some similarity to Rv2042c (265 aa), fasta scores, opt: 150 z-score:188.7 E(): 4.1e-05, 28.7% identity in 136 aa overlap"
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/product="hypothetical protein Rv0760c"
/protein_id="CAB02403.1"
/db_xref="GI:1550638"
/db_xref="SPTREMBL:P71817"
/transl_table="MTQTYQSPALIASQSSMRQVQAHDRBGMALMADVVIEDPIK
SVTNPDGSGIKGEAVGAFPDTHIANRLTYVCEETPFSSSPDEIAHILVLSPEPDG
FTSEVGRVFTYRVNKGALITNMKGWINDMMTMFGNOE"
/complement(4447..5574)
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/gene="adhB"
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/codon_start=1
/transl_table=11
/product="adhB"
/protein_id="CAB02404.1"
/db_xref="GI:1550639"
/db_xref="SPTREMBL:P71818"
/transl_table="MKTGALIMEPNQWSVEEIEIGDRPRDEKIQMEAGMGRSDH
HLVTDIDMAGFPVYLGHEGAGIYVEVGVDDFAPGCHVVLALFPGCGKPCQCOAG
RNLCIDLAGGLAGESVTGDSPRIARQGNVYPMTLTGTFSPYMWVHRSSVYKIDPSVP
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Job time: 9410 sec

misc_feature

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 /gene="adhB"

gene

/note="ps00059 zinc-containing alcohol dehydrogenases
 signature"
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 /gene="Rv0762c"

CDS

complement(5673..6218)
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/note="Rv0762c, (MTCY369.07c), len: 181; unknown, weak

Query Match

69.7%; Score 20.2; DB 3; Length 36850;

Best Local Similarity 88.0%; Pred. No. 5.5e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGCCGTGCGCGCTGTGTGGCGGC 27
 ||||| ||||| ||||| ||||| ||

Db 28617 CGCCGCGCGCGCTGTGTGGCGGC 28593

RESULT 15

AP003007/c

AP003007 348411 bp DNA

BCT 03-FEB-2001

LOCUS

Mesorhizobium loti DNA, complete genome, section 14/21, complete

DEFINITION

sequence.

ACCESSION

AP003007 BA000012

VERSION

AP003007.1 GI:11994982

KEYWORDS

HTG.

SOURCE

Mesorhizobium loti (strain:MAFF303099) DNA.

ORGANISM

Mesorhizobium loti

REFERENCE

Bacteria: Proteobacteria; alpha subdivision; Rhizobiaceae group;
 Phyllobacteriaceae; Mesorhizobium.

AUTHORS

1 (sites)
 Kaneko, T., Nakamura, Y., Sato, S., Asamizu, E., Kato, T., Sasamoto, S.,
 Watanabe, A., Idesawa, K., Ishikawa, A., Kawashima, K., Kimura, T.,
 Kishida, Y., Kiyokawa, C., Kohara, M., Matsumoto, M., Matsuno, A.,
 Mochizuki, Y., Nakayama, S., Nakazaki, N., Shimpō, S., Sugimoto, M.,
 Takeuchi, C., Yamada, M. and Tabata, S.

TITLE

Complete genome structure of the nitrogen-fixing symbiotic
 bacterium Mesorhizobium loti

JOURNAL

DNA Res. 7, 331-338 (2000)

REFERENCE

2 (bases 1 to 348411)

AUTHORS

Kaneko, T.

TITLE

Direct Submission

JOURNAL

Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research
 Institute, The First Laboratory for Plant Gene Research; Yana
 1532-3, Kisarazu, Chiba 292-0812, Japan
 (E-mail: kaneko@kazusa.or.jp)
 URL: http://www.kazusa.or.jp/rhizobase/, Tel: 81-438-52-3935,
 Fax: 81-438-52-3934

FEATURES

Location/Qualifiers

source

1.348411

BASE COUNT

67860 a 105626 c 106678 g 68247 t

ORIGIN

1.348411
 /organism="Mesorhizobium loti"
 /strain="MAFF303099"
 /db_xref="taxon:381"

Query Match

69.7%; Score 20.2; DB 2; Length 348411;

Best Local Similarity

88.0%; Pred. No. 2.2e+02;

Matches

22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

1 GGGCGCGTGGCGCGCTGTGTGGCG 25
 || ||||| ||||| ||||| ||||| ||

Db

263289 GGAGCGAGCGACGCTGTGTGGCG 263265

Search completed:

April 19, 2001, 23:58:53

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 21:25:58 ; Search time 547.68 Secqyds
(without alignments)
30.912 Million cell updates/sec

Title: US-09-016-464-8

Perfect score: 29
Sequence: 1 GGCGCGTGGCGCGCTTGTGTGGCGCGCG 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
N.Geneseq_0401: *
1: /SID52/gcgdata/geneseq/geneseq/NA1980.DAT: *
2: /SID52/gcgdata/geneseq/geneseq/NA1981.DAT: *
3: /SID52/gcgdata/geneseq/geneseq/NA1982.DAT: *
4: /SID52/gcgdata/geneseq/geneseq/NA1983.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	29	18 T76057	Human A2b adenosin
2	29	100.0	29	20 X53850	Human adenosine A2
3	29	100.0	29	21 F19415	Human adenosine A2
4	29	100.0	29	21 A33293	Low adenosine anti
5	29	100.0	29	21 A03695	Human adenosine A1
6	29	100.0	304	20 X54549	Human adenosine A2
7	29	100.0	304	21 F20118	Human low adenosin
8	29	100.0	304	21 A33996	Human adenosine re
9	29	100.0	1733	21 F20858	Human adenosine A2
10	29	100.0	1733	21 F20858	Human adenosine A2
11	29	100.0	1733	21 A34736	Human adenosine re

C	12	29	100.0	1733	21 A34747
C	13	29	100.0	7144	21 F21439
C	14	29	100.0	7144	21 F21439
C	15	29	100.0	7800	21 F20842
C	16	29	100.0	7800	21 A34720
C	17	29	100.0	7803	20 X55272
C	18	29	100.0	114955	20 X53491
C	19	29	100.0	117609	21 F21435
C	20	29	100.0	117609	21 F21435
C	21	22	76.6	610	21 F08099
C	22	19.4	66.9	1053	21 Z54533
C	23	19.4	66.9	1314	21 Z54534
C	24	19.4	66.9	10763	19 V39837
C	25	19.4	66.9	10763	20 X93688
C	26	19.4	66.9	14926	19 V62156
C	27	19.4	66.9	56609	21 A81459
C	28	19.4	66.9	117213	19 V62176
C	29	19.4	66.9	349980	21 F21609
C	30	18.6	63.4	711	20 Q98750
C	31	18.4	63.4	1087	19 V42701
C	32	18.4	63.4	1155	20 Z09784
C	33	18.4	63.4	1155	22 A39433
C	34	18.4	63.4	1155	22 A39433
C	35	18.4	63.4	1235	19 V38659
C	36	18.4	63.4	1611	19 V21655
C	37	18.4	63.4	1641	21 D00774
C	38	18.4	63.4	1872	19 V21649
C	39	18.4	63.4	1872	19 V21656
C	40	18.4	63.4	1872	21 D00773
C	41	18.4	63.4	3519	16 Q94352
C	42	18.4	63.4	3720	20 Z09790
C	43	18.4	63.4	4683	22 F23749
C	44	18.4	63.4	4718	21 D00772
C	45	18.4	63.4	4767	19 V21648

ALIGNMENTS

RESULT	1
ID	T76057 standard; DNA: 29 BP.
AC	T76057;
DF	11-SEP-1997 (first entry)
DE	Human A2b adenosine receptor antisense oligonucleotide HSA2BRECA51.
KM	Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW	chronic obstructive pulmonary disease; bronchitis; ss.
OS	Synthetic.
PN	WO9640162-A1.
PD	19-DEC-1996.
PF	06-JUN-1996; 96WO-US09306.
PR	07-JUN-1995; 95US-0474497.
PA	(UYEC-) UNIV EAST CAROLINA.
PI	Metzger WJ, Nyce JW;
DR	WPI: 1997-051871/05.
PT	Treatment of airway diseases such as asthma - by topically applying
PS	adenosine-free antisense oligo:nucleotide to airway epithelium of
PS	subject
PS	Claim 5; Page 24; 71pp; English.

CC The specification describes antisense oligonucleotides (X522865-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions

KW low adenosine aminase oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; ROS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

PT trigger adenosine receptors during metabolism, useful e.g. for treating

PS Claim 14; Page 124; 1592pp; English

CC The present invention describes low adenosine (A) content antisense

oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine, and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoreactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. F18434 to F21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 29 BP: 0 A; 9 C; 15 G; 5 T; 0 other;

Query Match 100.0%; Score 29; DB 21; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCGTGGCGTGTGGTGGCGCG 29
|||||
Db 1 ggcgcgctgcgcgctctgtggtgcgcg 29

RESULT 4
A33293
ID A33293 standard; DNA: 29 BP.
AC A33293;
XX

28-JUL-2000 (first entry)

Low adenosine antisense oligonucleotide SEQ ID NO:982.

Human: adenosine receptor; low adenosine antisense oligonucleotide;
phosphorothioate; impaired respiration; inflammation; allergy;
allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;
lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
respiratory distress syndrome; pain; cystic fibrosis; emphysema;
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

MO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99WO-US171712.

03-AUG-1998; 98US-0095212.

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WP1: 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.

Claim 18; Page 388; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytosstatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. A33313 to A35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 1815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323 to A33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

Sequence 29 BP: 0 A; 9 C; 15 G; 5 T; 0 other;

Query Match 100.0%; Score 29; DB 21; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCGTGGCGGCTGTGGTGGCGCG 29
|||||
Db 1 ggcgcgctgcgcgctctgtggtgcgcg 29

RESULT 5
A03695
ID A03695 standard; DNA: 29 BP.
AC A03695;
XX

19-MAY-2000 (first entry)

Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:979.

Human: adenosine A1 receptor; antisense oligonucleotide; hypoxia;
adenosine A2a receptor; adenosine Ab receptor; adenosine A3 receptor;
phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;
endotoxin release; ARDS; acute respiratory distress syndrome;
cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;
supraventricular tachycardia; allergic rhinitis; acute inflammation;
chronic obstructive pulmonary disease; ss.

Homo sapiens.

Synthetic.

WO9963938-A2.

16-DEC-1999.

PF 08-JUN-1999; 99WO-US12775.
 XX 08-JUN-1998; 98US-0088501.
 PR 09-JUN-1998; 98US-0088657.
 PR 09-JUN-1998; 98US-0093972.
 XX (EPIC-) EPIGENESIS PHARM INC.
 PA
 XX
 PI Nyce JW, Hill JL.
 DR WPI: 2000-116433/10.
 XX
 PT Novel composition for treating or preventing e.g. cardiopulmonary and
 PT renal injury -
 XX
 PS Claim 17; Page 39; 252pp; English.
 XX
 CC The present invention describes a pharmaceutical composition, comprising
 CC at least one agent (I) that prevents, alleviates and/or inhibits
 CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.
 CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide
 CC (Ib), containing less than 15% adenosine (A), that is antisense to
 CC target genes or corresponding RNA, to genomic flanking regions (i.e. 5'
 CC or 3' ends or segments between coding and non-coding sequences), or to
 CC all segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors,
 CC and has A1, A2b or A3 agonist activity or A2a antagonist activity (or at
 CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)
 CC and (Ib), and optionally also contains one or more surfactants. The
 CC compositions are used to prevent, alleviate and/or treat adenosine
 CC receptor-mediated cardiac, lung and/or renal damage or failure
 CC (particularly where associated with ischaemia, toxin release and/or
 CC administration of drugs or imaging agents, e.g. adenosine for treating
 CC supraventricular tachycardia); (adult) respiratory distress syndrome
 CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive
 CC pulmonary disease; cardiopulmonary hypoxia associated with administration
 CC of stress-test agents, particularly where such conditions are associated
 CC with acute inflammation. A02717, A02719, A02721 and A02723 to A03715
 CC represent specifically claimed phosphorothioate antisense
 CC oligonucleotides for use in the composition of the present invention.
 CC A02718, A02720, A02722 and A03716 to A03720 represent other
 CC phosphorothioate oligonucleotides used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 29 BP; 0 A; 9 C; 15 G; 5 T; 0 other;

Query Match 100.0%; Score 29; DB 21; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCGTGGCGGCTTGTGTGGCGCGG 29
 ||||||||||||||||||||||||||||
 DB 1 ggcgcgcgtgcgcgtctctgtg9gcg9cg 29

RESULT 6
 X54549
 ID X54549 standard; DNA: 304 BP.
 AC X54549;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human adenosine A2b receptor antisense oligonucleotide fragment.
 XX
 KW Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;

KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9913886-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19419.
 XX
 PR 09-JUN-1998; 98US-0093972.
 PR 17-SEP-1997; 97US-0059160.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 DR WPI: 1999-229400/19.
 XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 XX
 PS Disclosure; Page 43; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (X52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have
 CC metastasized to the lungs, including breast and prostate cancer.
 CC
 XX
 SQ Sequence 304 BP; 6 A; 131 C; 116 G; 45 T; 6 other;

Query Match 100.0%; Score 29; DB 20; Length 304;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCGTGGCGGCTTGTGTGGCGCGG 29
 ||||||||||||||||||||||||||||
 DB 1 ggcgcgcgtgcgcgtctctgtg9gcg9cg 29

RESULT 7
 F20118
 ID F20118 standard; DNA: 304 BP.
 AC F20118;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human low adenosine antisense oligonucleotide #1685.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; anti-inflammatory;
 KW immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;

XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
RW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
cancer; ss.
XX
OS Homo sapiens.
XX
PM WO20062736-A2.
PD
PN 26-OCT-2000.
PP
PR 24-MAR-2000; 2000WO-US08020.
PS 06-APR-1999; 99US-0127958.
PT (UYEC-) UNIV EAST CAROLINA.
PX (NYCE/) NYCE J W.
PY
PL Nycce JW;
DR WPJ; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX
XX Claim 14; Page 539-540; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antisthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and CC receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory stress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. F18454 to F21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 304 BP; 6 A; 131 C; 116 G; 45 T; 6 other:

Query Match 100.0%; Score 29; DB 21; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 GGCGCCGTCGCCGCCTTGGTGCGACGCG 29
|||||
DB 1 ggcgcctgcccgcgtcttggtgcgagcg 29

RESULT 8
A33996

ID	A33996	standard; DNA: 304 BP.
XX		
AC	A33996;	
XX		
DT	28-JUL-2000	(first entry)
XX		
DE	Human adenosine receptor related polynucleotide SEQ ID NO:1685.	
XX		
KW	Human; adenosine receptor; low adenosine antisense oligonucleotide;	
KW	phosphorocholate; impaired respiration; inflammation; allergy;	
KW	allergic disease; bronchoconstriction; inhibitor; antiinflammatory;	
KW	antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;	
KW	lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;	
KW	respiratory distress syndrome; pain; cystic fibrosis; emphysema;	
KW	pulmonary hypertension; chronic obstructive pulmonary disease; COPD;	
KW	cancer; leukemia; lymphoma; carcinoma; metastasis; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200009525-A2.	
XX		
PD	24-FEB-2000.	
XX		
PF	03-AUG-1999; 99WO-US17712.	
XX		
PR	03-AUG-1998; 98US-0095212.	
XX		
PA	(UYEC-) UNIV EAST CAROLINA.	
XX		
PI	Nyce JW;	
XX		
DR	WPI; 2000-205971/18.	
XX		
PT	New antisense oligonucleotides useful for treating e.g. pulmonary	
PT	vasoconstriction, inflammation, allergies, asthma, hypercemia, or	
PT	bronchitis, emphysema, respiratory distress syndrome, ischemia or	
PT	cancers -	
XX		
PS	Disclosure; Page 474; 1343pp; English.	
XX		
CC	The present invention describes a new composition comprising an antisense	
CC	oligonucleotide (ON) with low adenosine (up to 15%), which targets	
CC	nucleic acids involved in bronchoconstriction, allergies, and/or	
CC	inflammation. The ON can have antiinflammatory, antiallergic,	
CC	antiasthmatic, cytostatic and analgesic activities. The compositions are	
CC	useful for the treatment of diseases associated with inflammation,	
CC	impaired airways, including lung disease and diseases whose secondary	
CC	effects afflict the lungs of a subject. They can be used for treating	
CC	e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,	
CC	impaired respiration, respiratory distress syndrome, pain, cystic	
CC	fibrosis, pulmonary hypertension, emphysema, chronic obstructive	
CC	pulmonary disease (COPD), and cancers such as leukemias, lymphomas,	
CC	carcinomas, and cancers which may metastasize to the lungs, including	
CC	breast and prostate cancer. The reduction of the adenosine content of the	
CC	ONS reduces side effects. The A-containing ONS break down with the	
CC	release of deoxyadenosine which activates adenosine receptors causing	
CC	bronchoconstriction and inflammation. A32313 to A35312 represent the	
CC	nucleotide sequences given in the sequence listing from the present	
CC	invention, which correspond to SEQ ID NO:1 to 2815, and then the last	
CC	185 sequences are also called SEQ ID NO:1 to 185, but the sequences	
CC	differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323	
CC	to A33992) are specifically claimed ONS from the present invention.	
CC	N.B. Sequences given in the disclosure of the present invention do not	
CC	match up with their corresponding SEQ ID NO: sequences given in the	
CC	sequence listing.	
XX		
XX	Sequence 304 BP; 6 A; 131 C; 116 G; 45 T; 6 other;	
XX		
Query Match	100.0%; Score 29; DB 21; Length 304;	
Best Local Similarity	100.0%; Pred. No. 0.019;	
Matches 29; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	

OY 1 GGGCGCGCGCGCTGTGTCGGCGG 29
 ||||||||||||||||||||||||||||
 Db 1 ggcgcgcgcgcgcgtcttcgtgcgcg 29

RESULT 9

F20858/c
 ID F20858 standard; DNA: 1733 BP.

XX F20858;

XX 14-MAR-2001 (first entry)

XX Human adenosine A2b receptor polynucleotide fragment #2425.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 XX human; airway disorder; bronchoconstriction; lung inflammation;
 XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 XX immunosuppressive; antisthmatic; analgesic; hypotensive; cycostatic;
 XX respiratory obstruction; pulmonary obstruction; impeded respiration;
 XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 XX cancer; ss.

XX Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

XX 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX Nyce JW;

XX WPI: 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not
 XX trigger adenosine receptors during metabolism, useful e.g. for treating
 XX cancers and respiratory obstructions -

XX Disclosure; Page 123-124; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antisthmatic, hypotensive and cycostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary

CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.

XX Sequence 1733 BP; 352 A; 479 C; 485 G; 417 T; 0 other;

XX Query Match 100.0%; Score 29; DB 21; Length 1733;

XX Best Local Similarity 100.0%; Pred. No. 0.018;

XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCGCGCGCTGTGTCGGCGG 29
 Db 47 ggcgcgcgcgcgcgtcttcgtgcgcg 19

RESULT 10

F20869/c
 ID F20869 standard; DNA: 1733 BP.

XX F20869;

XX 14-MAR-2001 (first entry)

XX Human adenosine A2b receptor polynucleotide fragment #2436.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 XX human; airway disorder; bronchoconstriction; lung inflammation;
 XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 XX immunosuppressive; antisthmatic; analgesic; hypotensive; cycostatic;
 XX respiratory obstruction; pulmonary obstruction; impeded respiration;
 XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 XX cancer; ss.

XX Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

XX 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX Nyce JW;

XX WPI: 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not
 XX trigger adenosine receptors during metabolism, useful e.g. for treating
 XX cancers and respiratory obstructions -

XX Disclosure; Page 123; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antisthmatic, hypotensive and cycostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,

CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasodilative peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. Fl8434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.

CC Sequence 1733 BP; 352 A; 479 C; 485 G; 417 T; 0 other;

Query Match 100.0%; Score 29; DB 21; Length 1733;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCGTGGCGGCTGTGGTGGCGGCGG 29
Db 47 GGGCGCGTGGCGGCTGTGGTGGCGGCGG 19

RESULT 11

A34736/c
ID A34736 standard; DNA; 1733 BP.

AC A34736;

DT 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:2425.

Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inhibitor; antiinflammatory;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiasthmatic; antiallergic; cytosstatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

PN WO200009525-A2.

PD 24-FEB-2000.

PF 03-AUG-1999; 99WO-US17712.

PR 03-AUG-1998; 98US-0095212.

PA (UYEC-) UNIV EAST CAROLINA.

PI Nyce JW;

DR WPI; 2000-205971/18.

PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -

PS Disclosure; Page 575-576; 1343pp; English.

XX

CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiasthmatic,
CC antiasthmatic, cytosstatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A3213 to A3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.

CC Sequence 1733 BP; 352 A; 479 C; 485 G; 417 T; 0 other;

Query Match 100.0%; Score 29; DB 21; Length 1733;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCGCGTGGCGGCTGTGGTGGCGGCGG 29
Db 47 GGGCGCGTGGCGGCTGTGGTGGCGGCGG 19

RESULT 12

A34747/c
ID A34747 standard; DNA; 1733 BP.

AC A34747;

DT 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:2436.

Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inhibitor; antiinflammatory;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiasthmatic; antiallergic; cytosstatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

PN WO200009525-A2.

PD 24-FEB-2000.

PF 03-AUG-1999; 99WO-US17712.

PR 03-AUG-1998; 98US-0095212.

PA (UYEC-) UNIV EAST CAROLINA.

PI Nyce JW;

DR WPI; 2000-205971/18.

XX

XX 24-MAR-2000; 2000WO-US08020
PF

KM immunosuppressive; antihistaminic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM

KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 XX
 XX Homo sapiens.
 OS
 PN WO200062736-A2.
 XX
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIT EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 PI
 DR WPI; 2000-679539/66.
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 XX Disclosure; Page 121-123; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antispasmodic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating with
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 CC
 XX
 XX Sequence 7144 BP; 1460 A; 1973 C; 1972 G; 1733 T; 6 other;
 SQ
 Query Match 100.0%; Score 29; DB 21; Length 7144;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCGCGCGTGGCGTCTGTGGCGGCG 29
 ||||||||||||||||||||||||||||
 DB 5458 GCGCGCGTGGCGTCTGTGGCGGCG 5430
 RESULT 15
 F20842

ID F20842 standard; DNA; 7800 BP.
 XX
 AC F20842;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 XX Human multiple target antisense (MTA) oligonucleotide #2409.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antispasmodic; analgesic; hypotensive; cytostatic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 XX
 XX Homo sapiens.
 OS
 PN WO200062736-A2.
 XX
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIT EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 PI
 DR WPI; 2000-679539/66.
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 XX Claim 14; Page 634-636; 1592pp; English.
 PS
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antispasmodic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating with
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 CC
 XX
 XX Sequence 7800 BP; 403 A; 2525 C; 2530 G; 1986 T; 356 other;
 SQ

Query Match 100.0%; Score 29; DB 21; Length 780;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCCGCGTGGCGCTTGTGGCGCGG 29
 |||||
 Db 381 ggccgctgcccgtcttgggtggcgcg 409

Search completed: April 20, 2001, 00:12:45
 Job time: 10007 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 21:08:43 ; Search time 7150.85 Seconds
(without alignments)
0.593 Million cell updates/sec

Title: US-09-016-464-8

Perfect score: 29

Sequence: 1 GCGCGCGTGGCGCTTGTGTGGCGCGCGG 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	21.6	74.5	1032	171	BF979636 602287931
2	21	72.4	433	118	AM676731 DGL13.G0
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4	21	72.4	670	170	BF867753 963093605
5	21	72.4	749	212	AQ869084 nbe0033L
6	21	72.4	758	115	AW448097 BRY1648
7	21	72.4	869	212	AQ861446 nbe0016L
8	21	72.4	914	147	BF347938 602022831
9	21	72.4	946	169	BF795776 602260392
10	21	72.4	1105	146	BF338971 602036044
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15	20	69.0	452	149	BF483453 WHE2334.B
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22      20      69.0      1093      232      CNS05K00      AL341817      Tetradon
23      20      69.0      1120      231      CNS03SX0      AL259127      Tetradon
24      19.8      68.3      490      140      BE834560      BE834560      MR3-FN000
25      19.6      67.6      791      231      CNS03XFX      AL264967      Tetradon
26      19.6      67.6      876      151      BF695805      BF695805      601852352
27      19.6      67.6      1202      78      BE317249      BE317249      NF056D12L
28      19.4      66.9      223      148      BF430893      BF430893      OG05G0773
29      19.4      66.9      269      11      AA757376      AA757376      ah98b07.s
30      19.4      66.9      322      140      BE857081      BE857081      7923f10.x
31      19.4      66.9      335      29      AV389538      AV389538      AV389538
32      19.4      66.9      338      31      AV628672      AV628672      AV628672
33      19.4      66.9      365      118      AM676105      AM676105      832004B09
34      19.4      66.9      366      119      AM758035      AM758035      874005D04
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36      19.4      66.9      378      216      A2135188      A2135188      OSJNB011
37      19.4      66.9      402      137      BE599921      BE599921      P11_77_A1
38      19.4      66.9      405      31      AV637147      AV637147      AV637147
39      19.4      66.9      417      118      AM676084      AM676084      832003E06
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44      19.4      66.9      426      167      BE441969      BE441969      925009H04
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ALIGNMENTS

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RESULT 1
LOCUS   BF979636/c      1032 bp      mRNA      EST      23-JAN-2001
DEFINITION 602287931F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4373934 5',
            mRNA sequence.
ACCESSION BF979636
VERSION   BF979636.2
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
            1 (bases 1 to 1032)
            NIH-MGC http://mgi.mgi.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            On Jan 17, 2001 this sequence version replaced gi:12346760.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: Miklos Palcovits, M.D., Ph.D.
            CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshitaka and Piero Carninci (RIKEN)
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10036 row: m column: 07
            High quality sequence stop: 630.

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FEATURES

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    ); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',
    size-selected for average insert size 2.2 kb and

```

normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

Query Match 74.5%; Score 21.6; DB 171; Length 1032;
Best local Similarity 85.7%; Pred. No. 1e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

Qy      2      GCGCCGTGCGCGCTTGTGCGCGCG 29
          ||||||| ||| || |||||||||
Db      37      GCGCCGTGCGCGCGCTGAGTGGCGCG 10

```

```

RESULT 2
LOCUS   AM676731      433 bp      mRNA      EST      19-JUL-2000
DEFINITION DGL_13.G08.g1_A002 Dark Grown 1 (DGL) Sorghum bicolor cDNA, mRNA
            sequence.
ACCESSION AM676731
VERSION   AM676731.1
KEYWORDS  EST.
SOURCE    sorghum.
ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
            ; Andropogoneae; Sorghum.
            1 (bases 1 to 433)
            Cordnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudnan,M. and Pratt
            ,L.H.
            An EST database from Sorghum: dark-grown seedlings
            Unpublished (2000)
            Contact: Cordnier-Pratt MM
            Department of Botany
            The University of Georgia
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 542 1805
            Email: mmp@prattuga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: T7
            High quality sequence start: 2
            High quality sequence stop: 422
            POLYA-No.

```

FEATURES

```

source
1..433
    /organism="Sorghum bicolor"
    /db_xref="taxon:4558"
    /clone_lib="Dark Grown 1 (DGL)"
    /note="Organ: 5-day-old dark-grown seedlings; Vector:
    Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
    made from poly-A RNA in the cloning vector lambda Zap II.
    Clones to be sequenced were prepared by mass excision."
BASE COUNT      104 a      97 c      121 g      111 t
ORIGIN

```

Query Match 72.4%; Score 21; DB 118; Length 433;
Best local Similarity 82.8%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

Qy      1      GCGCCGTGCGCGCTTGTGCGCGCG 29
          ||||||| || ||||||| ||||| |||
Db      5      GCGCGGTTCGCGCTGAGTGGTGGCGG 33

```

RESULT 3


```
source      1. .758
/organism="Triticum aestivum"
```

equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three

CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM9501 row: 9 column: 11
 High quality sequence start: 4
 High quality sequence stop: 125.

FEATURES

source

1. 1105

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4184098"

/clone.lib="NCI_CGAP_Brn64"

/tissue.type="glioiblastoma with EGFR amplification"

/lab.host="DH10B (TI phage-resistant)"

/note="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.57 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT

292 a 341 c 224 g 248 t

ORIGIN

Query Match

Best Local Similarity 72.4%; Score 21; DB 146; Length 1105;

Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGCGCGTGGCGCTTGTGGCGGCGG 29

Db 280 GGGCGCGTGGCGCTTGTGGCGGCGG 308

RESULT 11

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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COMMENT

BASE COUNT 211 a 205 c 261 g 225 t
 ORIGIN

Query Match 71.7%; Score 20.8; DB 173; Length 902;
 Best Local Similarity 91.7%; Pred. No. 2.1e+02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGCGCGTGGCGCTTGTGGCGG 24

Db 819 GGGCGCGTGGCGCTTGTGGCGG 842

RESULT 12

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

COMMENT

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COMMENT

BASE COUNT 211 a 205 c 261 g 225 t
 ORIGIN

Query Match 70.3%; Score 20.4; DB 140; Length 212;
 Best Local Similarity 95.5%; Pred. No. 3.6e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCGCGTGGCGCTTGTGGCGG 23

Db 819 GGGCGCGTGGCGCTTGTGGCGG 842

RESULT 12

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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DB 25 GCGCGTGGCGCTTGTGTG 4

RESULT 13

LOCUS U60299 166 bp mRNA EST 22-JUL-1996

DEFINITION OS060299 FDRRC Oryza sativa cDNA clone pFDRRC197, mRNA sequence.

ACCESSION U60299

VERSION U60299.1 GI:1438549

KEYWORDS EST.

SOURCE Oryza sativa.

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 166)

AUTHORS Xiao, C.

TITLE Rice cDNA partial sequence

JOURNAL Unpublished (1995)

COMMENT Contact: Chuan Xiao

Fudan University

Handan Road 220#, Shanghai 200433, People's Republic of China.

FEATURES

source

1. 166

/organism="Oryza sativa"

/strain="Guang-Lu-AI No.4"

/db_xref="taxon:4530"

/clone="pFDRRC197"

/clone_1lb="FDRRC"

/tissue="type="root"

BASE COUNT 29 a 42 c 62 g 33 t

ORIGIN

Query Match 69.0%; Score 20; DB 157; Length 166;

Best Local Similarity 82.1%; Pred. No. 5.2e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GCGCGTGGCGCTTGTGTGCGCG 29

DB 31 GCGCGCGACTGCTTGTGTGCGCGCG 4

RESULT 14

LOCUS BE440240 439 bp mRNA EST 21-NOV-2000

DEFINITION sp3a02.y1 Gm-c1043 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1043-963 5' similar to SW:HMGL_SOYBN P26585 HMGL/2-LIKE PROTEIN ;, mRNA sequence.

ACCESSION BE440240

VERSION BE440240.1 GI:9439725

KEYWORDS soybean.

SOURCE Glycine max

ORGANISM Glycine max

REFERENCE 1 (bases 1 to 439)

AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Pearson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE Public Soybean EST Project

JOURNAL Unpublished (1999)

COMMENT Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com

Insert Length: 933 Std Error: 0.00

High quality sequence stop: 438.

FEATURES

source

1. 439

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1043-963"

/clone_1lb="Gm-c1043"

/tissue="type="Hypocotyl and plumule, germinating seeds"

/lab_host="DH10B"

/note="Vector: pT73Pac (Pharmacia); Site 1: EcoRI; Site 2: NotI; This cDNA library was constructed from mRNA isolated from hypocotyl and plumule tissues of seeds germinated for three days of the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and NotI. The cDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the pT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 150 a 79 c 136 g 73 t 1 others

ORIGIN

Query Match 69.0%; Score 20; DB 167; Length 439;

Best Local Similarity 82.1%; Pred. No. 4.6e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCGCGTGGCGCTTGTGTGCGCG 28

DB 95 GCGCGGCTTCTTGTGTGTGCGCG 68

RESULT 15

LOCUS BF483453 452 bp mRNA EST 06-DEC-2000

DEFINITION WHE2334_B01_C0225 wheat pre-anthesis spike cDNA library Trilicium aestivum cDNA clone WHE2334_B01_C02, mRNA sequence.

ACCESSION BF483453

VERSION BF483453.1 GI:11566754

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM Trilicium aestivum

REFERENCE 1 (bases 1 to 452)

AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.

TITLE The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20

Seq primer: StrataGene SK primer.

Location/Qualifiers

source

```

1. .452
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2334_B01_C02"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give phagemid
phagemids in the T7 close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
```

```

BASE COUNT      59 a      147 c      180 g      66 t
ORIGIN
```

```

Query Match      69.0%; Score 20; DB 149; Length 452;
Best Local Similarity 82.1%; Pred. No. 4.6e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 GCGCCGTGCGCGCTGTGTGTGCGCGCG 29
    ||| ||||| ||| ||||| |||||
Db 9 GCGAGTGTCTGTGTGTGTGCGCGCG 36
```

Search completed: April 19, 2001, 23:24:33
Job time: 8150 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 21:22:23 ; Search time 280.46 Seconds
(without alignments): 18.054 Million cell updates/sec

Title: US-09-016-464-8

Perfect score: 29

Sequence: 1 GGCCTGCGCGCTGTGTGCGCGCGG 29

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/lna/5A.COMB.seq:**

2: /cgn2_6/ptodata/2/lna/5B.COMB.seq:**

3: /cgn2_6/ptodata/2/lna/6A.COMB.seq:**

4: /cgn2_6/ptodata/2/lna/6B.COMB.seq:**

5: /cgn2_6/ptodata/2/lna/PTOS.COMB.seq:**

6: /cgn2_6/ptodata/2/lna/Backfile1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.4	66.9	10763	1 US-08-761-258-1	Sequence 1, Appl
C 2	19.4	66.9	10763	2 US-08-977-306-1	Sequence 1, Appl
C 3	18.6	64.1	12101	1 US-08-106-761-1	Sequence 1, Appl
C 4	18.4	63.4	3519	1 US-08-035-558-1	Sequence 1, Appl
5	18.4	63.4	10095	3 US-08-822-586-45	Sequence 45, Appl
6	17.8	61.4	360	4 US-09-060-756-455	Sequence 455, App
7	17.8	61.4	447	4 US-09-060-756-70	Sequence 70, Appl
8	17.8	61.4	1117	4 US-09-347-819-5	Sequence 50, Appl
9	17.8	61.4	1303	2 US-08-793-410-10	Sequence 10, Appl
C 10	17.8	61.4	1908	2 US-08-265-310-1	Sequence 1, Appl
C 11	17.8	61.4	1908	2 US-08-951-742-1	Sequence 1, Appl
C 12	17.8	61.4	2214	1 US-07-985-458-1	Sequence 1, Appl
C 13	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
14	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
15	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
16	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
17	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
18	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
19	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
20	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
21	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
22	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
23	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
24	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
25	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
26	17.8	61.4	4325	1 US-08-471-791-29	Sequence 29, Appl
C 27	17.4	60.0	1680	1 US-08-234-783-3	Sequence 36, Appl
			1680	1 US-08-456-907-3	Sequence 3, Appl
			1680	5 PCT-US95-05523-3	Sequence 3, Appl
			1691	3 US-08-917-299-3	Sequence 3, Appl

C 28	17.4	60.0	1691	4 US-09-422-662-3	Sequence 3, Appl
29	17	58.6	560	2 US-08-330-272-3	Sequence 3, Appl
30	17	58.6	560	2 PCT-US95-13663-3	Sequence 3, Appl
31	17	58.6	9515	1 US-08-920-812-13	Sequence 13, Appl
32	17	58.6	9515	1 US-08-920-827-13	Sequence 13, Appl
33	17	58.6	9515	1 US-08-921-177-13	Sequence 13, Appl
34	17	58.6	9515	1 US-08-362-577C-13	Sequence 13, Appl
35	17	58.6	9515	2 US-08-920-828-13	Sequence 13, Appl
C 36	17	58.6	13987	2 US-08-804-227C-13	Sequence 13, Appl
C 37	17	58.6	43280	2 US-08-804-227C-13	Sequence 1, Appl
C 38	16.8	57.9	346	1 US-08-488-144-15	Sequence 15, Appl
C 39	16.8	57.9	474	2 US-08-403-852D-14	Sequence 14, Appl
C 40	16.8	57.9	474	3 US-08-510-646B-14	Sequence 14, Appl
C 41	16.8	57.9	474	4 US-09-231-818-14	Sequence 14, Appl
C 42	16.8	57.9	491	1 US-08-133-711-37	Sequence 37, Appl
C 43	16.8	57.9	872	3 US-09-248-335-63	Sequence 63, Appl
C 44	16.8	57.9	1151	1 US-07-204-288C-2	Sequence 2, Appl
C 45	16.8	57.9	1151	1 US-08-093-372-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-761-258-1/C
; Sequence 1, Application US/08761258
; Patent No. 5756087
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Lam, Stephen T.
APPLICANT: Gaffney, Thomas D.
APPLICANT: Tokewitz, Nancy
TITLE OF INVENTION: Genetically Modified Pseudomonas Strains
TITLE OF INVENTION: with Enhanced Biocontrol Activity
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,258
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356 (aka MCG134 and aka BL915)
IMMEDIATE SOURCE:
CLONE: Plasmid pE11
FEATURE:

```

1 NAME/KEY: misc_feature
2 LOCATION: 210..1688
3
4 OTHER INFORMATION: /product= "methyltransferase"
5 OTHER INFORMATION: /note= "Coding sequence for methyltransferase has homology to
6 OTHER INFORMATION: the cher and frzF genes from E. coli and Myxococcus xanthus,
7 OTHER INFORMATION: respectively."
8 FEATURE:
9 NAME/KEY: misc_feature
10 LOCATION: 1906..3633
11
12 OTHER INFORMATION: /product= "sensor kinase"
13 OTHER INFORMATION: /note= "Coding sequence for sensor kinase has homology to the
14 OTHER INFORMATION: rcsC, frzE, and bvgS genes of E. coli, M. Xanthus, and
15 OTHER INFORMATION: Bordetella pertussis, respectively."
16 FEATURE:
17 NAME/KEY: misc_RNA
18 LOCATION: complement (4616..4691)
19 OTHER INFORMATION: /product= "tRNA"
20 OTHER INFORMATION: /note= "(complementary DNA strand) Homology to g1yw from E.
21 OTHER INFORMATION: coli."
22 FEATURE:
23 NAME/KEY: misc_feature
24 LOCATION: complement (4731..5318)
25
26 OTHER INFORMATION: /product=
27 OTHER INFORMATION: "GDP-diacylglycerol-glycerol-3-phosphate-3-phosph
28 OTHER INFORMATION: atidyltrans."
29 OTHER INFORMATION: /note= "Coding sequence for
30 OTHER INFORMATION: GDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltransf
31 OTHER INFORMATION: se has homology to psaA."
32 FEATURE:
33 NAME/KEY: misc_feature
34 LOCATION: complement (5574..7397)
35 OTHER INFORMATION: /product= "UVR exonuclease subunit
36 OTHER INFORMATION: C"
37 OTHER INFORMATION: /note= "Coding sequence for UVR exonuclease subunit C has
38 OTHER INFORMATION: homology to uvrC."
39 FEATURE:
40 NAME/KEY: misc_feature
41 LOCATION: complement (7400..8041)
42
43 OTHER INFORMATION: /function= "response
44 OTHER INFORMATION: regulator/transcription activator"
45 OTHER INFORMATION: /product= "gacA (aka gafA)"
46 OTHER INFORMATION: /note= "Coding sequence for gacA (aka gafA) has homology to t
47 OTHER INFORMATION: uvrY and gacA genes of E. coli and Ps. fluorescens,
48 OTHER INFORMATION: respectively."
49 US-08-761-258-1
50
51 Query Match 66.9%; Score 19.4; DB 1; Length 10763;
52 Best Local Similarity 79.3%; Pred. No. 23;
53 Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
54
55 QY 1 GGGCGCCGTGCGCGCTCTGTGTCGGCGCG 29
56 ||||||| ||||||| |||
57 Db 6873 GGGCGCCGTGCGCGCTCTGTGTCGGCGCG 6845
58
59 RESULT 2
60 US-08-977-306-1/c
61 ; Sequence 1, Application US/08977306
62 ; Patent No. 5955348
63 GENERAL INFORMATION:
64 APPLICANT: Ligon, James M.
65 APPLICANT: Hill, Dwight S.
66 APPLICANT: Gaffney, Thomas D.
67 APPLICANT: Torkewitz, Nancy
68 APPLICANT: Stafford, Jill M.
69 TITLE OF INVENTION: Genetically Modified Pseudomonas Strains
70 TITLE OF INVENTION: With Enhanced Biocontrol Activity
71 NUMBER OF SEQUENCES: 11
72 CORRESPONDENCE ADDRESSES:
73 ADDRESSEE: No. 5955348artis Corporation
74 STREET: 3054 Cornwallis Road
75 CITY: Research Triangle Park

```

```

STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977.306
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10763 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudomonas fluorescens
STRAIN: CGA267356 (aka MCG134 and aka BL915)
IMMEDIATE SOURCE:
CLONE: Plasmid pE11
FEATURE:
NAME/KEY: misc_feature
LOCATION: 210..1688
OTHER INFORMATION: /product= "methyltransferase"
OTHER INFORMATION: /note= "Coding sequence for methyltransferase has homology to the cheR and fitZ genes from E. coli and Myxococcus xanthus"
OTHER INFORMATION: respectively."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1906..3633
OTHER INFORMATION: /product= "sensor kinase"
OTHER INFORMATION: /note= "Coding sequence for sensor kinase has homology to rcsC, fitZ, and bvgS genes of E. coli, M. xanthus, and Bordetella pertussis, respectively."
OTHER INFORMATION: respectively."
FEATURE:
NAME/KEY: misc_RNA
LOCATION: complement (4616..4691)
OTHER INFORMATION: /product= "tRNA"
OTHER INFORMATION: /note= "(complementary DNA strand) Homology to glyc from E. coli."
OTHER INFORMATION: coli."
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (4731..5318)
OTHER INFORMATION: /product= "CDP-diacylglycerol-3-phosphate-3-phosphatidyltransferase"
OTHER INFORMATION: /note= "CDP-diacylglycerol-3-phosphate-3-phosphatidyltransferase"
OTHER INFORMATION: /note= "Coding sequence for CDP-diacylglycerol-3-phosphate-3-phosphatidyltransferase"
OTHER INFORMATION: se has homology to pgsA."
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (5574..7397)
OTHER INFORMATION: /product= "UVR exonuclease subunit C"
OTHER INFORMATION: /note= "Coding sequence for UVR exonuclease subunit C has homology to uvrC."
OTHER INFORMATION: regulator/transcription activator"
OTHER INFORMATION:

```


OTHER INFORMATION: /product= "gaca (aka gafa)"
OTHER INFORMATION: /note= "coding sequence for gaca (aka gafa) has homology to t
OTHER INFORMATION: uvry and gaca genes of E. coli and Ps. fluorescens,
OTHER INFORMATION: respectively."
US-08-977-306-1

Query Match 66.9%; Score 19.4; DB 2; Length 10763;
Best Local Similarity 79.3%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGGCGCGTGGCGCTTGTGGCGCG 29
DB 6873 GGGCGCGTGGCGCTTGTGGCGCG 6845

RESULT 3
US-08-106-761-1/c
Sequence 1, Application US/08106761
Patent No. 5445956
GENERAL INFORMATION:
APPLICANT: HAMMOCK, Bruce D.
APPLICANT: GRANT, David F.
APPLICANT: BERTHAM, Jeffrey K.
TITLE OF INVENTION: RECOMBINANT SOLUBLE EPOXIDE HYDROLASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
STREET: Stewart Street Tower, 20th Floor, One Market
Plaza
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/106,761
FILING DATE: 19930813
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 2307E-445
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 42..1703
US-08-106-761-1

Query Match 64.1%; Score 18.6; DB 1; Length 2101;
Best Local Similarity 84.0%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGGCGCGTGGCGCTTGTGGCGCG 25
DB 59 GGGCGCGTGGCGCTTGTGGCGCG 35

RESULT 4
US-08-035-558-1/c
Sequence 1, Application US/08035558
Patent No. 5462734
GENERAL INFORMATION:
APPLICANT: Letchworth, Geoffrey J.
APPLICANT: Israel, Barbara A.
TITLE OF INVENTION: HERPESVIRUS VACCINE AND METHOD
TITLE OF INVENTION: OF USING SAME
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: P.O. Box 2113
CITY: FIRST WISCONSIN PLAZA
STATE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,558
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/607,794
FILING DATE: 02-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Seay
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9629691682
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608)251-5000
TELEFAX: (608)251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3519 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: bovine herpesvirus-1
INDIVIDUAL ISOLATE: P8-2 strain
FEATURE:
NAME/KEY: coding sequence for g1 glycoprotein
LOCATION: 379 to 3165
IDENTIFICATION METHOD: sequence analysis
PUBLICATION INFORMATION:
AUTHORS: Mistra, Vikram
AUTHORS: Nelson, Randy
AUTHORS: Smith, Michael
TITLE: Sequence of a Bovine Herpesvirus Type-1 etc.
JOURNAL: Virology
VOLUME: 166
PAGES: 542-549
DATE: 1988
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 379 TO 3165
US-08-035-558-1

Query Match 63.4%; Score 18.4; DB 1; Length 3519;
Best Local Similarity 78.6%; Pred. No. 55;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGGCGCGTGGCGCTTGTGGCGCG 28

DB 3326 GCGCCCTCCCTGCGCCGCGTGGCGCG 3239

RESULT 5

US-08-822-586-45

Sequence 45, Application US/08822586

Patent No. 6015890

GENERAL INFORMATION:

APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND

APPLICANT: AMALIO TELENTO

TITLE OF INVENTION: AN EMBCAB OPERON OF MYCOBACTERIA AND

TITLE OF INVENTION: MUTANTS THEREOF

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: AKSTER, ROTHSTEIN & EBENSTEIN

STREET: 90 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: U.S.A.

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE

MEDIUM TYPE: DISKETTE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/822,586

FILING DATE: MARCH 20, 1997

ATTORNEY/AGENT INFORMATION:

NAME: ELIZABETH A. BOGOSIAN

REGISTRATION NUMBER: 39,911

TELEPHONE: (212) 697-5995

TELEFAX: (212) 286-0854 or 286-0082

TELEX: TWX 710-581-4766

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 10095

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

US-08-822-586-45

Query Match 63.4%; Score 18.4; DB 3; Length 10095;

Best Local Similarity 78.6%; Pred. No. 53;

Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GCGCCGTGCGCGCTGTGTGGCGCGCG 29

DB 3863 GTGGCGTTCGCGACGTGGCGCGCG 3890

RESULT 6

US-09-060-756-455

Sequence 455, Application US/09060756

Patent No. 6183957

GENERAL INFORMATION:

APPLICANT: Cole, Stewart

APPLICANT: Buchleser-Brosch, Roland

APPLICANT: Gordon, Stephen

APPLICANT: Billault, Alain

TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM

TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

FILE REFERENCE: 3495-0169

CURRENT APPLICATION NUMBER: US/09/060,756

CURRENT FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 743

SOFTWARE: Patentlin Ver. 2.0

SEQ ID NO 455

LENGTH: 360

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis

FEATURE:

NAME/KEY: unsure

LOCATION: (various positions within the sequence)

OTHER INFORMATION: applicants are uncertain of bases designated as "n"

US-09-060-756-455

Query Match 61.4%; Score 17.8; DB 4; Length 360;

Best Local Similarity 75.9%; Pred. No. 97;

Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCGCCGTGCGCGCTGTGTGGCGCGCG 29

DB 63 ggcgtgctgctgctgctgctgctgctgctg 91

RESULT 7

US-09-060-756-70

Sequence 70, Application US/09060756

Patent No. 6183957

GENERAL INFORMATION:

APPLICANT: Cole, Stewart

APPLICANT: Buchleser-Brosch, Roland

APPLICANT: Gordon, Stephen

APPLICANT: Billault, Alain

TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM

TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

FILE REFERENCE: 3495-0169

CURRENT APPLICATION NUMBER: US/09/060,756

CURRENT FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 743

SOFTWARE: Patentlin Ver. 2.0

SEQ ID NO 70

LENGTH: 447

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis

US-09-060-756-70

Query Match 61.4%; Score 17.8; DB 4; Length 447;

Best Local Similarity 75.9%; Pred. No. 96;

Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCGCCGTGCGCGCTGTGTGGCGCGCG 29

DB 191 ggcgtgctgctgctgctgctgctgctgctg 219

RESULT 8

US-09-347-819-5

Sequence 5, Application US/09347819

Patent No. 6184036

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Rafalski, J. Antoni

APPLICANT: Palco, S. Carl

TITLE OF INVENTION: Ornithine Biosynthesis Enzymes

FILE REFERENCE: BB-1174-C

CURRENT APPLICATION NUMBER: US/09/347,819

CURRENT FILING DATE: 1999-07-02

EARLIER APPLICATION NUMBER: 60/093,209

EARLIER FILING DATE: July 17, 1998

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Microsoft Office 97

SEQ ID NO 5

LENGTH: 1117

```
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (225)
FEATURE:
NAME/KEY: unsure
LOCATION: (227)
FEATURE:
NAME/KEY: unsure
LOCATION: (229)
FEATURE:
NAME/KEY: unsure
LOCATION: (246)
FEATURE:
NAME/KEY: unsure
LOCATION: (255)
FEATURE:
NAME/KEY: unsure
LOCATION: (308)
FEATURE:
NAME/KEY: unsure
LOCATION: (320)
FEATURE:
NAME/KEY: unsure
LOCATION: (1043)
FEATURE:
NAME/KEY: unsure
LOCATION: (1068)
FEATURE:
NAME/KEY: unsure
LOCATION: (1070)
FEATURE:
NAME/KEY: unsure
LOCATION: (1084)
FEATURE:
NAME/KEY: unsure
LOCATION: (1100)
FEATURE:
NAME/KEY: unsure
LOCATION: (1114)
FEATURE:
NAME/KEY: unsure
LOCATION: (1116)
US-09-347-819-5
```

```
Query Match 61.4%; Score 17.8; DB 4; Length 1117;
Best Local Similarity 75.9%; Pred. No. 94;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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```
QY 1 GCGCGCGTCCGCGTCTTGTCGGCGCGG 29
||||| 111111111111111111111111
DB 153 ggcgtg99g9gc9cgtcacg9c9c9g 181
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RESULT 9

US-08-793-410-10

```
; Sequence 10, Application US/08793410
; Patent No. 5955650
; GENERAL INFORMATION:
; APPLICANT: HITZ, WILLIAM DEAN
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF CANOLA
; TITLE OF INVENTION: AND SOYBEAN PALMITOYL-ACP THIO-
; TITLE OF INVENTION: ESTERASE GENES AND THEIR USE IN
; TITLE OF INVENTION: THE REGULATION OF FATTY ACID
; TITLE OF INVENTION: CONTENT OF THE OILS OF SOYBEAN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
```

```
STATE: DELAWARE
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,410
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10627
FILING DATE: AUGUST 25, 1995
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNN M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: CR-9567-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-793-410-10
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Query Match 61.4%; Score 17.8; DB 2; Length 1303;
Best Local Similarity 75.9%; Pred. No. 93;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY 1 GCGCGCGTCCGCGTCTTGTCGGCGCGG 29
||||| 111111111111111111111111
DB 1202 GCGCGCGTGCAGCGTTTGTGCGCGG 1230
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RESULT 10

US-08-173-508-1/C

```
; Sequence 1, Application US/08173508
; Patent No. 5616485
; GENERAL INFORMATION:
; APPLICANT: Bartfeld, Daniel
; APPLICANT: Butler, Michael J.
; APPLICANT: Hedary, Dany
; APPLICANT: Jenish, David
; APPLICANT: Krieger, Timothy
; TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
; TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,508
; FILING DATE: 23-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29, 768
REFERENCE/DOCKET NUMBER: 18740/125/CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 146..1759
FEATURE:
NAME/KEY: misc-feature
LOCATION: 146..148
OTHER INFORMATION: /note="Met at position -39
OTHER INFORMATION: represents fmet"

US-08-173-508-1

Query Match 61.4%; Score 17.8; DB 1; Length 1908;
Best Local Similarity 75.9%; Pred. No. 92;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCGCCGTCGCGCGCTTCGCGCGCGG 29
1 1111 11 1111 11111111
Db 1150 GCGCCGACGCGCTTCGCGCGCGG 1122

RESULT 11
US-08-265-310-1/c
Sequence 1, Application US/08265310
Patent No. 5856166
GENERAL INFORMATION:
APPLICANT: Bartfeld, Daniel
APPLICANT: Butler, Michael J.
APPLICANT: Hadary, Dany
APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
APPLICANT: Malek, Lawrence T.
APPLICANT: Soostmeyer, Gisela
APPLICANT: Walczyk, Eva
APPLICANT: Krzyzman, Phyllis
APPLICANT: Garven, Sheila
TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,310
FILING DATE: 24-JUN-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,508
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29, 768
REFERENCE/DOCKET NUMBER: 18740/133/CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 146..1759
FEATURE:
NAME/KEY: misc-feature
LOCATION: 146..148
OTHER INFORMATION: /note="Met at position -39
OTHER INFORMATION: represents fmet"

US-08-265-310-1

Query Match 61.4%; Score 17.8; DB 2; Length 1908;
Best Local Similarity 75.9%; Pred. No. 92;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCGCCGTCGCGCGCTTCGCGCGCGG 29
1 1111 11 1111 11111111
Db 1150 GCGCCGACGCGCTTCGCGCGCGG 1122

RESULT 12
US-08-951-742-1/c
Sequence 1, Application US/08951742
Patent No. 6127144
GENERAL INFORMATION:
APPLICANT: Bartfeld, Daniel
APPLICANT: Michael J. Butler
APPLICANT: Dany Hadary
APPLICANT: David Jenish
APPLICANT: Tim Krieger
APPLICANT: Lawrence T. Malek
APPLICANT: Gisela Soostmeyer
APPLICANT: Eva Walczyk
APPLICANT: Phyllis Krzyzman
APPLICANT: Sheila Garven
TITLE OF INVENTION: METHOD FOR EXPRESSION OF PROTEINS IN
TITLE OF INVENTION: BACTERIAL HOST CELLS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,742
FILING DATE: 16-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 0189740/0140
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 146..1756
FEATURE:
NAME/KEY: misc_feature
LOCATION: 146..148
OTHER INFORMATION: /product="Met at position -39
OTHER INFORMATION: represents fMet"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 146..262
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 263..1756
US-08-951-742-1

Query Match      61.4%; Score 17.8; DB 4; Length 1908;
Best Local Similarity 75.9%; Pred. No. 92;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCGCGCGTCCGCGTCTTGTCGCGCGCG 29
DB 1150 GCGCGCGAGCGCTCTTCGCGCGCGG 1122

RESULT 13
US-07-985-458-1
Sequence 1, Application US/07985458
Patent No. 5344777
GENERAL INFORMATION:
APPLICANT: Tamaki, Toshimi;
APPLICANT: Takemura, Hiroshi;
APPLICANT: Tayama, Kenji;
APPLICANT: Fukaya, Masahito;
APPLICANT: Okumura, Hajime and
APPLICANT: Kawamura, Yoshiya
TITLE OF INVENTION: Structural Gene of Membrane-Bound
TITLE OF INVENTION: Alcohol Dehydrogenase Complex. Plasmid
TITLE OF INVENTION: Containing The Same And Transformed Acetic Acid
TITLE OF INVENTION: Bacteria
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frischauf, Holztz, Goodman & Woodward, P.C.
STREET: 600 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10016-2088
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72 mb
COMPUTER: IBM PC compatible (NEC PC-9801 ES)
OPERATING SYSTEM: MS DOS
SOFTWARE: ASCII form
CURRENT APPLICATION DATA:
```

```

APPLICATION NUMBER: US/07/985,458
FILING DATE: 19921203
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/658,221
FILING DATE: 20-FEB-1991
APPLICATION NUMBER: 73440/1990
FILING DATE: 26-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Herbert
REGISTRATION NUMBER: 17081
REFERENCE/DOCKET NUMBER: 910134/HG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
TELEFAX: (212)370-1622
TELEX: 236268
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2214 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Acetobacter alioacetigenes
PUBLICATION INFORMATION:
STRAIN: MH-24
AUTHORS: Tamaki, Toshimi;
AUTHORS: Fukaya, Masahito;
AUTHORS: Takemura, Hiroshi;
AUTHORS: Tayama, Kenji;
AUTHORS: Okumura, Hajime;
AUTHORS: Kawamura, Yoshiya;
AUTHORS: Nishiyama, Makoto;
AUTHORS: Horinouchi, Sueharu and
AUTHORS: Beppu, Teruniko
TITLE: Cloning and Sequencing of the Gene Cluster
TITLE: Encoding Two Subunits of Membrane-Bound
TITLE: Alcohol Dehydrogenase from Acetobacter
TITLE: polyoxogenes
JOURNAL: Biochimica et Biophysica Acta.
VOLUME: 1088
PAGES: 292-300
DATE: 1991
US-07-985-458-1

Query Match      61.4%; Score 17.8; DB 1; Length 2214;
Best Local Similarity 75.9%; Pred. No. 92;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCGCGCGTCCGCGTCTTGTCGCGCGCG 29
DB 802 GCGCGCTGAGCCGCGCAGGTCGCGCGG 830

RESULT 14
US-08-453-924-2
Sequence 2, Application US/08453924
Patent No. 5608152
GENERAL INFORMATION:
APPLICANT: Knauf, Vic C.
APPLICANT: Kridl, Jean C.
TITLE OF INVENTION: Seed-Specific Transcriptional Regulation
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weill, Gotshal & Manges
STREET: 2882 Sand Hill Road, Ste. 280
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
```

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,924
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/742,834
FILING DATE: 08-AUGUST-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/550,804
FILING DATE: 09-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/147,781
FILING DATE: 25-JANUARY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/078,538
FILING DATE: 28-JULY-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/891,529
FILING DATE: 31-JULY-1986
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Ventler, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE-037/04US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FRAGMENT TYPE: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 2152..2703
US-08-453-924-2

Query Match 61.4%; Score 17.8; DB 1; Length 4325;
Best Local Similarity 75.9%; Pred. No. 90;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGCGCGTGCCTTGTGTGGCGCG 29
DB 3811 GGCGCGCGCGACGTTTGTGTGGCGCG 3839

RESULT 15
US-08-471-791-29
Sequence 29, Application US/08471791
Patent No. 5723595
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knaut, Y/C
TITLE OF INVENTION: Plant Desaturases-Compositions
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 2.0 MB storage
COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: MicrosoftWord 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,791
FILING DATE: 6-JUNE-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/762,762
FILING DATE: 16-SEPT-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 69-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-471-791-29

Query Match 61.4%; Score 17.8; DB 1; Length 4325;
Best Local Similarity 75.9%; Pred. No. 90;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGCGCGTGCCTTGTGTGGCGCG 29
DB 3811 GGCGCGCGCGACGTTTGTGTGGCGCG 3839

Search completed: April 20, 2001, 00:03:25
Job time: 9662 sec

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This search was run on the machines we identify as Compugen1, abss03, abss04, or abss05. The databases on these machines are exactly the same as those on the other machines. However, for searches run on the listed machines, two sets of results are now generated when the Pending Nucleic Acid and/or Pending Amino Acid databases are searched. The Pending databases have been split into two parts to reduce the amount of time required for their daily update.

Searches run against the Nucleic Acid Pending database will produce two sets of results, with the extensions **.rnpn** and **.rnpn**

Searches run against the Amino Acid Pending database will produce two sets of results, with the extensions **.rapn** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:25:13 ; Search time 1165 Seconds
(without alignments)
13.523 Million cell updates/sec

Title: US-09-016-464-8
Perfect score: 29
Sequence: 1 GGCCTCGCTGCTTGTGTGCGCGCG 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13168883 segs, 2603265903 residues

Total number of hits satisfying chosen parameters: 26337766

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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35: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	29	100.0	29	8	US-08-474-497-8	Sequence 8, Appli
2	29	100.0	29	14	US-09-016-464-8	Sequence 8, Appli
3	29	100.0	29	14	US-09-093-972C-979	Sequence 979, App
4	29	100.0	29	19	US-09-509-152A-982	Sequence 982, App
5	29	100.0	304	19	US-09-509-152A-1685	Sequence 1685, App
6	29	100.0	1333	57	US-60-258-273-239	Sequence 239, App
7	29	100.0	1747	30	US-09-770-173-3143	Sequence 3143, App
8	29	100.0	1784	53	US-60-213-360-1179	Sequence 1179, App
9	29	100.0	7800	19	US-09-509-152A-2409	Sequence 2409, App
10	29	100.0	34503	57	US-60-258-273-31	Sequence 31, Appl
11	22.2	76.6	610	20	US-09-533-559-622	Sequence 622, App
12	21.6	74.5	427	29	US-09-721-588-2477	Sequence 2477, App
13	21.6	74.5	782	29	US-09-721-588-4972	Sequence 4972, App
14	21.6	74.5	3305	16	US-09-205-070-2471	Sequence 2471, App
15	21.6	74.5	6215	17	US-09-340-623-2471	Sequence 2471, App
16	21.6	74.5	32768	54	US-60-213-846-496	Sequence 496, App
17	21.6	74.5	32768	54	US-60-229-515-46	Sequence 46, Appl
18	21	72.4	283	16	US-09-266-640A-2107	Sequence 2107, App
19	21	72.4	283	16	US-09-266-640B-2107	Sequence 2107, App
20	21	72.4	283	25	US-09-654-617-36169	Sequence 36169, App
21	21	72.4	283	27	US-09-684-016-36169	Sequence 36169, App
22	21	72.4	331	52	US-60-207-458-93141	Sequence 93141, App
23	21	72.4	377	52	US-60-207-458-44741	Sequence 44741, App
24	21	72.4	394	17	US-09-394-745-38366	Sequence 38366, App
25	21	72.4	394	22	US-09-565-306-58880	Sequence 58880, App
26	21	72.4	444	47	US-09-155-006-2646	Sequence 2646, App
27	21	72.4	497	25	US-09-654-617-175615	Sequence 175615, App
28	21	72.4	497	27	US-09-684-016-175615	Sequence 175615, App
29	21	72.4	555	25	US-09-654-617-278382	Sequence 278382, App
30	21	72.4	555	27	US-09-684-016-278382	Sequence 278382, App
31	21	72.4	721	24	US-09-620-392-21788	Sequence 21788, App
32	21	72.4	1154	24	US-09-620-392-55447	Sequence 55447, App
33	21	72.4	1154	28	US-09-702-134-1102	Sequence 1102, App
34	21	72.4	1210	24	US-09-620-392-64393	Sequence 64393, App
35	21	72.4	1751	28	US-09-702-134-12423	Sequence 12423, App
36	21	72.4	2675	24	US-09-620-392-52914	Sequence 52914, App
37	21	72.4	2675	28	US-09-702-134-47824	Sequence 47824, App
38	21	72.4	4675	24	US-09-620-392-67867	Sequence 67867, App
39	21	72.4	6405	24	US-09-620-392-72055	Sequence 72055, App
40	21	72.4	6587	28	US-09-702-134-6483	Sequence 6483, App
41	21	72.4	9067	24	US-09-620-392-48114	Sequence 48114, App
42	21	72.4	11471	24	US-09-702-134-15888	Sequence 15888, App
43	21	72.4	11471	24	US-09-620-392-52603	Sequence 52603, App
44	21	72.4	12883	28	US-09-702-134-8867	Sequence 8867, App
45	21	72.4	13586	28	US-09-702-134-7646	Sequence 7646, App

ALIGNMENTS

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RESULT 1
US-08-474-497-8
; Sequence 8, Application US/08474497
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,497
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-497-8

Query Match          100.0%; Score 29; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. NO. 0.47;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCGCGTCCGCGTCTTGTCGGCGCG 29
    |||||||||||||||||||||||||||
Db 1 GGGCGCGTCCGCGTCTTGTCGGCGCG 29

RESULT 2
US-09-016-464-8
; Sequence 8, Application US/09016464
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,464
FILING DATE: 30-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,497
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-016-464-8

Query Match          100.0%; Score 29; DB 14; Length 29;
Best Local Similarity 100.0%; Pred. NO. 0.47;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCGCGTCCGCGTCTTGTCGGCGCG 29
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Db 1 GGGCGCGTCCGCGTCTTGTCGGCGCG 29

RESULT 3
US-09-093-972C-979
; Sequence 979, Application US/09093972C
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; TITLE OF INVENTION: & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; TITLE OF INVENTION: BRONCHOCONSTRICION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 966
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIDENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
```

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; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 979:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 979:
US-09-093-972C-979

Query Match          100.0%; Score 29; DB 14; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCGTGGCGGCTTGTGTGGCGGCG 29
Db 1 GGGCGCGTGGCGGCTTGTGTGGCGGCG 29

RESULT 4
US-09-509-152A-982
; Sequence 982, Application US/09509152A
; GENERAL INFORMATION:
; APPLICANT: NCE, JONATHAN W.
; TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
; FORMULATIONS, KITS & APPLICATIONS
; NUMBER OF SEQUENCES: 2419
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 CLARKE DRIVE
; CITY: CRANBURY
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/509,152A
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,160
; FILING DATE: 1997-09-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 982:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 982:
US-09-509-152A-982

Query Match          100.0%; Score 29; DB 19; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGGCGCGTGGCGGCTTGTGTGGCGGCG 29
Db 1 GGGCGCGTGGCGGCTTGTGTGGCGGCG 29

RESULT 5
US-09-509-152A-1685
; Sequence 1685, Application US/09509152A
; GENERAL INFORMATION:
; APPLICANT: NCE, JONATHAN W.
; TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
; FORMULATIONS, KITS & APPLICATIONS
; NUMBER OF SEQUENCES: 2419
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 CLARKE DRIVE
; CITY: CRANBURY
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/509,152A
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,160
; FILING DATE: 1997-09-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1685:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 304 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1685:
US-09-509-152A-1685

Query Match          100.0%; Score 29; DB 19; Length 304;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCGTGGCGGCTTGTGTGGCGGCG 29
Db 1 GGGCGCGTGGCGGCTTGTGTGGCGGCG 29

RESULT 6
US-60-258-273-239/C
; Sequence 239, Application US/60258273
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
; TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001042-PROV
; CURRENT APPLICATION NUMBER: US/60/258,273
; CURRENT FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 239
LENGTH: 1733
TYPE: DNA
ORGANISM: Human
US-60-258-273-239

Query Match 100.0%; Score 29; DB 57; Length 1733;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCCGTCGCCGCTTGTGTGGCGCGG 29
|||||
DB 48 GGGCCGTCGCCGCTTGTGTGGCGCGG 20

RESULT 7
US-09-770-173-3143/c
; Sequence 3143, Application US/09770173
; GENERAL INFORMATION:
; APPLICANT: Pan, David
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600, 2059-001
; CURRENT APPLICATION NUMBER: US/09/770,173
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,876
; NUMBER OF SEQ ID NOS: 3167
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3143
; LENGTH: 1747
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-770-173-3143

Query Match 100.0%; Score 29; DB 30; Length 1747;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCCGTCGCCGCTTGTGTGGCGCGG 29
|||||
DB 44 GGGCCGTCGCCGCTTGTGTGGCGCGG 16

RESULT 8
US-60-213-360-1179/c
; Sequence 1179, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preel
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; TITLE OF INVENTION: Identified Thereby
; FILE REFERENCE: CA-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8347
; SOFTWARE: PERL Program
; SEQ ID NO 1179
; LENGTH: 1784
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 349694.1
US-60-213-360-1179

Query Match 100.0%; Score 29; DB 53; Length 1784;

Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCCGTCGCCGCTTGTGTGGCGCGG 29
|||||
DB 47 GGGCCGTCGCCGCTTGTGTGGCGCGG 19

RESULT 9
US-09-509-152A-2409
; Sequence 2409, Application US/09509152A
; GENERAL INFORMATION:
; APPLICANT: NYCE, JONATHAN W.
; TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
; FORMULATIONS, KITS & APPLICATIONS
; NUMBER OF SEQUENCES: 2419
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 CLARKE DRIVE
; CITY: CRANBURY
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/509,152A
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,160
; FILING DATE: 1997-09-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2409:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2409:
US-09-509-152A-2409

Query Match 100.0%; Score 29; DB 19; Length 7800;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCCGTCGCCGCTTGTGTGGCGCGG 29
|||||
DB 381 GGGCCGTCGCCGCTTGTGTGGCGCGG 409

RESULT 10
US-60-258-273-31
; Sequence 31, Application US/60258273
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
; FILE REFERENCE: CLO01042-P-PROV
; CURRENT APPLICATION NUMBER: US/60/258,273
; CURRENT FILING DATE: 2000-12-27

NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 34503
TYPE: DNA
ORGANISM: Human
US-60-258-273-31

Query Match 100.0%; Score 29; DB 57; Length 34503;
Best Local Similarity 100.0%; Pred. No. 0.32; Mismatches 0; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 GCGCCGTGCGCGCTGTGTGTCGCGCG 29
|||||
Db 32458 ggcgcgtgacgcgctgtgtggtgcgcg 32486

RESULT 11
US-09-533-559-622
Sequence 622, Application US/09533559
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Key
APPLICANT: Jeffrey R. Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
FILE REFERENCE: 5849,200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 622
LENGTH: 610
TYPE: DNA
ORGANISM: Fusarium venenatum
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(610)
OTHER INFORMATION: n = A,T,C or G
US-09-533-559-622

Query Match 76.6%; Score 22.2; DB 20; Length 610;
Best Local Similarity 88.9%; Pred. No. 1.3e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 3 GCGCGTCCGCGCTGTGTGTCGCGCG 29
|||||
Db 280 cgcctgacgcgctgtgtggtgcgcg 306

RESULT 12
US-09-721-588-2477
Sequence 2477, Application US/09721588
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Villeval, Jean-Luc
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600,2046-001
CURRENT APPLICATION NUMBER: US/09/721,588
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/167,381
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 5410
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2477
LENGTH: 427
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(427)
OTHER INFORMATION: n = A,T,C or G
US-09-721-588-2477

Query Match 74.5%; Score 21.6; DB 29; Length 427;
Best Local Similarity 85.7%; Pred. No. 2.2e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Y 2 GCGCCGTGCGCGCTGTGTGTCGCGCG 29
|||||
Db 54 ggcgcgtgacgcgctgtgtggtgcgcg 81

RESULT 13
US-09-721-588-4972
Sequence 4972, Application US/09721588
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Villeval, Jean-Luc
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600,2046-001
CURRENT APPLICATION NUMBER: US/09/721,588
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/167,381
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 5410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4972
LENGTH: 782
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(782)
OTHER INFORMATION: n = A,T,C or G
US-09-721-588-4972

Query Match 74.5%; Score 21.6; DB 29; Length 782;
Best Local Similarity 85.7%; Pred. No. 2.1e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Y 2 GCGCCGTGCGCGCTGTGTGTCGCGCG 29
|||||
Db 55 ggcgcgtgacgcgctgtgtggtgcgcg 82

RESULT 14
US-09-205-070-2471
Sequence 2471, Application US/09205070
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL COMPOS OBTAINED FROM VARIOUS CDNA
FILE REFERENCE: 20411-748
CURRENT APPLICATION NUMBER: US/09/205,070
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2471
LENGTH: 3305
TYPE: DNA
ORGANISM: Homo sapiens
US-09-205-070-2471

GenCore version 4.5
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 21:37:43 ; Search time 101.94 Seconds
(without alignments)
39.365 Million cell updates/sec

Title: US-09-016-464-8

Perfect score: 29
Sequence: 1 GGCGCCGTCGCGCTGTGTGCGCGCGC 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 seqs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PC7_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	29	US-09-543-679A-982	Sequence 982, App
2	29	100.0	304	US-09-543-679A-1685	Sequence 1685, Ap
3	29	100.0	1733	US-09-543-679A-2425	Sequence 2425, Ap
4	29	100.0	1733	US-09-543-679A-2436	Sequence 2436, Ap
5	29	100.0	7144	US-09-543-679A-3006	Sequence 3006, Ap
6	29	100.0	7144	US-09-543-679A-3006	Sequence 3006, Ap
7	29	100.0	7800	US-09-543-679A-2409	Sequence 2409, Ap
8	29	100.0	117608	US-09-543-679A-3002	Sequence 3002, Ap
9	29	100.0	117608	US-09-543-679A-3002	Sequence 3002, Ap
10	19.4	66.9	858	US-09-739-449-1026	Sequence 1026, Ap
11	19.4	66.9	801	US-09-813-206-117	Sequence 117, App
12	19.4	65.5	1497	US-09-739-449-5379	Sequence 5379, App
13	19.4	65.5	318095	US-09-739-449-215	Sequence 215, App
14	18.4	63.4	506	US-08-276-1630-15236	Sequence 15236, A
15	18.4	63.4	600	US-09-739-449-7065	Sequence 7065, Ap
16	18.4	63.4	807	US-09-739-449-4007	Sequence 4007, Ap
17	18.4	63.4	867	US-09-739-449-7521	Sequence 7521, Ap
18	18.4	63.4	945	US-09-739-449-2742	Sequence 2742, Ap
19	18.4	63.4	99070	US-09-739-449-200	Sequence 200, App
20	18.4	63.4	138954	US-09-739-449-204	Sequence 204, App
21	18.4	63.4	542340	US-09-739-449-219	Sequence 219, App
22	18.2	62.8	150	US-09-543-679A-1196	Sequence 119, App
23	18.2	62.8	869	US-09-543-679A-1782	Sequence 1782, Ap
24	18.2	62.8	869	US-09-543-679A-1785	Sequence 1785, Ap
25	18.2	62.8	1087	US-09-739-449-1041	Sequence 1041, Ap
26	18.2	62.8	7033	US-09-543-679A-2411	Sequence 2411, Ap
27	18.2	62.8	209274	US-09-543-679A-3004	Sequence 3004, Ap

28	18	62.1	660	US-09-739-449-7870	Sequence 7870, Ap
29	18	62.1	801	US-09-739-449-6247	Sequence 6247, Ap
30	18	62.1	1320	US-09-739-449-7530	Sequence 7530, Ap
31	18	62.1	1371	US-09-739-449-3733	Sequence 3733, Ap
32	18	62.1	143551	US-09-739-449-203	Sequence 203, App
33	18	62.1	202491	US-09-739-449-201	Sequence 201, App
34	17.8	61.4	1359	US-09-739-449-5000	Sequence 5000, Ap
35	17.8	61.4	308503	US-09-739-449-214	Sequence 214, App
36	17.4	60.0	199	US-09-487-566A-3241	Sequence 3241, Ap
37	17.4	60.0	312	US-09-739-449-7969	Sequence 7969, Ap
38	17.4	60.0	873	US-09-739-449-4067	Sequence 4067, Ap
39	17.4	60.0	1005	US-09-739-449-6354	Sequence 6354, Ap
40	17.4	60.0	1023	US-09-739-449-5399	Sequence 5399, Ap
41	17.4	60.0	1803	US-09-739-449-5289	Sequence 5289, Ap
42	17.4	60.0	3705	US-09-739-449-3247	Sequence 3247, Ap
43	17.4	60.0	77826	US-09-739-449-198	Sequence 198, App
44	17.4	60.0	138954	US-09-739-449-204	Sequence 204, App
45	17.4	60.0	184668	US-09-739-449-207	Sequence 207, App

ALIGNMENTS

RESULT 1
US-09-543-679A-982
; Sequence 982, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICITION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: EPTIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 982:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 982:
; US-09-543-679A-982
; Query Match 100.0%; Score 29; DB 5; Length 29;
; Best local Similarity 100.0%; Pred. No. 0.0011;
; Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCGTCCGCTTGTGGCGCGG 29
|||||
Db 1 GGGCGCGTCCGCTTGTGGCGCGG 29

RESULT 2

US-09-543-679A-1685
; Sequence 1685, Application US/09543679A
; GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LONG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <UNKNOWN>

INFORMATION FOR SEQ ID NO: 1685:

SEQUENCE CHARACTERISTICS:

LENGTH: 304 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1685:

US-09-543-679A-1685

Query Match 100.0%; Score 29; DB 5; Length 304;

Best Local Similarity 100.0%; Pred. No. 0.00087;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCGTCCGCTTGTGGCGCGG 29
|||||
Db 1 GGGCGCGTCCGCTTGTGGCGCGG 29

RESULT 3

US-09-543-679A-2425/C

; Sequence 2425, Application US/09543679A

; GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT

OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LONG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <UNKNOWN>

INFORMATION FOR SEQ ID NO: 2425:

SEQUENCE CHARACTERISTICS:

LENGTH: 1733 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2425:

US-09-543-679A-2425

Query Match 100.0%; Score 29; DB 5; Length 1733;

Best Local Similarity 100.0%; Pred. No. 0.00075;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCGTCCGCTTGTGGCGCGG 29
|||||
Db 47 GGGCGCGTCCGCTTGTGGCGCGG 19

RESULT 4

US-09-543-679A-2436/C

; Sequence 2436, Application US/09543679A

; GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LONG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

```

;
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
;   NAME: Amzel, Viviana
;   REGISTRATION NUMBER: 30,930
;   REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 609-409-3035
;   TELEFAX: 413-254-9245
;   TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 2436:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1733 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2436:
US-09-543-679A-2436

Query Match          100.0%; Score 29; DB 5; Length 1733;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCCGCGTGGCGCTTGTGGTGGCGCG 29
    ||||||||||||||||||||||||||||
DB 47 GGGCCGCGTGGCGCTTGTGGTGGCGCG 19

RESULT 5
US-09-543-679A-3006
; Sequence 3006, Application US/09543679A
; GENERAL INFORMATION:
;   APPLICANT: NYCE, Jonathan W.
;   TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;     COMPOSITIONS, KIT & METHOD FOR TREATMENT
;     OF AIRWAY DISORDERS ASSOCIATED WITH
;     BRONCHOCONSTRICITION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;   STREET: 7 Claire Drive
;   CITY: Cranbury
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08512
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: CD-R
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: N/A
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/543,679A
;   FILING DATE: 13-Apr-2000
;   CLASSIFICATION: UNKNOWN
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/127,958
;     FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
;   NAME: Amzel, Viviana
;   REGISTRATION NUMBER: 30,930
;   REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 609-409-3035
;   TELEFAX: 413-254-9245
;   TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 3006:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 7144 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3006:
US-09-543-679A-3006
```

```

;
; Query Match          100.0%; Score 29; DB 5; Length 7144;
; Best Local Similarity 100.0%; Pred. No. 0.00067;
; Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCCGCGTGGCGCTTGTGGTGGCGCG 29
    ||||||||||||||||||||||||||||
DB 5458 GGGCCGCGTGGCGCTTGTGGTGGCGCG 5430

RESULT 6
US-09-543-679A-3006/c
; Sequence 3006, Application US/09543679A
; GENERAL INFORMATION:
;   APPLICANT: NYCE, Jonathan W.
;   TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;     COMPOSITIONS, KIT & METHOD FOR TREATMENT
;     OF AIRWAY DISORDERS ASSOCIATED WITH
;     BRONCHOCONSTRICITION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;   STREET: 7 Claire Drive
;   CITY: Cranbury
;   STATE: NJ
;   COUNTRY: USA
;   ZIP: 08512
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: CD-R
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: N/A
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/543,679A
;   FILING DATE: 13-Apr-2000
;   CLASSIFICATION: UNKNOWN
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/127,958
;     FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
;   NAME: Amzel, Viviana
;   REGISTRATION NUMBER: 30,930
;   REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 609-409-3035
;   TELEFAX: 413-254-9245
;   TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 3006:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 7144 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3006:
US-09-543-679A-3006

Query Match          100.0%; Score 29; DB 5; Length 7144;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCCGCGTGGCGCTTGTGGTGGCGCG 29
    ||||||||||||||||||||||||||||
DB 5458 GGGCCGCGTGGCGCTTGTGGTGGCGCG 5430

RESULT 7
US-09-543-679A-2409
; Sequence 2409, Application US/09543679A
; GENERAL INFORMATION:
;   APPLICANT: NYCE, Jonathan W.
;   TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;     COMPOSITIONS, KIT & METHOD FOR TREATMENT
;     OF AIRWAY DISORDERS ASSOCIATED WITH
;     BRONCHOCONSTRICITION, LUNG INFLAMMATION,
```

```
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2409:
SEQUENCE CHARACTERISTICS:
LENGTH: 7800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2409:
US-09-543-679A-2409

Query Match      100.0%; Score 29; DB 5; Length 7800;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCGTCCCGCTTGTGTGGCGGCG 29
    |||
DB 381 GGGCGCGTCCCGCTTGTGTGGCGGCG 409

RESULT 8
US-09-543-679A-3002
; Sequence 3002, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICTION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 3002:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117608 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3002:
US-09-543-679A-3002
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APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 3002:
SEQUENCE CHARACTERISTICS:
LENGTH: 117608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3002:
US-09-543-679A-3002

Query Match      100.0%; Score 29; DB 5; Length 117608;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCGTCCCGCTTGTGTGGCGGCG 29
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DB 381 GGGCGCGTCCCGCTTGTGTGGCGGCG 409

RESULT 9
US-09-543-679A-3002/c
; Sequence 3002, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICTION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 3002:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117608 base pairs
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RESULT 14
US-08-276-163D-15236
; Sequence 15236, Application US/08276163D
; GENERAL INFORMATION:
; APPLICANT: Adams, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
; FILE REFERENCE: POI4
; CURRENT APPLICATION NUMBER: US/08/276,163D
; NUMBER OF SEQ ID NOS: 15314
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15236
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)
; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (11)
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; NAME/KEY: misc feature

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; NAME/KEY: misc feature
; LOCATION: (489)
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; NAME/KEY: misc feature
; LOCATION: (491)

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; OTHER INFORMATION: n equals a,t,g, or c
 US-08-276-163D-15236

Query Match 63.4%; Score 18.4; DB 4; Length 506;
 Best Local Similarity 86.4%; Pred. No. 13;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 TGGCGCGCTTGGTGGCGGCG 29
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 Db 40 tgcgcgctmgtgagcgcgcg 61

RESULT 15
 US-09-739-449-7065/C
 ; Sequence 7065, Application US/09739449
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15490)C
 ; CURRENT APPLICATION NUMBER: US/09/739,449
 ; CURRENT FILING DATE: 2000-12-19
 ; PRIOR APPLICATION NUMBER: US 09/514,000
 ; PRIOR FILING DATE: 2000-02-23
 ; NUMBER OF SEQ ID NOS: 13351
 ; SEQ ID NO 7065
 ; LENGTH: 600
 ; TYPE: DNA
 ; ORGANISM: Agrobacterium tumefaciens
 US-09-739-449-7065

Query Match 63.4%; Score 18.4; DB 5; Length 600;
 Best Local Similarity 78.6%; Pred. No. 13;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGCGCGCTTGGTGGCGGCG 28
 ||||| ||||| ||||| |||||
 Db 342 GGTGGCGTCCGCCCTCGGTGACGGCG 315

Search completed: April 20, 2001, 00:14:49
 Job time: 9426 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:58:53 ; Search time 2028.86 Seconds
(without alignments)
51.598 Million cell updates/sec

Title: US-09-016-464-9

Perfect score: 17
Sequence: 1 TTTCCTCCGCTCTTCC 17

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
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5: gb_in2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	17	100.0	99	9	AX039241
2	17	100.0	99	9	AX039242
3	17	100.0	99	9	AX039481
4	17	100.0	99	9	AX039482
5	17	100.0	894	93	HUMICERB
6	17	100.0	11298	9	AR040667
7	17	100.0	11298	93	HUMRICBCHA
8	17	100.0	123861	82	AP001181
9	17	100.0	179447	73	AC060806
10	17	100.0	182638	90	CNS01DT7
11	16	94.1	454	54	HS793C17S

C 12 16 94.1 7452 9 AR096107 Sequence
C 13 16 94.1 7452 9 ARI00869
C 14 16 94.1 7452 9 HSGPV
C 15 16 94.1 14315 94 RATCYP2A3A
16 94.1 30377 92 HSLUCA1
17 94.1 56415 92 HSLUCA1
C 18 16 94.1 80465 80 AL359386
C 19 16 94.1 91826 85 AB045320
C 20 16 94.1 119071 92 HSDJ79416
21 16 94.1 120689 83 CDS01RGS
22 16 94.1 126732 86 AC007114
23 16 94.1 143321 89 AL135932
C 24 16 94.1 149897 90 CDS01DSV
25 16 94.1 157419 69 AC025389
C 26 16 94.1 162084 70 AC025700
27 16 94.1 170498 71 AC034127
28 16 94.1 170635 65 AC018862
C 29 16 94.1 170635 65 AC018862
30 16 94.1 171279 67 AC022183
31 16 94.1 173379 90 AP002360
32 16 94.1 173591 62 AC011693
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34 16 94.1 180157 67 AC021548
35 16 94.1 181627 80 AL359264
36 16 94.1 182513 66 AC020695
37 16 94.1 183197 82 AP002000
C 38 16 94.1 187413 86 AC007567
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C 40 16 94.1 195932 67 AC021710
41 16 94.1 201144 79 AL160290
42 16 94.1 209889 61 AC009158
C 43 16 94.1 212250 65 AC016717
C 44 15.4 90.6 962 53 CDS07115
C 45 15.4 90.6 1712 14 SCPDX3

ALIGNMENTS

RESULT 1
LOCUS AX039241/c 99 bp DNA PAT 18-NOV-2000
DEFINITION Sequence 42 from Patent WO0063372.
ACCESSION AX039241
VERSION AX039241.1 GI:11229346
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 99)
AUTHORS Lawson, A.D. and Finney, H.M.
TITLE Synthetic signalling molecules
JOURNAL Patent: WO 0063372-A 42 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="A9000"
BASE COUNT 33 a 16 c 25 g 25 t
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Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCTGGGCTTCC 17
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Db 90 TTTCCTGGGCTTCC 74

RESULT 2

AX039242
LOCUS AX039242 99 bp DNA PAT 18-NOV-2000
DEFINITION Sequence 43 from Patent WO0063372.
ACCESSION AX039242
VERSION AX039242.1 GI:11229347
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 99)
AUTHORS Lawson, A.D. and Finney, H.M.
TITLE Synthetic signalling molecules
JOURNAL Patent: WO 0063372-A 43 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 TTTCCTGGGCTTCC 30

RESULT 3
LOCUS AX039481/c 99 bp DNA PAT 18-NOV-2000
DEFINITION Sequence 36 from Patent WO0063360.
ACCESSION AX039481
VERSION AX039481.1 GI:11229512
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 99)
AUTHORS Finney, H.M. and Lawson, A.D.
TITLE Combinatorial method for producing nucleic acids
JOURNAL Patent: WO 0063360-A 36 26-OCT-2000;
CELLTECH THERAPEUTICS LIMITED (GB)
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 17; DB 9; Length 99;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCTGGGCTTCC 17
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Db 90 TTTCCTGGGCTTCC 74

RESULT 4
LOCUS AX039482 99 bp DNA PAT 18-NOV-2000
DEFINITION Sequence 37 from Patent WO0063360.
ACCESSION AX039482
VERSION AX039482.1 GI:11229513
KEYWORDS
SOURCE synthetic construct.

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ORGANISM      synthetic construct
REFERENCE      artificial sequence.
AUTHORS        1 (bases 1 to 99)
TITLE          Flinney,H.M. and Lawson,A.D.
JOURNAL        Combinatorial method for producing nucleic acids
                Patent: WO 0063360-A 37 26-Oct-2000;
                CELLTech THERAPEUTICS LIMITED (GB)
FEATURES       location/Qualifiers
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Query Match    100.0%; Score 17; DB 9; Length 99;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTCCCTGGGCTTCC 17
        |||||||
Db      14 TTTCCCTGGGCTTCC 30

RESULT  5
HUMIGRB/c  HUMIGRB      894 bp      mRNA      PRI      02-FEB-1999
DEFINITION Homo sapiens mRNA for Ige receptor beta subunit, complete cds.
ACCESSION   D10583
VERSION     D10583.1 GI:219881
KEYWORDS    high-affinity Ige receptor; Ige receptor beta subunit;
SOURCE      Homo sapiens umbilical cord blood basophils cDNA to mRNA.
ORGANISM    Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 894)
AUTHORS     Harada,S.
TITLE       Direct Submission
JOURNAL     Submitted (24-FEB-1992) to the DDBJ/EMBL/GenBank databases.
MEDLINE     Mishigenori Harada, Shimonogi Institute for Medical Science; 2-5-1
FEATURES     Mishima, Setasu, Osaka 566, Japan (Tel:06-382-2612,
                Fax:06-382-2598)
                2 (bases 1 to 894)
                Maelawa,K., Imagawa,N., Tanaka,Y. and Harada,S.
                Determination of the sequence coding for the beta subunit of the
                human high-affinity Ige receptor
                FEBS Lett. 302 (2), 161-165 (1992)
                92339505
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                WGAIFESISGMSIISERRNATYIVRSGIANTFASISNGTGITLITINIKKSLAYIH
                IHSCKFEFTKCFMASFESEIVVMLEFLTILIGLSAVSLTTCGAGEELKGNKVPEDRV
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                YELNIVSATTSLEDDPGEMSPIDL"
BASE COUNT     254 a      184 c      198 g      258 t
ORIGIN
Query Match    100.0%; Score 17; DB 93; Length 894;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTCCCTGGGCTTCC 17

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Db      762 TTTCCCTGGGCTTCC 746
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RESULT  6
AR040667/c  AR040667      11298 bp      DNA      PAT      29-SEP-1999
LOCUS       Sequence 2 from patent US 5807988.
DEFINITION AR040667
ACCESSION   AR040667
VERSION     AR040667.1 GI:5960030
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 11298)
AUTHORS     Kinet,J. and Jouvin,M.
TITLE       Isolation, characterization, and use of the human and subunit of
                the high affinity receptor for immunoglobulin E
                Patent: US 5807988-A 2 15-SEP-1998;
                Location/Qualifiers
                1..11298
                /organism="unknown"
BASE COUNT     3470 a      2113 c      2283 g      3415 t      17 others
ORIGIN
Query Match    100.0%; Score 17; DB 9; Length 11298;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTCCCTGGGCTTCC 17
        |||||||
Db      7299 TTTCCCTGGGCTTCC 7283

RESULT  7
HUMIGRBCHA/c  HUMIGRBCHA  11298 bp      DNA      PRI      09-JAN-1995
LOCUS       Human high affinity Ige receptor beta chain gene, complete cds.
DEFINITION   M89796
ACCESSION   M89796
VERSION     M89796.1 GI:337417
KEYWORDS    Ige receptor beta chain.
SOURCE      Homo sapiens DNA.
ORGANISM    Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 11298)
AUTHORS     Kuster,H., Zhang,L., Brini,A.T., MacGlashan,D.W. and Kinet,J.P.
TITLE       The gene and cDNA for the human high affinity immunoglobulin E
                receptor beta chain and expression of the complete human receptor
                J. Biol. Chem. 267 (18), 12782-12787 (1992)
                92316966
                Location/Qualifiers
                1..11298
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                /db_xref="taxon:9606"
                /cell_type="leukocyte"
                /protein_id="leukocyte"
                /join(354..511,1381..1510,2026..2160,4475..4531,5079..5237,
                5640..5738,7224..7322)
                /gene="high affinity Ige receptor beta chain"
                /product="high affinity Ige receptor beta chain"
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                /gene="high affinity Ige receptor beta chain"
                /number=1
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                5640..5738,7224..7322)
                /gene="high affinity Ige receptor beta chain"
                /codon_start=1
                /product="high affinity Ige receptor beta chain"
                /protein_id="AAA60269.1"
                /db_xref="GI:337418"

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 IHSOKFETKCPMASFSTETVWMLFLTIIGLSAVSLTICGAGEELKQKNVPEDRV
 YELNIYATYSELEDPKSPIDL"

512..1380
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 1511..2025
 /gene="high affinity Ige receptor beta chain"
 /number=2
 2026..2160
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 /number=4
 4532..5078
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 /number=6
 5739..7223
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 7224..10214
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 /number=7
 3470 a 2113 c 2283 g 3415 t 17 others
 BASE COUNT
 ORIGIN
 Query Match 100.0%; Score 17; DB 93; Length 11298;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TITLE JOURNAL

COMMENT

Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 Direct Submission
 Submitted (16-FEB-2000) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-15-1 Kitasato, Sagami-hara, Kanagawa 228-8555, Japan
 (E-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
 Tel: 81-42-778-9923, Fax: 81-42-778-9924)
 On Oct 7, 2000 this sequence version replaced g1:8117626.
 ----- Genome Center
 Center: RIKEN Genomic Sciences Center(GSC)
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gsc.riken.go.jp
 ----- Project Information
 Center project name: HumDraFtl1
 Center clone name: CMB9-2M23
 ----- Summary Statistics
 Sequencing vector: PCR products; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 119519 bases at least Q40
 Consensus quality: 121114 bases at least Q30
 Consensus quality: 121877 bases at least Q20
 Insert size: 122461; sum-of-coverage
 Quality coverage: 8.64x in Q20 bases; sum-of-coverage

 NOTE: This is a 'working draft' sequence. It currently consists of
 15 contigs. The true order of the pieces is not known and their
 order in this sequence record is arbitrary. Gaps between the
 contigs are represented as runs 'N', but the exact sizes of the gaps
 are unknown. This record will be updated with the finished sequence
 as soon as it is available and the accession number will be
 preserved.
 1 30921 contig of 30921 bp in length
 31022 45002 contig of 13981 bp in length
 45103 58778 contig of 13676 bp in length
 58879 68977 contig of 10099 bp in length
 69078 78474 contig of 9397 bp in length
 78575 88158 contig of 9584 bp in length
 88259 94978 contig of 6720 bp in length
 94978 95078 contig of 100 bp in length
 95079 99841 contig of 4763 bp in length
 99842 99941 contig of 100 bp in length
 99942 105080 contig of 5139 bp in length
 * 30921: contig of 30921 bp in length
 * 30922 31021: gap of 100 bp
 * 31022 45002: contig of 13981 bp in length
 * 45003 45102: gap of 100 bp
 * 45103 58778: contig of 13676 bp in length
 * 58779 58878: gap of 100 bp
 * 58879 68977: contig of 10099 bp in length
 * 68978 69077: gap of 100 bp
 * 69078 78474: contig of 9397 bp in length
 * 78475 78574: gap of 100 bp
 * 78575 88158: contig of 9584 bp in length
 * 88159 88258: gap of 100 bp
 * 88259 94978: contig of 6720 bp in length
 * 94978 95078: gap of 100 bp
 * 95079 99841: contig of 4763 bp in length
 * 99842 99941: gap of 100 bp
 * 99942 105080: contig of 5139 bp in length
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of 'N', but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

* 105081 105180: gap of 100 bp
* 105181 109464: contig of 4284 bp in length
* 109465 109564: gap of 100 bp
* 109565 114210: contig of 4646 bp in length
* 114211 114310: gap of 100 bp
* 114311 118663: contig of 4353 bp in length
* 118664 118763: gap of 100 bp
* 118764 121220: contig of 2457 bp in length
* 121221 121320: gap of 100 bp
* 121321 122902: contig of 1582 bp in length
* 122903 123002: gap of 100 bp
* 123003 123861: contig of 859 bp in length.
Location/Qualifiers
1. 123861

```

```

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q12"
/clone="CMB9-2M23"
1. 30921
misc_feature
/note="assembly_fragment"
31022..45002
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/note="assembly_fragment"
45103..58778
misc_feature
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78575..88158
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88259..94978
misc_feature
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99942..105080
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105181..109464
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109565..114210
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118764..121220
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121321..122902
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/note="assembly_fragment"
123003..123861
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123861..22984
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22984..24073
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24073..37298
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/note="assembly_fragment clone_end:SP6 vector_side:left"
37298..1400
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1400..others
BASE COUNT 38106 a 22984 c 24073 g 37298 t 1400 others
ORIGIN

```

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Query Match 100.0% Score 17; DB 82; Length 123861;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCCCTGGGCTTC 17
1111111111111111
Db 67663 TTTCCCTGGGCTTC 67647

```

```

RESULT 9
AC060806/c 179447 bp DNA HTG 28-MAY-2000
LOCUS Homo sapiens chromosome 11 clone RP11-773M18 map 11, WORKING DRAFT
DEFINITION SEQUENCE, 37 unordered pieces.
AC060806 AC060806
VERSION AC060806.2 GI:8099915
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE

1 (bases 1 to 179447)
 Birren, B., Linton, L., Nusbaum, C., and Lander, E.
 Homo sapiens chromosome 11, clone RP11-773M18
 Unpublished
 2 (bases 1 to 179447)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barua, N., Bastien, V., Bedd, F.,
 Boguslavsky, L., Bouckhalter, B., Brown, A., Burkett, G.,
 Campiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
 Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
 Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L.,
 Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
 Klein, J., Labocque, K., Lamazares, R., Landers, T., Lehotzky, J.,
 Levine, R., Liu, G., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McKeeters, R.,
 Meldrum, J., Menus, L., Mihova, T., Miranda, C., Mianga, V., Morrow, J.,
 Murphy, T., Naylor, T.M., Norman, C.H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
 Pisanil, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Testaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE

Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On May 28, 2000 this sequence version replaced gi:7622470.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L9780
 Center clone name: 773_M18
 ----- Summary Statistics
 Sequencing vector: M13; M7815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 159493 bases at least Q40
 Consensus quality: 169539 bases at least Q30
 Consensus quality: 173498 bases at least Q20
 Insert size: 17100; agarose-fp
 Insert size: 175847; sum-of-contigs
 Quality coverage: 4.0 in Q20 bases; agarose-fp
 Quality coverage: 3.9 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 37 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1044: contig of 1044 bp in length
 * 1045 1144: gap of 100 bp
 * 1145 2541: contig of 1397 bp in length
 * 2542 2641: gap of 100 bp
 * 2642 4192: contig of 1551 bp in length
 * 4193 4292: gap of 100 bp
 * 4293 6402: contig of 2110 bp in length
 * 6403 6502: gap of 100 bp
 * 6503 6981: contig of 479 bp in length
 * 6982 7081: gap of 100 bp
 * 7082 8985: contig of 1904 bp in length

```

* 8986 9085: gap of 100 bp
* 9086 11477: contig of 2392 bp in length
* 11478 11577: gap of 100 bp
* 11578 12982: contig of 1405 bp in length
* 12983 13082: gap of 100 bp
* 13083 16059: contig of 2977 bp in length
* 16060 16159: gap of 100 bp
* 16160 18669: contig of 2510 bp in length
* 18670 18769: gap of 100 bp
* 18770 20954: contig of 2185 bp in length
* 20955 21054: gap of 100 bp
* 21055 23279: contig of 2225 bp in length
* 23280 23379: gap of 100 bp
* 23380 27208: contig of 3829 bp in length
* 27209 27308: gap of 100 bp
* 27309 30059: contig of 2751 bp in length
* 30060 30159: gap of 100 bp
* 30160 32764: contig of 2605 bp in length
* 32765 32864: gap of 100 bp
* 32865 35950: contig of 3086 bp in length
* 35951 36050: gap of 100 bp
* 36051 38750: contig of 2700 bp in length
* 38751 38850: gap of 100 bp
* 38851 42486: contig of 3636 bp in length
* 42487 42586: gap of 100 bp
* 42587 45258: contig of 2672 bp in length
* 45259 45358: gap of 100 bp
* 45359 48964: contig of 3606 bp in length
* 48965 49064: gap of 100 bp
* 49065 52693: contig of 3629 bp in length
* 52694 52793: gap of 100 bp
* 52794 56025: contig of 3232 bp in length
* 56026 56125: gap of 100 bp
* 56126 60774: contig of 4649 bp in length
* 60775 60874: gap of 100 bp
* 60875 64900: contig of 4026 bp in length
* 64901 65000: gap of 100 bp
* 65001 70301: contig of 5301 bp in length
* 70302 70401: gap of 100 bp
* 70402 75584: contig of 5183 bp in length
* 75585 75684: gap of 100 bp
* 75685 82095: contig of 6411 bp in length
* 82096 82195: gap of 100 bp
* 82196 88039: contig of 5844 bp in length
* 88040 88139: gap of 100 bp
* 88140 95954: contig of 7815 bp in length
* 95955 96054: gap of 100 bp
* 96055 105465: contig of 9411 bp in length
* 105466 105565: gap of 100 bp
* 105566 114274: contig of 8709 bp in length
* 114275 114374: gap of 100 bp
* 114375 122628: contig of 8254 bp in length
* 122629 122728: gap of 100 bp
* 122729 132969: contig of 10241 bp in length
* 132970 133069: gap of 100 bp
* 133070 142278: contig of 9209 bp in length
* 142279 142378: gap of 100 bp
* 142379 152398: contig of 9920 bp in length
* 152399 152398: gap of 100 bp
* 152399 167711: contig of 15313 bp in length
* 167712 167811: gap of 100 bp
* 167812 179447: contig of 11636 bp in length.

```

FEATURES

```

source
1..179447
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /chromosome="11"
  /map="11"
  /clone="RP11-773M18"
  /clone_1lb="RC1-11 Human Male BAC"
  1..1044
  /note="assembly_fragment"
  1145..2541

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/note="assembly_fragment"
2642..4192
/note="assembly_fragment"
4293..6402
/note="assembly_fragment"
6503..6981
/note="assembly_fragment
clone_end:SP6
vector_side:left"
7082..8985
/note="assembly_fragment"
9086..11477
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11578..12982
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13083..16059
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16160..18669
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27309..30059
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30160..32764
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36051..38750
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38851..42486
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45359..48964
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49065..52693
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52794..56025
/note="assembly_fragment"
56126..60774
/note="assembly_fragment"

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Query Match 100.0%; Score 17; DB 73; Length 179447;
Best Local Similarity 94.1%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 TTTCCCTGGGCTTCC 17
DB 16378 TTCCCTGGGCTTCC 16362

```

```

RESULT 10
CNS01D7 182638 bp DNA PRI 25-MAY-2000
DEFINITION Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-131n24
of library RC1-11 from chromosome 14 of Homo sapiens (human),
complete sequence.
ACCESSION AL132642
VERSION AL132642.3 GI:8217878
KEYWORDS HTG; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 182638)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-2000) to the EMBL/GenBank/DBJ databases
COMMENT On Jun 3, 2000 this sequence version replaced gi:6850919.

```

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . . even if efforts are made to eliminate these contaminating sequences. The following BAC sequence is oriented from the T7 to the SP6 end.

Upstream BAC (overlapping the T7 end) : R-187A6
Downstream BAC (overlapping the SP6 end) : R-1089B7

Overall quality chart :

```

Range : bases
0 : 21
1 - 9 : 424
10 - 19 : 1092
20 - 29 : 4077
30 - 39 : 14404
40 - 49 : 10333
50 - 59 : 14505
60 - 69 : 35481
70 - 79 : 60302
80 - 89 : 30903
90 - 99 : 11096

```

Percentage of bases with a quality value >= 40 : 89 %.

FEATURES

source

Location/Qualifiers

1..182638

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="14"

/clone.lib="RPC1-11"

/clone="R-131H24"

BASE COUNT 46698 a 44813 c 44885 g 46221 t 21 others

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 17; DB 90; Length 182638;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTCTCC 17

Db 18148 TTTCCTGGGCTCTCC 18164

RESULT 11

LOCUS

HS793C17S 454 bp DNA STS 24-NOV-2000

DEFINITION H.sapiens STS from genomic clone 793C17, sequence tagged site.

ACCESSION AL450368

VERSION AL450368.1 GI:11344481

KEYWORDS STS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 454)

AUTHORS Deloukas, P., Holden, J., Harrison, P., Huckle, E., Taylor, R. and Hunt, S.

TITLE Direct Submission

JOURNAL Submitted (23-NOV-2000) E-mail contact: humquerry@sanger.ac.uk

Marker std793C17SP6 (Primer A : AAAATCCAACTGCCCATTTG; Primer B :

GACTGGAGTGGGAGATGA; amplicon size : 86 bp) is from sequence

generated from the SP6 end of PAC 793C17 793C17 is part of the

bacterial clone contigs constructed by the Chromosome 20 Mapping

Group. (http://www.sanger.ac.uk/HGP/Chr20/).

FEATURES

source

1..454

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="20"

/clone="793C17"

BASE COUNT 122 a 146 c 102 g 84 t

ORIGIN

Query Match

Best Local Similarity 94.1%; Score 16; DB 54; Length 454;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTTCCTGGGCTCTCC 17

Db 413 TTTCCTGGGCTCTCC 428

RESULT 12

LOCUS

AR096107/c 7452 bp DNA PAT 08-SEP-2000

DEFINITION Sequence 1 from patent US 6005089.

ACCESSION AR096107

VERSION AR096107.1 GI:10024609

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 7452)

AUTHORS Lanza, F., Phillips, D.R. and Cazenave, J.

TITLE Platelet glycoprotein V gene and uses

JOURNAL Patent: US 6005089-A 1 21-DEC-1999;

FEATURES

source

1..7452

/organism="unknown"

BASE COUNT 1822 a 1778 c 1793 g 2059 t

ORIGIN

Query Match

Best Local Similarity 94.1%; Score 16; DB 9; Length 7452;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTTCCTGGGCTCTCC 17

Db 1125 TTTCCTGGGCTCTCC 1110

RESULT 13

LOCUS

ARI00869/c 7452 bp DNA PAT 14-FEB-2001

DEFINITION Sequence 1 from patent US 6083688.

ACCESSION ARI00869

VERSION ARI00869.1 GI:12811667

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 7452)

AUTHORS Lanza, F., Phillips, D.R. and Cazenave, J.

TITLE Platelet glycoprotein V gene and uses

JOURNAL Patent: US 6083688-A 1 04-JUL-2000;

FEATURES

source

1..7452

/organism="unknown"

BASE COUNT 1822 a 1778 c 1793 g 2059 t

ORIGIN

Query Match

Best Local Similarity 94.1%; Score 16; DB 9; Length 7452;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTTCCTGGGCTCTCC 17

Db 1125 TTTCCTGGGCTCTCC 1110

RESULT 14
LOCUS HSGPV 7452 bp DNA PRI 23-NOV-1993
DEFINITION H.sapiens GPV gene encoding platelet glycoprotein V precursor.
ACCESSION Z23091 GI:312501
KEYWORDS platelet glycoprotein; platelet glycoprotein V.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 7452)
Lanza, F., Morales, M., de La Salle, C., Cazeneuve, J.P.,
Clemetson, K.J., Shimomura, T. and Phillips, D.R.
Cloning and characterization of the gene encoding the human
platelet glycoprotein V. A member of the leucine-rich glycoprotein
family cleaved during thrombin-induced platelet activation
J. Biol. Chem. 268 (28), 20801-20807 (1993)
94012616
2 (bases 1 to 7452)
Lanza, F.
Direct Submission
Submitted (23-JUN-1993) Lanza F., Centre Regional De Transfusion
Sanguine, INSERM U.311, 10 rue Spielemann, STRASBOURG, FRANCE, 67085
FEATURES
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DB 1125 TTCCCCTGGGCTTCC 1110
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DEFINITION Rat cytochrome P450 II A3 (CYP2A3) gene, complete cds.
ACCESSION M33190
VERSION M33190.1 GI:203750
KEYWORDS coumarin 7-hydroxylase; cytochrome P450 IIA3.
SOURCE Rat (Sprague-Dawley) DNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 14315)
Ueno, T. and Gonzalez, F.
Complete sequence of the rat CYP2A3 gene specifically transcribed
in lung
JOURNAL Nucleic Acids Res. 18, 4623-4623 (1990)
MEDLINE 90356430
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by F.Gonzalez 23-MAR-1990, for release after publication.
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LYEMFSSVMKHLPPQDAFKELOGLEDFTTKVQONQRTLDPSNPRDTSFLIRML
EKKRNPNTEEFMKMLVITTLNLFPAGTETVSTLRVGYFLILMKHPDIEAKVHEIDRY

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:45 ; Search time 547.68 Seconds
(without alignments)
18.121 Million cell updates/sec

Title: US-09-016-464-9
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	18	T76070 Human IGE receptor
2	17	100.0	17	20	X53868 Human IGE receptor
3	17	100.0	17	21	F19433 Human IGE receptor
4	17	100.0	17	21	A33311 Low adenosine anti
5	17	100.0	99	21	C66486 Chimaeric receptor
6	17	100.0	99	21	C66487 Chimaeric receptor
7	17	100.0	99	21	C68014 Oligonucleotide A9
8	17	100.0	99	21	C68015 Oligonucleotide A9
9	17	100.0	133	20	X54558 Human IGE receptor
10	17	100.0	133	21	F20127 Human IGE receptor
11	17	100.0	133	21	A34005 Human adenosine re

C 12	17	100.0	735	16	087807	IGE receptor gene.
C 13	17	100.0	894	21	F20936	Human high affinity
C 14	17	100.0	894	21	A34814	Human adenosine re
C 15	17	100.0	7800	21	F20842	Human multiple tar
C 16	17	100.0	7800	21	A34720	Human adenosine re
C 17	17	100.0	7803	20	X55272	Human receptor-rel
C 18	17	100.0	11298	19	V54661	Human beta subunit
C 19	17	100.0	11298	21	F20937	Human high affinity
C 20	17	100.0	11298	21	A34815	Human adenosine re
C 21	17	100.0	11357	14	Q51024	Human FcERI beta c
C 22	17	100.0	21742	21	F20938	Human high affinity
C 23	17	100.0	21742	21	A34816	Human adenosine re
C 24	17	100.0	114955	20	X53491	Human adenosine A1
C 25	17	100.0	117609	21	F21435	Human receptor-rel
C 26	17	100.0	117609	21	F21435	Human receptor-rel
C 27	16	94.1	1842	21	C73875	Human secreted pro
C 28	16	94.1	7452	16	Q85594	Human glycoprotein
C 29	16	94.1	7452	21	Z61217	DNA encoding human
C 30	15.4	90.6	11298	18	T86756	Human high affinity
C 31	15	88.2	2406	20	X13245	Enterococcus faeca
C 32	14.4	84.7	231	21	A36783	Human dysferlin re
C 33	14.4	84.7	231	21	X82874	Human dysferlin DN
C 34	14.4	84.7	278	21	F21388	Human low adenosin
C 35	14.4	84.7	278	21	A35266	Human adenosine re
C 36	14.4	84.7	410	19	V49738	Chicken HMGI-C CDN
C 37	14.4	84.7	890	19	V34291	Human secreted pro
C 38	14.4	84.7	996	18	T59473	Human onset Alzhei
C 39	14.4	84.7	1053	21	A75683	DNA encoding a hum
C 40	14.4	84.7	1092	17	T40040	Presentin-1 exon
C 41	14.4	84.7	1092	19	T99669	Human presentin-1
C 42	14.4	84.7	1226	15	Q70664	Scfv-BSRase fusio
C 43	14.4	84.7	1235	15	Q70663	Scfv-BSRase fusio
C 44	14.4	84.7	1259	15	Q70662	Scfv-BSRase fusio
C 45	14.4	84.7	1260	15	Q70668	H17-DIP. Tox. -BSRN

ALIGNMENTS

RESULT 1	
ID T76070	standard: DNA: 17 BP.
AC T76070;	
XX	
DT 11-SEP-1997	(first entry)
XX	
DE Human IGE receptor beta antisense oligonucleotide HUMIGEBetars1.	
XX	
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;	
KW chronic obstructive pulmonary disease; bronchitis; immunoglobulin; ss.	
XX	
OS Synthetic.	
XX	
PN W09640162-A1.	
XX	
PD 19-DEC-1996.	
XX	
PE 06-JUN-1996;	96MO-US09306.
XX	
PR 07-JUN-1995;	95US-0474497.
XX	
PA (UYEC-) UNIV EAST CAROLINA.	
XX	
PI Metzger WJ, Nyce JW;	
XX	
DR WPI; 1997-051871/05.	
XX	
PT Treatment of airway diseases such as asthma - by topically applying	
PT adenosine-free antisense oligo:nucleotide to airway epithelium of	
PT subject	
XX	
PS Claim 5; Page 24; 71pp; English.	

XX A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC HMMgebetaASI specific for the human IGE receptor beta. The method
CC can be used to treat airway diseases such as cystic fibrosis, asthma,
CC chronic obstructive pulmonary disease, bronchitis and other airway
CC diseases characterized by an inflammatory response. By eliminating
CC adenosine from the antisense ON, its liberation upon antisense
CC degradation is prevented, thereby preventing adenosine-induced
CC bronchoconstriction in patients with hyper-reactive airways.
XX
SQ Sequence 17 BP: 0 A; 7 C; 3 G; 7 T; 0 other;

Query Match 100.0%; Score 17; DB 18; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCCGTGGCTTCC 17
Db 1 ttccccggtctcc 17

RESULT 2
X53868
ID X53868 standard; DNA; 17 BP.
XX
AC X53868;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human IGE receptor beta antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;
KW Impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
XX Synthetic.
OS
PN WO913886-A1.
XX
XX 25-MAR-1999.
PD
XX 17-SEP-1998; 98WO-US19419.
PF
XX 09-JUN-1998; 98US-0093972.
PR
XX 17-SEP-1997; 97US-0059160.
PR
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction
XX
PS Disclosure: Page 43; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (X52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding

CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences X55272-74. These multiple target
CC oligonucleotides (specifically X55180-271) can be used for the antisense
CC treatment of diseases and conditions. Typical diseases and conditions
CC are those associated with impaired respiration and inflammation,
CC including lung diseases, pulmonary vasoconstriction, inflammation,
CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC metastases, as well as all types of cancers which may metastasize or have
CC metastasized to the lungs, including breast and prostate cancer.
XX
SQ Sequence 17 BP: 0 A; 7 C; 3 G; 7 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCCGTGGCTTCC 17
Db 1 ttccccggtctcc 17

RESULT 3
F19433
ID F19433 standard; DNA; 17 BP.
XX
AC F19433;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human IGE receptor beta polynucleotide fragment #1000.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX Homo sapiens.
OS
XX WO200062736-A2.
PN
XX 26-OCT-2000.
PD
XX 24-MAR-2000; 2000WO-US08020.
PF
XX 06-APR-1999; 99US-0127958.
PR
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX (NYCE/) NYCE J W.
PA
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
XX trigger adenosine receptors during metabolism, useful e.g. for treating
XX cancers and respiratory obstructions -
XX
XX Claim 14; Page 130; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense

CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.

XX Sequence 17 BP; 0 A; 7 C; 3 G; 7 T; 0 other;

Query Match 100.0%; Score 17; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTCTTC 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 ttccctgggtcttc 17

RESULT 4
A33311 ID A33311 standard; DNA; 17 BP.

XX AC A33311;

DT 28-JUL-2000 (first entry)

XX DE Low adenosine antisense oligonucleotide SEQ ID NO:1000.

XX KM Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antiasthmatic; cycostatic; analgesic; impeded airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX OS Homo sapiens.

XX PN WO200009525-A2.

XX PD 24-FEB-2000.

XX PF 03-AUG-1999; 99WO-US17712.

XX PR 03-AUG-1998; 98US-0095212.

XX PA (UYEC-) UNIV EAST CAROLINA.

XX NYCE JW;

XX WPI; 2000-205971/18.

XX PT New antisense oligonucleotides useful for treating e.g. pulmonary

PT vasoconstriction, inflammation, allergies, asthma, hypertension or

PT bronchitis, emphysema, respiratory distress syndrome, Ischemia or

PS cancers

XX Claim 18; Page 390; 1343pp; English.

CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cycostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A3213 to A3512 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.

XX Sequence 17 BP; 0 A; 7 C; 3 G; 7 T; 0 other;

Query Match 100.0%; Score 17; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTCTTC 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 ttccctgggtcttc 17

RESULT 5

XX C66486/C ID C66486 standard; DNA; 99 BP.

XX AC C66486;

DT 14-FEB-2001 (first entry)

XX DE Chimeric receptor construction oligonucleotide A9000.

XX KM Synthetic signalling molecule; signalling cascade; infection;

XX autoimmune disease; cancer; allergy; congenital disease; ds.

XX OS Synthetic.

XX PN WO200063372-A1.

XX PD 26-OCT-2000.

XX PF 17-APR-2000; 2000WO-GB01456.

XX PR 16-APR-1999; 99GB-0008807.

XX PA (CILT) CELLTech THERAPEUTICS LTD.

```
PI Lawson ADG, Finney HM;
XX
XX WPI: 2000-687176/67.
XX
XX Nucleic acids encoding synthetic signaling molecules comprising two or
PT more sequence blocks having different primary signaling motifs linked
PT in new arrangement, for modulating the level of intracellular signaling
PT
XX
XX Example 1; Fig 4; 74pp; English.
XX
XX The present invention is concerned with a number of synthetic signalling
CC molecules which are made up of at least two sequence blocks (SBS) linked
CC in a non-natural manner. These sequences are based upon the signalling
CC motifs from immunoglobulin tyrosine receptor-based activation motifs
CC (ITAMs). The sequences can be used in the treatment of infectious
CC diseases such as HIV, inflammatory and autoimmune diseases such as
CC rheumatoid arthritis, osteoarthritis and inflammatory bowel disease,
CC cancer, allergic and atopic diseases including asthma and eczema,
CC congenital diseases such as cystic fibrosis and sickle cell anaemia,
CC dermatologic diseases including psoriasis, neurologic diseases such as
CC multiple sclerosis, organ transplant rejection, graft versus host
CC disease and metabolic or idiopathic diseases such as diabetes.
XX
XX Sequence 99 BP; 33 A; 16 C; 25 G; 25 T; 0 other;
SQ

Query Match          100.0%; Score 17; DB 21; Length 99;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGCTTCC 17
   |||||||
Db  90 TTTCCCTGGGCTTCC 74

RESULT 6
C66487
ID C66487 standard; DNA: 99 BP.
XX
XX C66487:
XX
XX 14-FEB-2001 (first entry)
XX
XX Chimaeric receptor construction oligonucleotide A9001.
XX
XX Synthetic signalling molecule; signalling cascade; infection;
XX autoimmune disease; cancer; allergy; congenital disease; ds.
XX
XX Synthetic.
XX
XX WO200063372-A1.
XX
XX 26-OCT-2000.
XX
XX 17-APR-2000; 2000WO-GB01456.
XX
XX 16-APR-1999; 99GB-0008807.
XX
XX (CLLT ) CELLTech THERAPEUTICS LTD.
XX
XX Lawson ADG, Finney HM;
XX
XX WPI: 2000-687176/67.
XX
XX Nucleic acids encoding synthetic signaling molecules comprising two or
PT more sequence blocks having different primary signaling motifs linked
PT in new arrangement, for modulating the level of intracellular signaling
PT
XX
XX Example 1; Fig 4; 74pp; English.
XX
XX The present invention is concerned with a number of synthetic signalling
```

```
CC molecules which are made up of at least two sequence blocks (SBS) linked
CC in a non-natural manner. These sequences are based upon the signalling
CC motifs from immunoglobulin tyrosine receptor-based activation motifs
CC (ITAMs). The sequences can be used in the treatment of infectious
CC diseases such as HIV, inflammatory and autoimmune diseases such as
CC rheumatoid arthritis, osteoarthritis and inflammatory bowel disease,
CC cancer, allergic and atopic diseases including asthma and eczema,
CC congenital diseases such as cystic fibrosis and sickle cell anaemia,
CC dermatologic diseases including psoriasis, neurologic diseases such as
CC multiple sclerosis, organ transplant rejection, graft versus host
CC disease and metabolic or idiopathic diseases such as diabetes.
XX
XX Sequence 99 BP; 25 A; 25 C; 16 G; 33 T; 0 other;
SQ

Query Match          100.0%; Score 17; DB 21; Length 99;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGCTTCC 17
   |||||||
Db  14 ttccctgggtctcc 30

RESULT 7
C68014/C
ID C68014 standard; DNA: 99 BP.
XX
XX C68014:
XX
XX 19-FEB-2001 (first entry)
XX
XX Oligonucleotide A9000 used in sequence block construction.
XX
XX Oligonucleotide library; sequence block; ss.
XX
XX Unidentified.
XX
XX WO200063360-A1.
XX
XX 26-OCT-2000.
XX
XX 17-APR-2000; 2000WO-GB01498.
XX
XX 16-APR-1999; 99GB-0008814.
XX
XX (CLLT ) CELLTech THERAPEUTICS LTD.
XX
XX PI Finney HM, Lawson ADG;
XX
XX WPI: 2000-679595/66.
XX
XX Generating a library of DNA molecules of varying length and sequence in
PT a desired orientation comprises ligating a mixture of double-stranded
PT DNA molecules, and cutting ligated molecules in undesired orientations
PT
XX
XX Example 2; Fig 4; 50pp; English.
XX
XX The present invention relates to a method for generating a library of
CC oligonucleotides of varying length and sequence in a desired orientation.
CC The method comprises ligating a double-stranded oligonucleotide mixture
CC having 5' and 3' ends compatible to each other and corresponding to
CC cleavage products of different but compatible restriction enzymes, and
CC cutting ligated oligonucleotide, such that only molecules that are
CC ligated in undesired orientations are cut, to produce a sequence block.
CC The present sequence is one such oligonucleotide used in the present
CC invention to generate a sequence block.
XX
XX Sequence 99 BP; 33 A; 16 C; 25 G; 25 T; 0 other;
SQ

Query Match          100.0%; Score 17; DB 21; Length 99;
```


XX 14-MAR-2001 (first entry)
 DT Human Ige receptor beta polynucleotide fragment #1694.
 XX
 XX
 DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 XX human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 KW
 OS Homo sapiens.
 XX
 XX WO200062736-A2.
 XX
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NVEC/) NICE J M.
 XX
 PI Nyce JW;
 XX
 DR WPI: 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS
 XX Claim 14; Page 130; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (1) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (1) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cyostatic activities. The antisense oligonucleotides and (1) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. F18434 to F21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 133 BP; 8 A; 37 C; 16 G; 64 T; 8 other:

Query Match 100.0%; Score 17; DB 21; Length 133;

Best Local Similarity 100.0%; Pred. No. 14;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCCTGGGCTTCC 17
 ||||||||||||||||
 Db 1 ttcccttggtcttc 17

RESULT 11
 A34005
 ID A34005 standard; DNA; 133 BP.
 AC A34005;
 DT 28-JUL-2000 (first entry)
 XX
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:1694.
 XX
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 KW
 OS Homo sapiens.
 XX
 XX WO200009525-A2.
 XX
 XX 24-FEB-2000.
 PD
 XX 03-AUG-1999; 99WO-US17712.
 PF
 XX 03-AUG-1998; 98US-0095212.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX
 PI Nyce JW;
 XX
 DR WPI: 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS
 XX Disclosure: Page 475; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cyostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. A33313 to A35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32223 to A33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not

CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.

XX
 SQ Sequence 133 BP; 8 A; 37 C; 16 G; 64 T; 8 other;

Query Match 100.0%; Score 17; DB 21; Length 133;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTCTCC 17
 1 tttcccttggtctctcc 17

RESULT 12
 087807/c
 ID 087807 standard; DNA; 735 BP.

XX 087807;

XX 14-NOV-1995 (first entry)

DE Ige receptor gene.

XX Probe; immunoglobulin; Ige; receptor; beta; allergic disease;
 KW detection; screening; diagnosis; ss.

XX Homo sapiens.

PN EP649910-A.

PD 26-APR-1995.

XX 21-OCT-1994; 94EP-0307751.

PR 22-OCT-1993; 93JP-0265144.

PA (SUME) SUMITOMO ELECTRIC IND CO.

PI Miyabe Y, Nakata M, Osoegawa M, Ra C, Suzuki K;

DR WPI; 1995-156760/21.

PT Probes for mutation(s) in beta chain gene of a high affinity Ige
 PT receptor - for the diagnosis of allergic disease, esp. in
 PT neonate(s)

PS Disclosure; Figures 1 and 2; 17pp; English.

XX DNA probes (See 087799-803) having sequences identical or
 CC complementary to parts of the immunoglobulin E (Ige) receptor, are
 CC used to detect genes associated with allergic disease (diseases
 CC involving mutations in the beta chain gene). They may be used in
 CC neonatal screening, prenatal diagnosis etc. Two primers (087805,
 CC 087806) were used to amplify mRNA in blood samples transcribed from
 CC the Ige receptor gene to produce cDNA. The cDNA is then conjugated
 CC with a probe and an Ige ligand (See 087804) which is immobilised on
 CC a support is then used to bind to probe/Ige receptor gene
 CC conjugates. The probe is then eluted by a gradual rise in
 CC temperature. This sequence is the Ige gene. It was found that
 CC individuals with allergies had one of the following point mutations
 CC in their Ige receptor gene: 173 A-T; 380 T-C; 473 A-C; 543 T-C and
 CC 597 C-T.

XX Sequence 735 BP; 207 A; 149 C; 168 G; 211 T; 0 other;

Query Match 100.0%; Score 17; DB 16; Length 735;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTCTCC 17

DB 712 TTTCCTGGGCTCTCC 696

RESULT 13

ID F20936/c

ID F20936 standard; DNA; 894 BP.

XX F20936;

DT 14-MAR-2001 (first entry)

DE Human high affinity Ige receptor polynucleotide fragment #2503.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiallergic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX Homo sapiens.

PN WO200062736-A2.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US08020.

PR 06-APR-1999; 99US-0127958.

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PI Nyce JW;

DR WPI; 2000-679539/66.

PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 PS Disclosure; Page 138; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),

CC pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. F18434 to F21543 represent human polynucleotide fragments CC and antisense oligonucleotides used in the exemplification of the CC present invention.

CC SQ Sequence 894 BP; 254 A; 184 C; 198 G; 258 T; 0 other:

Query Match 100.0%; Score 17; DB 21; Length 894;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGCTTCC 17
|||||
Db 762 TTTCCCTGGGCTTCC 746

RESULT 14
A34814/C
ID A34814 standard; DNA; 894 BP.

AC A34814;

DT 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide SEQ ID NO:2503.

DE Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiasthmatic; cytosstatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS WO200009525-A2.

PN 24-FEB-2000.

XX 03-AUG-1999; 99WO-US17712.

PD 03-AUG-1998; 98US-0095212.

XX (UYEC-) UNIV EAST CAROLINA.

PA NYCE JW;

PI WPI: 2000-205971/18.

DR New antisense oligonucleotides useful for treating e.g. pulmonary vasospasm, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers -

XX Disclosure: Page 655; 1343pp; English.

PS The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets CC nucleic acids involved in bronchoconstriction, allergies, and/or CC inflammation. The ON can have antiinflammatory, antiasthmatic, antiasthmatic, cytosstatic and analgesic activities. The compositions are CC useful for the treatment of diseases associated with inflammation, CC impaired airways, including lung disease and diseases whose secondary CC effects afflict the lungs of a subject. They can be used for treating CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma, CC impaired respiration, respiratory distress syndrome, pain, cystic CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas, CC carcinomas, and cancers which may metastasize to the lungs, including CC breast and prostate cancer. The reduction of the adenosine content of the

CC ONs reduces side effects. The A-containing ONs break down with the CC release of deoxyadenosine which activates adenosine receptors causing CC bronchoconstriction and inflammation. A32313 to A35312 represent the CC nucleotide sequences given in the sequence listing from the present CC invention, which correspond to SEQ ID NO:1 to 185, and then the last CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323 CC to A33992) are specifically claimed ONs from the present invention. CC N.B. Sequences given in the disclosure of the present invention do not CC match up with their corresponding SEQ ID NO: sequences given in the CC sequence listing.

XX SQ Sequence 894 BP; 254 A; 184 C; 198 G; 258 T; 0 other:

Query Match 100.0%; Score 17; DB 21; Length 894;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGCTTCC 17
|||||
Db 762 TTTCCCTGGGCTTCC 746

RESULT 15
F20842
ID F20842 standard; DNA; 7800 BP.

AC F20842;

DT 14-MAR-2001 (first entry)

XX Human multiple target antisense (MTA) oligonucleotide #2409.

DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosstatic; respiratory obstruction; pulmonary obstruction; impaired respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

XX Homo sapiens.

OS WO200062736-A2.

PN 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

PD 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.

PA NYCE JW;

PI WPI: 2000-679539/66.

DR Low adenosine (A) content antisense oligonucleotides which do not PT trigger adenosine receptors during metabolism, useful e.g. for treating PT cancers and respiratory obstructions -

XX Claim 14; Page 634-636; 1592pp; English.

PS The present invention describes low adenosine (A) content antisense CC oligonucleotides and compositions (I) comprising them. In the antisense CC oligonucleotides the A is replaced by a 'universal' or alternative base. CC (II) can have respiratory, bronchodilator, antiinflammatory, analgesic, CC immunosuppressive, antiasthmatic, hypotensive and cytosstatic activities.

CC The antisense oligonucleotides and (1) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.

CC
 XX
 SQ Sequence 7800 BP; 403 A; 2525 C; 2530 G; 1986 T; 356 other;

Query Match 100.0%; Score 17; DB 21; Length 7800;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 |||
 Db 898 ttcccttggtcttc 914

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3	16	94.1	211	17	AT211672	AT211672 q0912a1.r
4	16	94.1	341	170	BF912247	BF912247 L12-PT007
5	16	94.1	1074	141	BE912438	BE912438 601666054
6	15.4	90.6	165	222	A2500921	A2500921 IM0339102
7	15.4	90.6	180	19	AT329583	AT329583 b6f06ne.r
8	15.4	90.6	190	153	H24592	H24592 y140g07.s1
9	15.4	90.6	212	122	BB001591	BB001591 BB001591
10	15.4	90.6	228	134	BB486354	BB486354 BB486354
11	15.4	90.6	239	2	AA076894	AA076894 7B04G06 C
12	15.4	90.6	278	108	AV079156	AV079156 AV079156
13	15.4	90.6	282	130	BB326864	BB326864 BB326864
14	15.4	90.6	300	160	BB549107	BB549107 BB549107
15	15.4	90.6	306	132	BB403120	BB403120 BB403120
16	15.4	90.6	315	123	BB023191	BB023191 BB023191
17	15.4	90.6	323	129	BB274667	BB274667 BB274667
18	15.4	90.6	335	8	AA493192	AA493192 ne56f08.s

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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19 15.4 90.6 346 8 AA480258
20 15.4 90.6 372 210 AQ709897
21 15.4 90.6 381 158 W83801
22 15.4 90.6 385 103 A1913928
23 15.4 90.6 398 121 AM938392
24 15.4 90.6 406 1 AA000441
25 15.4 90.6 423 158 W17436
26 15.4 90.6 428 156 R68705
27 15.4 90.6 440 232 CNS05LYC
28 15.4 90.6 441 2 AA084870
29 15.4 90.6 467 152 H17254
30 15.4 90.6 482 148 BF433951
31 15.4 90.6 486 222 A2500131
32 15.4 90.6 492 23 A1635680
33 15.4 90.6 507 8 AA480084
34 15.4 90.6 508 149 BF516039
35 15.4 90.6 513 213 AQ934781
36 15.4 90.6 516 167 BE477302
37 15.4 90.6 526 159 Z71886
38 15.4 90.6 529 214 AZ007432
39 15.4 90.6 532 169 BF830671
40 15.4 90.6 552 221 AZ414707
41 15.4 90.6 569 162 BE046325
42 15.4 90.6 570 220 AZ362720
43 15.4 90.6 587 215 AZ077265
44 15.4 90.6 607 230 CNS020VK
45 15.4 90.6 611 206 AQ401361

```

ALIGNMENTS

```

/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site: 1;
EcoRI, Site: 2; EcoRI, Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      112 a      110 c      119 g      108 t
ORIGIN
Query Match      100.0%; Score 17; DB 218; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1      TTTCCCTGGGCTTCC 17
          |||||
Db      66      TTTCCTGGGCTTCC 50

```

```

RESULT 2
LOCUS      BF854137      512 bp      mRNA      EST      16-JAN-2001
DEFINITION MR2-EN0092-261200-001-a12 EN0092 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF854137
VERSION     BF854137.1 GI:12241881
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE 1 (bases 1 to 512)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.

```

```

TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
COMMENT    Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-EN0092-
            261200-001-a12&t3=2000-12-26&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 8
            High quality sequence stop: 511.

```

FEATURES

source

1. 512 location/Qualifiers

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="EN0092"
/dev_stage="Adult"
/notes="Organ: lung,normal; Vector: puc18; Site: 1; SmaI;
Site: 2; SmaI: A mini-library was made by cloning products
derived from ORESNES PCR (U.S. letters patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

FEATURES

source

1. 449 location/Qualifiers

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-14206"

```

```

RESULT 1
LOCUS      AZ265149/c      449 bp      DNA      GSS      26-JUL-2000
DEFINITION RPCI-23-14206.TV RPCI-23 Mus musculus genomic clone RPCI-23-14206.
ACCESSION  AZ265149
VERSION     AZ265149.1 GI:9476954
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 449)
            Zhao,S., Nierman,W., Feiblyum,T., Malek,J., Shatsman,S., Akirret
            ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
            Mouse BAC End Sequences from Library RPCI-23
            Unpublished (1999)
            Other_GSSs: RPCI-23-14206.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 142 row: 0 column: 6
            Seq primer: SP6
            Class: BAC ends.

```

BASE COUNT 171 a 101 c 102 g 138 t
ORIGIN

Query Match 100.0%; Score 17; DB 170; Length 512;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCTGGGCTTCC 17
|||||
DB 298 TTTCCTGGGCTTCC 314

RESULT 3

LOCUS AI211672 211 bp mRNA EST 19-OCT-1998
DEFINITION 90g12a1.r1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Aspergillus nidulans cDNA clone 90g12a1 5', mRNA sequence.

ACCESSION AI211672 GI:3773614
VERSION AI211672
KEYWORDS EST
SOURCE Aspergillus nidulans.
ORGANISM Aspergillus nidulans

REFERENCE 1 (bases 1 to 211)
AUTHORS Kuper, D., Gray, J., Hausner, J., Lai, H., Martin, W., Aramayo, R., Prade, R., and Roe, B.

TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Other ESTs: 90g12a1.f1

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Putative full length read
The vector to vector length is 212
Seq primer: 73.

FEATURES
source location/Qualifiers

1..211
/organism="Aspergillus nidulans"
/strain="FGSC A26"
/db_xref="taxon:5072"
/clone="90g12a1"
/clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library"
/issue_type="vegetative mycelia, asexual structures"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 38 a 73 c 39 g 61 t
ORIGIN

Query Match 94.1%; Score 16; DB 17; Length 211;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTTCCTGGGCTTCC 17
|||||
DB 160 TTTCCTGGGCTTCC 175

RESULT 4
LOCUS BF912247/c 341 bp mRNA EST 18-JAN-2001
DEFINITION IL2-UT0073-131100-245-C03 UT0073 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF912247 GI:12303705
VERSION BF912247.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 341)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. J., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
CONTACT: Simpson A.J.G.
LABORATORY: Laboratory of Cancer Genetics
LUDWIG INSTITUTE FOR CANCER RESEARCH
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LIRC Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?IL2&C2-IL2-UT0073-131100-245-C03&C3-2000-11-13&t4-1)
Seq primer: puc 18 forward
High quality sequence stop: 340.

FEATURES
source location/Qualifiers

1..341
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UT0073"
/dev_stage="Adult"
/note="Organ: uterus; tumor: Vector: puc18; site_1: SmaI; site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (O.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 111 a 61 c 71 g 98 t
ORIGIN

Query Match 94.1%; Score 16; DB 170; Length 341;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTTCCTGGGCTTCC 17
|||||
DB 48 TTTCCTGGGCTTCC 33

RESULT 5
LOCUS BE912438/c 1074 bp mRNA EST 29-SEP-2000
DEFINITION 60166054F1 NC1_CGAP_Maml Mus musculus cDNA clone IMAGE:3966109 5', mRNA sequence.
ACCESSION BE912438 GI:10409425
VERSION BE912438
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1074)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM9138 row: 1 column: 14
High quality sequence stop: 633.
Location/Qualifiers
1. 1074
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3966109"
/clone.lib="NCI CGAP Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: Salt; Site_2: Not; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 244 a 319 c 343 g 168 t
ORIGIN

Query Match 94.1%; Score 16; DB 141; Length 1074;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTTCCTGGGCTTCC 17
|||||
Db 840 TTCCCTGGGCTTCC 825

RESULT 6
AZ500921 165 bp DNA GSS 05-OCT-2000
LOCUS 1M0339102R Mouse 10kb plasmid UGCLM library Mus musculus genomic
DEFINITION clone UGCLM0339102 R, DNA sequence.
ACCESSION AZ500921
VERSION AZ500921.1 GI:10682237
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 165)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0338 row: 1 column: 02
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 165.

FEATURES
source Location/Qualifiers
1. 165
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0339102"
/clone.lib="Mouse 10kb plasmid UGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-gold, M1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 38 a 26 c 39 g 62 t
ORIGIN

Query Match 90.6%; Score 15.4; DB 222; Length 165;
Best Local Similarity 94.1%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCCTGGGCTTCC 17
|||||
Db 22 TTTCCTGGGCTTCC 38

RESULT 7
AI329583 180 bp mRNA EST 28-DEC-1998
LOCUS b6f06ne.r1 Neurospora crassa evening CDNA library Neurospora crassa
DEFINITION CDNA clone b6f06ne 3', mRNA sequence.
ACCESSION AI329583
VERSION AI329583.1 GI:4066142
KEYWORDS EST.
SOURCE Neurospora crassa.
ORGANISM Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
1 (bases 1 to 180)
Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.
Two Neurospora crassa EST Databases
Unpublished (1998)
Other_ESTS: b6f06ne.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Seq primer: Universal Reverse Primer
High quality sequence stop: 171.
Location/Qualifiers
1. 180
/organism="Neurospora crassa"
/strain="Strain 30-7 (bd, A)"

```

/db_xref="taxon:5141"
/clone="b6f06ne"
/clone_lib="Neurospora crassa evening cDNA library"
/linkage_type="cDNA harvested following 22hr growth in dark"
/note="Vector: pBluescript SK-; Site.1: XbaI; Site.2: EcoRI; See: Bell-Pedersen,D., et al., PNAS 93:13096, 1996. 5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI site of pBluescript"
BASE COUNT      38 a      48 c      31 g      63 t
ORIGIN
Query Match      90.6%; Score 15.4; DB 19; Length 180;
Best Local Similarity 94.1%; Pred. No. 1,5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Oy 1 TTATCCCTGAGCTTCC 17
      ||| ||||| |||||
Db 65 TTATCCCTGAGCTTTC 81

RESULT 8
H24592/c
LOCUS
DEFINITION
H24592 190 bp mRNA EST 07-JUL-1995
Y110g07.s1 Soares breast 3MDHbSt Homo sapiens cDNA clone
IMAGE:160764 3' similar to gb:U07548 AMINOACYLASE-1 (HUMAN);, mRNA
sequence.
H24592
H24592.1 GI:893491
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 190)
AUTHORS
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maitra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1577
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1577 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers
1..190
/organism="Homo sapiens"
/db_xref="CDB:574837"
/db_xref="taxon:9606"
/clone="IMAGE:160764"
/clone_lib="Soares breast 3MDHbSt"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: breast; Vector: PT73D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5
TGTTACCAATCTGAAGTGGAGGCGGCCCTTTTCTTTTCTTTTCTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors

```

(Pharmacelia), digested with Not I and cloned into the Not and Eco RI sites of a modified pUT73 vector (Pharmacelia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Patima Bonaïdo."

Query Match 90.6%; Score 15.4; DB 153; Length 190;
 Best Local Similarity 94.1%; Pred. No. 1.5e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGGCTTCC 17
 |||||
 Db 47 TTTCCCTGGGGCTTCC 31

RESULT 9
 LOCUS BB001591 212 bp mRNA EST 22-JUN-2000
 DEFINITION BB001591 RIKEN full-length enriched, 14, 17 days embryo head Mus
 musculus cDNA clone 3201002K04 3', mRNA sequence.
 ACCESSION BB001591
 VERSION BB001591.1 GI:7841519
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 212)
 Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arikawa, T., Carninci
 , P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
 Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
 Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
 Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
 , Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
 Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya
 , T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
 , M., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Kono, H., et al.)
 Unpublished (2000)
 TITLE Genome Exploration Research Group, Life Science Tsukuba Center,
 JOURNAL Genome Science Laboratory
 COMMENT The Institute of Physical and Chemical Research (RIKEN), Genomic
 Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: +81-298-36-9093
 Fax: +81-298-36-9098
 Email: genome-res@rtc.riken.go.jp,
 URL: http://genome.rtc.riken.go.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
 , N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermoactivation of the chromatinase enzymes
 by trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2): 520-524 (1998)
 Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
 , Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5): 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.
 Location/Qualifiers
 1..212 /organism="Mus musculus"

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3201002K04"
/clone_lib="RIKEN full-length enriched, 14, 17 days embryo
head"
/sex="mixed"
/tissue_type="head"
/dev_stage="14, 17 days embryo"
/lab_host="DH10B"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGACGAGACGATCCAGACCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGACGAGATTCGAGTTAATTAATTAATCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I"

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BASE COUNT      57 a      47 c      37 g      71 t
ORIGIN
Query Match      90.6%; Score 15.4; DB 122; Length 212;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 TTTCCTCCGCTCTCC 17
      11111111111111111111
Db      43 TTTCCTCCGCTCTCC 59

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RESULT 10
LOCUS      BB486354      228 bp      mRNA      EST      23-JUL-2000
DEFINITION BB486354 RIKEN full-length enriched, 13 days embryo lung Mus
ACCESSION  BB486354
VERSION     BB486354.1 GI:9403963
KEYWORDS
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 228)

```

```

REFERENCE
AUTHORS      Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koyu,S., Kurihara,C., Kusabe,M.,
Katsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,
Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suganara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya,
T., Tsunoda,Y., Watabiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098

```

```

Email: genome-res@rtc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermolabile enzymes by
thermostabilization and thermoactivation of the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.

```

FEATURES

source

```

Location/Qualifiers
1..228
/organism="Mus musculus"
/db_xref="taxon:10090"
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lung"
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/lab_host="DH10B"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGACGAGACGCGCCGACCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGACGAGATTCGAGTTAATTAATTAATCCCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."

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BASE COUNT

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60 a      61 c      49 g      58 t

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Query Match      90.6%; Score 15.4; DB 134; Length 228;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 TTTCCTCCGCTCTCC 17
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Db      84 TTTCCTCCGCTCTCC 100

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RESULT 11
LOCUS      AA076894      239 bp      mRNA      EST      24-SEP-1999
DEFINITION 7B04G06 Chromosome 7 Fetal Brain cDNA library Homo sapiens cDNA
clone 7B04G06, mRNA sequence.
ACCESSION  AA076894
VERSION     AA076894.1 GI:1836368
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 239)

```

```

REFERENCE
AUTHORS      Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L.,
Robbins,C.M., Nussbaum,J.C., Lovett,M. and Green,E.D.
2006 expressed-sequence tags derived from human chromosome
7-enriched cDNA libraries
Genome Res. 7 (3), 281-292 (1997)
JOURNAL

```

```

MEDLINE      97228905
COMMENT      Contact: Eric D. Green
              Genome Technology Branch
              National Human Genome Research Institute/NIH
              49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
              Tel: 3014020201
              Fax: 3014024735
              Email: egreen@hgrl.nih.gov
              Plate: 04 row: G column: 06
              Seq primer: 21M13 (ABI)

FEATURES
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      /db_xref="taxon:9606"
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      /dev_stage="pool of 9 week and 12 week"
      /lab_host="E. coli strain DH5 alpha"
      /note="Organ: brain; Vector: pAMP10; cDNA was generated
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      hexamers and oligo(dT). From this pool of cDNA, human
      chromosome 7-enriched cDNA was isolated by direct cDNA
      selection using chromosome 7 genomic DNA (cosmids). The
      resulting direct-selected cDNA was cloned into a plasmid
      vector using a non-directional uracil DNA glycosylase (UDG
      )-mediated cloning strategy."

BASE COUNT   54 a      57 c      52 g      72 t      4 others
ORIGIN
Query Match      90.6%; Score 15.4; DB 2; Length 239;
Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 12
LOCUS      AV079156      278 bp      mRNA      EST      24-JUN-1999
DEFINITION AV079156 Mus musculus stomach C57BL/6J adult Mus musculus cDNA
ACCESSION  AV079156
VERSION     AV079156.1 GI:5198984
KEYWORDS
SOURCE
  ORGANISM  Mus musculus
            house mouse.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
            1 (bases 1 to 278)
            Carinini,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Alawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Nitsuna,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y., Tomioka,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
            RIKEN Mouse ESTs
            Unpublished (1999)
TITLE
JOURNAL
COMMENT
  3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan
  Tel: 81-298-36-9145
  Fax: 81-298-36-9098
  Email: genome-res@rc.riken.go.jp
  Thermostabilization and thermoactivation of thermostable enzymes by
  trehalose and its application for the synthesis of full length cDNA

```

```

(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.

FEATURES
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      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="2210408C21"
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Best Local Similarity 94.1%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      46 TTTCCCTGCGTCTTCC 62

RESULT 13
LOCUS      BB326864      282 bp      mRNA      EST      11-JUL-2000
DEFINITION BB326864 RIKEN full-length enriched, 4 days neonate male adipose
            Mus musculus cDNA clone B430212N18.3' similar to AF093671 Mus
            musculus peroxisomal biogenesis factor (Pex11b) mRNA, mRNA
            sequence.
            BB326864
            BB326864.1 GI:9035627
            EST.
            SOURCE
            house mouse.
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 282)
            Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carinini
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kado,C., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
            Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomioka,N., Toya
            T., Tsunoda,Y., Watanabe,S., Watanabe,S., Yamamura,T., Yamana,I.,
            Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            M., Muramatsu,M. and Hayashizaki,Y.
            RIKEN Mouse ESTs (Konno,H., et al.)
            Unpublished (2000)
TITLE
JOURNAL
COMMENT
  3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan
  Tel: 81-298-36-9013
  Fax: 81-298-36-9098
  Email: genome-res@rc.riken.go.jp,
  URL: http://genome.rtc.riken.go.jp/
  Carinini,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S., Sasaki
  N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  Thermostabilization and thermoactivation of thermostable enzymes by
  trehalose and its application for the synthesis of full length
  cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
  Itoh,M., Kitsumi,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

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11

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:25 ; Search time 280.46 Seconds
(without alignments)
10.583 Million cell updates/sec

Title: US-09-016-464-9
Perfect score: 17
Sequence: 1 TTTCCTCGGCTTCC 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfillseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	17	100.0	11298	1	US-08-201-879A-2
3	17	100.0	11298	4	US-09-103-663-31
4	16	94.1	7452	3	US-08-592-500-1
5	16	94.1	7452	3	US-08-195-006-1
6	16	94.1	7452	5	PCT-US94-07644A-1
7	14.4	84.7	1092	2	US-08-967-101-150
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11	14.4	84.7	1092	4	US-09-127-480-150
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21	14.4	84.7	1342	4	US-09-372-498-1
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23	14.4	84.7	1488	3	US-08-670-964-3
24	14.4	84.7	1750	3	US-08-670-964-1
25	14.4	84.7	1762	3	US-08-670-964-1
26	14.4	84.7	1914	2	US-08-670-964-1
27	14.4	84.7	2764	3	US-08-923-454A-9

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29	14.4	84.7	2791	2	US-08-967-101-1	Sequence 1, Appli
30	14.4	84.7	2791	2	US-08-967-101-133	Sequence 133, App
31	14.4	84.7	2791	2	US-08-592-541-1	Sequence 1, Appli
32	14.4	84.7	2791	2	US-08-592-541-133	Sequence 133, App
33	14.4	84.7	2791	4	US-09-124-698-1	Sequence 1, Appli
34	14.4	84.7	2791	4	US-09-124-698-133	Sequence 133, App
35	14.4	84.7	2791	4	US-09-127-480-1	Sequence 1, Appli
36	14.4	84.7	2791	4	US-09-127-480-133	Sequence 133, App
37	14.4	84.7	2791	4	US-08-496-841C-1	Sequence 1, Appli
38	14.4	84.7	2792	4	US-08-496-841C-133	Sequence 133, App
39	14.4	84.7	3086	3	US-08-888-077A-3	Sequence 3, Appli
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42	14.4	84.7	3087	4	US-09-124-698-5	Sequence 5, Appli
43	14.4	84.7	3087	4	US-09-127-480-5	Sequence 5, Appli
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45	13.8	81.2	206	1	US-08-480-552-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-07-869-933-31/C
; Sequence 31, Application us/07869933
; Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11298 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: homo sapien
STRAIN: FCRI beta
US-07-869-933-31

Query Match 100.0%; Score 17; DB 1; Length 11298;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCTGGGCTTCC 17
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Db 7299 TTTCCTGGGCTTCC 7283

RESULT 2

US-08-201-879A-2/C
; Sequence 2, Application US/08201879A
; Patent No. 5807988
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; APPLICANT: JOUVIN, Marie-Helene
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,879A
; FILING DATE: 24-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/869,933
; FILING DATE: 16-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03419
; FILING DATE: 16-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/234/NIND
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11298 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: FcRI beta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(456..511, 1381..1510, 2026..2160, 4475..4531,
; LOCATION: 5079..5237, 5640..5738, 7224..7319)
; US-08-201-879A-2

Query Match 100.0%; Score 17; DB 1; Length 11298;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 7299 TTTCCTGGGCTTCC 7283

RESULT 3
US-09-103-663-31/c

; Sequence 31, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 31
; LENGTH: 11298
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-103-663-31

Query Match 100.0%; Score 17; DB 4; Length 11298;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCTGGGCTTCC 17
|||||
Db 7299 TTTCCTGGGCTTCC 7283

RESULT 4

US-08-592-500-1/C
; Sequence 1, Application US/08592500
; Patent No. 6005089
; GENERAL INFORMATION:
; APPLICANT: Lanza, Francois
; APPLICANT: Phillips, David R.
; APPLICANT: Cazenave, Jean-Pierre
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,500
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

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ORIGINAL SOURCE:
FEATURE: ORGANISM: Homo sapiens
NAME/KEY: Intron
LOCATION: 1462..2419
FEATURE:
NAME/KEY: CDS
LOCATION: 2422..4101
FEATURE:
NAME/KEY: misc_signal
LOCATION: 68..76
OTHER INFORMATION: /function= "Putative TPA responsive
OTHER INFORMATION: element"
FEATURE:
NAME/KEY: misc_signal
LOCATION: 471..478
OTHER INFORMATION: /function= "Ets-1 cis-acting
OTHER INFORMATION: sequence"
FEATURE:
NAME/KEY: misc_signal
LOCATION: 493..502
OTHER INFORMATION: /function= "Ets-1 cis-acting
OTHER INFORMATION: sequence"
FEATURE:
NAME/KEY: repeat_region
LOCATION: 593..881
OTHER INFORMATION: /rpt_type= "other"
OTHER INFORMATION: /label= Alu
FEATURE:
NAME/KEY: misc_signal
LOCATION: 897..904
OTHER INFORMATION: /function= "Ets-1 cis-acting
OTHER INFORMATION: sequence"
FEATURE:
NAME/KEY: misc_biding
LOCATION: 1142..1149
OTHER INFORMATION: /function= "Spi binding site"
OTHER INFORMATION: /standard_name= "Spi"
FEATURE:
NAME/KEY: misc_signal
LOCATION: 1178..1184
OTHER INFORMATION: /function= "Ets-1 cis-acting
OTHER INFORMATION: sequences"
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 1199..1203
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 1263..1269
FEATURE:
NAME/KEY: misc_biding
LOCATION: 1285..1289
OTHER INFORMATION: /function= "GATA-1 binding site"
FEATURE:
NAME/KEY: misc_biding
LOCATION: 1321..1326
OTHER INFORMATION: /function= "GATA-1 binding site"
FEATURE:
NAME/KEY: misc_signal
LOCATION: 1365..1372
OTHER INFORMATION: /function= "Ets-1 cis-acting
OTHER INFORMATION: sequences"
FEATURE:
NAME/KEY: repeat_region
LOCATION: 6133..6440
OTHER INFORMATION: /rpt_type= "other"
OTHER INFORMATION: /label= Alu

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FEATURE:
NAME/KEY: misc_signal
LOCATION: 5610..5615
OTHER INFORMATION: /standard_name= "Polyadenylation
OTHER INFORMATION: signal sequence"
FEATURE:
NAME/KEY: misc_signal
LOCATION: 6966..6971
OTHER INFORMATION: /standard_name= "Polyadenylation
OTHER INFORMATION: signal sequence"
FEATURE:
NAME/KEY: misc_signal
LOCATION: 7224..7229
OTHER INFORMATION: /standard_name= "Polyadenylation
OTHER INFORMATION: signal sequence"
FEATURE:
NAME/KEY: misc_signal
LOCATION: 7358..7363
OTHER INFORMATION: /standard_name= "Polyadenylation
OTHER INFORMATION: signal sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..7452
OTHER INFORMATION: /standard_name= "Nucleotide
OTHER INFORMATION: sequence containing the human GPy gene"
US-08-592-500-1

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Query Match          94.18; Score 16; DB 3; Length 7452;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2  TTCCCTGGGCTTCC 17
Db      1125 TTCCCTGGGCTTCC 1110

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RESULT      5
US-08-195-006-1/c
; Sequence 1, Application US/08195006
; Patent No. 6083688
; GENERAL INFORMATION:
; APPLICANT: Ianza, Francois
; APPLICANT: Phillips, David R.
; APPLICANT: Cazenave, Jean-Pierre
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,006
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422

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	1	INFORMATION FOR SEQ ID NO: 1:
	2	SEQUENCE CHARACTERISTICS:
	3	LENGTH: 7452 base pairs
	4	TYPE: nucleic acid
	5	STRANDEDNESS: single
	6	TOPOLOGY: linear
	7	MOLECULE TYPE: DNA (genomic)
	8	ORIGINAL SOURCE:
	9	ORGANISM: Homo sapiens
	10	FEATURE:
	11	NAME/KEY: Intron
	12	LOCATION: 1462..2419
	13	FEATURE:
	14	NAME/KEY: CDS
	15	LOCATION: 2422..4101
	16	FEATURE:
	17	NAME/KEY: misc_signal
	18	LOCATION: 68..76
	19	OTHER INFORMATION: /function= "Purified TPA responsive"
	20	OTHER INFORMATION: element"
	21	OTHER INFORMATION: /label= TRE
	22	FEATURE:
	23	NAME/KEY: misc_signal
	24	LOCATION: 471..478
	25	OTHER INFORMATION: /function= "Ets-1 cis-acting
	26	OTHER INFORMATION: sequence"
	27	OTHER INFORMATION: /label= Ets-1
	28	FEATURE:
	29	NAME/KEY: misc_signal
	30	LOCATION: 493..502
	31	OTHER INFORMATION: /function= "Ets-1 cis-acting
	32	OTHER INFORMATION: sequence"
	33	OTHER INFORMATION: /label= Ets-1
	34	FEATURE:
	35	NAME/KEY: repeat_region
	36	LOCATION: 593..881
	37	OTHER INFORMATION: /rpl_type= "other"
	38	OTHER INFORMATION: /label= Alu
	39	FEATURE:
	40	NAME/KEY: misc_signal
	41	LOCATION: 897..904
	42	OTHER INFORMATION: /function= "Ets-1 cis-acting
	43	OTHER INFORMATION: sequence"
	44	OTHER INFORMATION: /label= Ets-1
	45	FEATURE:
	46	NAME/KEY: misc_binding
	47	LOCATION: 1142..1149
	48	OTHER INFORMATION: /function= "Sp1 binding site"
	49	OTHER INFORMATION: /standard_name= "Sp1"
	50	FEATURE:
	51	NAME/KEY: misc_signal
	52	LOCATION: 1178..1184
	53	OTHER INFORMATION: /function= "Ets-1 cis-acting
	54	OTHER INFORMATION: sequences"
	55	OTHER INFORMATION: /label= Ets-1
	56	FEATURE:
	57	NAME/KEY: TATA_signal
	58	LOCATION: 1199..1203
	59	FEATURE:
	60	NAME/KEY: TATA_signal
	61	LOCATION: 1263..1269
	62	FEATURE:
	63	NAME/KEY: misc_binding
	64	LOCATION: 1285..1289
	65	OTHER INFORMATION: /function= "GATTA-1 binding site"
	66	FEATURE:
	67	NAME/KEY: misc_binding
	68	LOCATION: 1321..1326
	69	OTHER INFORMATION: /function= "GATTA-1 binding site"
	70	FEATURE:
	71	NAME/KEY: misc_signal
	72	LOCATION: 1365..1372
	73	OTHER INFORMATION: /function= "Ets-1 cis-acting

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OTHER INFORMATION: sequences"
OTHER INFORMATION: /label= Ets-1
FEATURE:
NAME/KEY: repeat_region
LOCATION: 6133..6440
OTHER INFORMATION: /rpt_type= "other"
OTHER INFORMATION: /label= Alu
FEATURE:
NAME/KEY: misc_signal
LOCATION: 5610..5615
OTHER INFORMATION: /standard_name= "Polyadenylation"
OTHER INFORMATION: signal sequence"
FEATURE:
NAME/KEY: misc_signal
LOCATION: 6966..6971
OTHER INFORMATION: /standard_name= "Polyadenylation"
OTHER INFORMATION: signal sequence"
FEATURE:
NAME/KEY: misc_signal
LOCATION: 7224..7229
OTHER INFORMATION: /standard_name= "Polyadenylation"
OTHER INFORMATION: signal sequence"
FEATURE:
NAME/KEY: misc_signal
LOCATION: 7358..7363
OTHER INFORMATION: /standard_name= "Polyadenylation"
OTHER INFORMATION: signal sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..7452
OTHER INFORMATION: /standard_name= "Nucleotide"
OTHER INFORMATION: sequence containing the human GFY gene"
US-08-195-006-1

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Query Match	94.18;	Score 16;	DB 3;	Length 7452;
Best Local Similarity	100.08;	Pred. No. 13;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2	TTCCCTGGGCTCTCC	17
Db	1125	TTCCCTGGGCTCTCC	1110

RESULT 6
PCT-US94-07644A-1/c
Sequence 1, Application PC/TUS9407644A
GENERAL INFORMATION:
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07644A
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 012418-003000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1462..2419
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2422..4101
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 68..76
; OTHER INFORMATION: /function= "Pulitive TPA responsive
; OTHER INFORMATION: element"
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 471..478
; OTHER INFORMATION: /function= "Ets-1 cis-acting
; OTHER INFORMATION: sequence"
; OTHER INFORMATION: /label= Ets-1
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 493..502
; OTHER INFORMATION: /function= "Ets-1 cis-acting
; OTHER INFORMATION: sequence"
; OTHER INFORMATION: /label= Ets-1
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 593..881
; OTHER INFORMATION: /rpt_type= "other"
; OTHER INFORMATION: /label= Alu
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 897..904
; OTHER INFORMATION: /function= "Ets-1 cis-acting
; OTHER INFORMATION: sequence"
; OTHER INFORMATION: /label= Ets-1
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1142..1149
; OTHER INFORMATION: /function= "Spl binding site"
; OTHER INFORMATION: /standard_name= "Spl"
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 1178..1184
; OTHER INFORMATION: /function= "Ets-1 cis-acting
; OTHER INFORMATION: sequences"
; OTHER INFORMATION: /label= Ets-1
; FEATURE:
; NAME/KEY: TATA_signal
; LOCATION: 1199..1203
; FEATURE:
; NAME/KEY: TATA_signal
; LOCATION: 1263..1269
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1285..1289
; OTHER INFORMATION: /function= "GATA-1 binding site"
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1321..1326
; OTHER INFORMATION: /function= "GATA-1 binding site"
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 1365..1372
; OTHER INFORMATION: /function= "Ets-1 cis-acting

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; OTHER INFORMATION: sequences"
; OTHER INFORMATION: /label= Ets-1
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 6133..6440
; OTHER INFORMATION: /rpt_type= "other"
; OTHER INFORMATION: /label= Alu
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 5610..5615
; OTHER INFORMATION: /standard_name= "Polyadenylation
; OTHER INFORMATION: signal sequence"
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 6966..6971
; OTHER INFORMATION: /standard_name= "Polyadenylation
; OTHER INFORMATION: signal sequence"
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 7224..7229
; OTHER INFORMATION: /standard_name= "Polyadenylation
; OTHER INFORMATION: signal sequence"
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: 7358..7363
; OTHER INFORMATION: /standard_name= "Polyadenylation
; OTHER INFORMATION: signal sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..7452
; OTHER INFORMATION: /standard_name= "Nucleotide
; OTHER INFORMATION: sequence containing the human GYV gene"
; PCT-US94-07644A-1

Query Match          94.1%; Score 16; DB 5; Length 7452;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TTCCCTGGGCTCTCC 17
Db      1125 TTCCCTGGGCTCTCC 1110

RESULT      7
US-08-967-101-150/c
; Sequence 150, Application US/08967101
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROWMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,101
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541

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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 1092 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-967-101-150

Query Match 84.7%; Score 14.4; DB 2; Length 1092;
Best Local Similarity 93.8%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGCTTC 16
DB 624 TTTCCCTGGGCTTC 609

RESULT 8

US-08-592-541-150/c
Sequence 150, Application US/08592541
Patent No. 5960054

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 1092 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-592-541-150

Query Match 84.7%; Score 14.4; DB 2; Length 1092;
Best Local Similarity 93.8%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGCTTC 16
DB 624 TTTCCCTGGGCTTC 609

DB 624 TTTCCCTGGGCTTC 609

RESULT 9

US-08-888-077A-13/c
Sequence 13, Application US/08888077A
Patent No. 6020143

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLTZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
CITY: WESTFIELD
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/888,077A

FILING DATE: 03-JUL-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/592,541

FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: PALISI, THOMAS M

REGISTRATION NUMBER: 36,629

REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 654-5000

TELEFAX: (908) 654-7866

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 1092 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: misc.feature

LOCATION: 1..1092

OTHER INFORMATION: /note="1ex11"

US-08-888-077A-13

Query Match 84.7%; Score 14.4; DB 3; Length 1092;
Best Local Similarity 93.8%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGCTTC 16
DB 624 TTTCCCTGGGCTTC 609

RESULT 10

US-09-124-698-150/c

Sequence 150, Application US/09124698
Patent No. 6117978

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMENS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 183

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
;; STREET: High Street Tower - 125 High Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: U.S.A.
;; ZIP: 02110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/124,698
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/592,541
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pitcher, Edmund R.
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 150:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1092 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; US-09-124-698-150

Query Match 84.7%; Score 14.4; DB 4; Length 1092;
Best Local Similarity 93.8%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCCTGCTGCTTC 16
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Db 624 TTTCCTGCTGCTTC 609

RESULT 11
US-09-127-480-150/c
; Sequence 150, Application US/09127480
; Patent No. 6194153
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,480
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pitcher, Edmund R.
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 150:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1092 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; US-09-127-480-150

Query Match 84.7%; Score 14.4; DB 4; Length 1092;
Best Local Similarity 93.8%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCCTGCTGCTTC 16
||||| |||||||||
Db 624 TTTCCTGCTGCTTC 609

RESULT 12
US-08-496-841C-150/c
; Sequence 150, Application US/08496841C
; Patent No. 6210919
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,841C
; FILING DATE: 28-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul F. Fehlner, Ph.D.
; REGISTRATION NUMBER: 35,135
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1092 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 150:
US-08-496-841C-150

Query Match 84.7%; Score 14.4; DB 4; Length 1092;
Best Local Similarity 93.8%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTTCCTGCTGCTTC 16

; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
US-08-491-988-27

Query Match 84.7%; Score 14.4; DB 2; Length 1202;
Best Local Similarity 93.8%; Pred. No. 66;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 932 TTTCCTGCTCTTC 917

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Job time: 9664 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
7.928 Million cell updates/sec

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Sequence: 1 TTTCCTGCTTCC 17

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Gapop 10.0 , Gapext 1.0

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26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	US-08-474-497-9	Sequence 9, Appli
2	17	100.0	17	US-09-016-464-9	Sequence 9, Appli
3	17	100.0	17	US-09-509-152A-1000	Sequence 1000, Ap
4	17	100.0	133	US-09-509-152A-1694	Sequence 1694, Ap
5	17	100.0	434	US-09-637-888-6267	Sequence 6267, Ap
6	17	100.0	565	US-09-540-229-130511	Sequence 130511,
7	17	100.0	735	US-08-326-514-18	Sequence 18, Appl
8	17	100.0	735	US-08-326-514-19	Sequence 19, Appl
9	17	100.0	735	US-08-326-514-20	Sequence 20, Appl
10	17	100.0	7800	US-09-509-152A-2409	Sequence 2409, Ap
11	17	100.0	11298	US-08-201-873-2	Sequence 2, Appli
12	17	100.0	11298	US-09-103-663-31	Sequence 31, Appli
13	16	94.1	433	US-60-197-873-1456	Sequence 41456, A
14	16	94.1	507	US-09-398-253-953	Sequence 953, App
15	16	94.1	1842	PCT-US00-07506-21	Sequence 21, Appl
16	16	94.1	7452	US-08-884-571-1	Sequence 92, Appli
17	16	94.1	7452	US-09-365-164-92	Sequence 1, Appli
18	16	94.1	7452	US-09-775-803-13	Sequence 13, Appli
19	16	94.1	7452	US-09-560-814-1	Sequence 1400, Ap
20	16	94.1	21393	PCT-US01-01324-4400	Sequence 1340, Ap
21	16	94.1	30377	US-60-226-176-1340	Sequence 1340, Ap
22	16	94.1	30377	US-60-233-468-1340	Sequence 7728, Ap
23	16	94.1	241	US-60-208-063-7728	Sequence 63070, A
24	15.4	90.6	287	US-60-211-750-69070	Sequence 340, App
25	15.4	90.6	309	US-09-128-809-340	Sequence 2422, Ap
26	15.4	90.6	309	US-09-539-813-2422	Sequence 8596, Ap
27	15.4	90.6	348	US-60-217-080-8596	Sequence 9364, Ap
28	15.4	90.6	352	US-60-172-375-9364	Sequence 29131, A
29	15.4	90.6	372	US-09-359-067-29131	Sequence 4803, App
30	15.4	90.6	382	US-09-474-436-4803	Sequence 528, App
31	15.4	90.6	384	US-60-208-063-528	Sequence 7981, Ap
32	15.4	90.6	394	US-09-354-899-7981	Sequence 2577, Ap
33	15.4	90.6	395	US-09-574-454-2577	Sequence 7559, Ap
34	15.4	90.6	395	US-09-519-705-2577	Sequence 2397, App
35	15.4	90.6	405	US-09-474-436-7959	Sequence 1816, A
36	15.4	90.6	409	US-09-652-123-2997	Sequence 9503, Ap
37	15.4	90.6	421	US-09-287-618-1816	Sequence 1383, Ap
38	15.4	90.6	422	US-09-698-010-9503	Sequence 650, App
39	15.4	90.6	442	US-09-189-835-1383	Sequence 9700, Ap
40	15.4	90.6	442	US-09-189-835-1383	Sequence 1725, Ap
41	15.4	90.6	442	US-09-189-835-1383	
42	15.4	90.6	449	US-09-667-547-650	
43	15.4	90.6	449	US-09-667-547-650	
44	15.4	90.6	456	US-09-431-517-9700	
45	15.4	90.6	461	US-08-346-731-1725	

ALIGNMENTS

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RESULT 1
US-08-474-497-9
; Sequence 9, Application US/08474497
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,497
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-497-9

Query Match      100.0% Score 17; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTCTCC 17
    |||||
DB 1 TTTCCTGGGCTCTCC 17

RESULT 2
US-09-016-464-9
; Sequence 9, Application US/09016464
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,464
FILING DATE: 30-Jan-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,497
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-016-464-9

Query Match      100.0% Score 17; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTCTCC 17
    |||||
DB 1 TTTCCTGGGCTCTCC 17

RESULT 3
US-09-509-152A-1000
; Sequence 1000, Application US/09509152A
; GENERAL INFORMATION:
; APPLICANT: NYCE, JONATHAN W.
; TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
; FORMULATIONS, KITS & APPLICATIONS
; NUMBER OF SEQUENCES: 2419
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 CLARKE DRIVE
; CITY: CRANBURY
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/509,152A
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,160
; FILING DATE: 1997-09-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 1000:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1000:
US-09-509-152A-1000

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCCTGGGCTCTCC 17
|||||
Db 1 TTTCCCTGGGCTCTCC 17

RESULT 4

US-09-509-152A-1694

Sequence 1694, Application US/09509152A

GENERAL INFORMATION:

APPLICANT: NICE, JONATHAN W.

TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION

FORMULATIONS, KITS & APPLICATIONS

NUMBER OF SEQUENCES: 2419

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 CLARKE DRIVE

CITY: CRANBURY

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/509,152A

FILING DATE: 17-Mar-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/059,160

FILING DATE: 1997-09-17

ATTORNEY/AGENT INFORMATION:

NAME: AMZEL, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-00991

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1694:

SEQUENCE CHARACTERISTICS:

LENGTH: 133 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1694:

US-09-509-152A-1694

Query Match 100.0%; Score 17; DB 19; Length 133;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCCTGGGCTCTCC 17
|||||
Db 1 TTTCCCTGGGCTCTCC 17

RESULT 5

US-09-637-888-6267/c

Sequence 6267, Application US/09637888

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A. J.

APPLICANT: Gearing, David P.

APPLICANT: Kingsbury, Gillian A.

APPLICANT: Holzman, Douglas A.

APPLICANT: Welch, Nadine S.

APPLICANT: Fraser, Christopher C.

APPLICANT: Villevial, Jean-Luc M.G.

APPLICANT: Goodearl, Andrew

APPLICANT: Silos-Santiago, Immaculada

APPLICANT: Pan, Yang

APPLICANT: White, David

APPLICANT: Hodge, Martin

TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 1600.1155-001

CURRENT APPLICATION NUMBER: US/09/637,888

CURRENT FILING DATE: 2000-08-06

PRIOR APPLICATION NUMBER: 60/147,937

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 10569

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6267

LENGTH: 434

TYPE: DNA

ORGANISM: Homo sapiens

US-09-637-888-6267

Query Match 100.0%; Score 17; DB 24; Length 434;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCCTGGGCTCTCC 17
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Db 29 TTTCCCTGGGCTCTCC 13

RESULT 6

US-09-540-229-130511/c

Sequence 130511, Application US/09540229

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.

APPLICANT: Deleagane, Angelo M.

APPLICANT: Stuart, Susan G.

APPLICANT: Stuve, Laura L.

APPLICANT: Mullahy, Sara J.

APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS

FILE REFERENCE: PD-1033 CIP

CURRENT APPLICATION NUMBER: US/09/540,229

CURRENT FILING DATE: 2000-03-31

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 193582

SOFTWARE: PERL Program

SEQ ID NO 130511

LENGTH: 565

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc. feature

OTHER INFORMATION: Incyte ID No: hu01208122

US-09-540-229-130511

Query Match 100.0%; Score 17; DB 21; Length 565;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCCTGGGCTCTCC 17
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Db 279 TTTCCCTGGGCTCTCC 263

RESULT 7
US-08-326-514-18/c
; Sequence 18, Application US/08326514
; GENERAL INFORMATION:
; APPLICANT: Osoegawa, Misako
; APPLICANT: Miyabe, Yuki
; APPLICANT: Nakata, Motomi
; APPLICANT: Ra, Chisai
; APPLICANT: Suzuki, Katsuhiko
; TITLE OF INVENTION: DNA PROBE FOR DETECTING ALLERGIC
; TITLE OF INVENTION: DISEASE, AND DETECTION PROCESS OF ALLERGIC DISEASE GENE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,514
; FILING DATE: 20-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mills, Demetra J.
; REGISTRATION NUMBER: 34,506
; REFERENCE/DOCKET NUMBER: 715-099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; TELEX: CABLE AMERPAT
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 735 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-326-514-18

Query Match 100.0%; Score 17; DB 7; Length 735;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCCTGGGCTTCC 17
|||||
DB 712 TTTCCCTGGGCTTCC 696

RESULT 8
US-08-326-514-19/c
; Sequence 19, Application US/08326514
; GENERAL INFORMATION:
; APPLICANT: Osoegawa, Misako
; APPLICANT: Miyabe, Yuki
; APPLICANT: Nakata, Motomi
; APPLICANT: Ra, Chisai
; APPLICANT: Suzuki, Katsuhiko
; TITLE OF INVENTION: DNA PROBE FOR DETECTING ALLERGIC
; TITLE OF INVENTION: DISEASE, AND DETECTION PROCESS OF ALLERGIC DISEASE GENE
; NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,514
; FILING DATE: 20-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mills, Demetra J.
; REGISTRATION NUMBER: 34,506
; REFERENCE/DOCKET NUMBER: 715-099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; TELEX: CABLE AMERPAT
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 735 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-326-514-19

Query Match 100.0%; Score 17; DB 7; Length 735;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCCTGGGCTTCC 17
|||||
DB 712 TTTCCCTGGGCTTCC 696

RESULT 9
US-08-326-514-20/c
; Sequence 20, Application US/08326514
; GENERAL INFORMATION:
; APPLICANT: Osoegawa, Misako
; APPLICANT: Miyabe, Yuki
; APPLICANT: Nakata, Motomi
; APPLICANT: Ra, Chisai
; APPLICANT: Suzuki, Katsuhiko
; TITLE OF INVENTION: DNA PROBE FOR DETECTING ALLERGIC
; TITLE OF INVENTION: DISEASE, AND DETECTION PROCESS OF ALLERGIC DISEASE GENE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,514
; FILING DATE: 20-OCT-1994

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mills, Demetra J.
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 715-099
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
TELEX: CABLE AMERPAT
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
AMTI-SENSE: NO
US-08-326-514-20

Query Match 100.0%; Score 17; DB 7; Length 735;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCTGGGCTTCC 17
|||||
DB 712 TTTCCTGGGCTTCC 696

RESULT 10

US-09-509-152A-2409
Sequence 2409, Application US/09509152A

GENERAL INFORMATION:

APPLICANT: NICE, JONATHAN W.

TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS

NUMBER OF SEQUENCES: 2419

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 CLARK DRIVE

CITY: CRANBURY

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A

FILING DATE: 17-Mar-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160

FILING DATE: 1997-09-17

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-00991

TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 2409:

SEQUENCE CHARACTERISTICS:

LENGTH: 7800 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2409:

US-09-509-152A-2409

Query Match 100.0%; Score 17; DB 19; Length 7800;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCTGGGCTTCC 17
|||||
DB 898 TTTCCTGGGCTTCC 914

RESULT 11

US-08-201-879-2/c

Sequence 2, Application US/08201879

GENERAL INFORMATION:

APPLICANT: KINET, Jean-Pierre

TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF

TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR

TITLE OF INVENTION: IMMUNOGLOBULIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,879

FILING DATE: 24-FEB-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/869,933

FILING DATE: 16-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40399/234 NIH

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 11298 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

ORIGINAL SOURCE:

ORGANISM: homo sapien

STRAIN: Fcrl beta

US-08-201-879-2

Query Match 100.0%; Score 17; DB 6; Length 11298;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCTGGGCTTCC 17
|||||

DB 7299 TTTCCTGGGCTTCC 7283

RESULT 12

US-09-103-663-31/c

Sequence 31, Application US/09103663

GENERAL INFORMATION:

APPLICANT: KINET, Jean-Pierre

```

; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,663
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/869,933
; FILING DATE: 16-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIND
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11298 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: FCRI beta
; US-09-103-663-31

Query Match          100.0%; Score 17; DB 15; Length 11298;
Best Local Similarity 100.0%; Pred. No. 4,7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTTC 17
DB 7299 TTTCCTGGGCTTC 7283

RESULT 13
US-60-197-873-41456
; Sequence 41456, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Betanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81,US1,PRO
; CURRENT APPLICATION NUMBER: US/60/197,873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent. pm
; SEQ ID NO 41456
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-197-873-41456
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Query Match          94.1%; Score 16; DB 51; Length 433;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTTC 16
DB 83 ttccccgggtcttc 98

RESULT 14
US-09-398-253-953/c
; Sequence 953, Application US/09398253
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN POLYNUCLEOTIDES AND THE
; FILE REFERENCE: 8535-0026-999
; CURRENT APPLICATION NUMBER: US/09/398,253
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/095,989
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/100,917
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 953
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(507)
; OTHER INFORMATION: n = A,T,C or G
; US-09-398-253-953

Query Match          94.1%; Score 16; DB 17; Length 507;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTTC 16
DB 245 TTTCCTGGGCTTC 230

RESULT 15
PCT-US00-07506-21
; Sequence 21, Application PC/TUS0007506
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P5523PCT
; CURRENT APPLICATION NUMBER: PCT/US00/07506
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/126,505
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/172,412
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 1842
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1134)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1210)
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; OTHER INFORMATION: n equals a,t,g, or c
PCF-US00-07506-21

Query Match 94.1%; Score 16; DB 1; Length 1842;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGSGTCTTC 16
|||||
Db 1035 ttccctggtcttc 1050

Search completed: April 20, 2001, 03:21:06
Job time: 14153 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:14:49 ; Search time 101.94 Seconds
(without alignments)
23.076 Million cell updates/sec

Title: US-09-016-464-9

Perfect score: 17
Sequence: 1 TTTCCTGCTGCTTCC 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 segs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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2: /cgn2_6/prodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/prodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/prodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/prodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/prodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	US-09-543-679A-1000	Sequence 1000, Ap
2	17	100.0	133	US-09-543-679A-1694	Sequence 1694, Ap
3	17	100.0	894	US-09-543-679A-2503	Sequence 2503, Ap
4	17	100.0	7800	US-09-543-679A-2409	Sequence 2409, Ap
5	17	100.0	11298	US-09-543-679A-2504	Sequence 2504, Ap
6	17	100.0	21742	US-09-543-679A-2505	Sequence 2505, Ap
7	17	100.0	117608	US-09-543-679A-3002	Sequence 3002, Ap
8	17	100.0	117608	US-08-276-163D-1882	Sequence 1882, Ap
9	15.4	90.6	507	US-08-276-163D-1882	Sequence 577, App
10	15	88.2	33059	US-09-543-679A-2955	Sequence 2955, Ap
11	14.4	84.7	278	US-08-276-163D-1925	Sequence 1925, A
12	14.4	84.7	504	US-08-276-163D-11729	Sequence 11729, A
13	14.4	84.7	509	US-09-543-679A-2965	Sequence 2965, Ap
14	13.8	81.2	186	US-08-276-163D-1330	Sequence 1330, A
15	13.8	81.2	433	US-09-543-679A-1123	Sequence 1123, Ap
16	13.8	81.2	497	US-08-276-163D-8674	Sequence 8674, Ap
17	13.8	81.2	503	US-08-276-163D-1809	Sequence 1809, A
18	13.8	81.2	504	US-09-533-077-387	Sequence 387, App
19	13.8	81.2	843	US-09-739-449-7650	Sequence 7650, Ap
20	13.8	81.2	1015	US-09-739-449-1283	Sequence 1283, Ap
21	13.8	81.2	1445	US-09-814-951-1	Sequence 1, App1
22	13.8	81.2	2615	US-09-543-679A-2465	Sequence 2465, Ap
23	13.8	81.2	3490	US-09-814-951-3	Sequence 3, App1
24	13.8	81.2	9704	US-09-543-679A-2466	Sequence 2466, Ap
25	13.8	81.2	17365	US-60-248-505-217	Sequence 217, App
26	13.8	81.2	39449	US-60-248-505-537	Sequence 537, App
27	13.8	81.2	39449	US-60-248-505-537	Sequence 537, App

C 28	13.8	81.2	45977	6	US-60-248-505-540	Sequence 540, App
C 29	13.8	81.2	47614	6	US-60-248-505-75	Sequence 75, App1
C 30	13.8	81.2	90543	6	US-60-248-505-84	Sequence 84, App1
C 31	13.8	81.2	127420	6	US-60-248-505-413	Sequence 413, App
C 32	13.8	81.2	143068	5	US-09-543-679A-2672	Sequence 2672, Ap
C 33	13.8	81.2	143068	5	US-09-543-679A-2839	Sequence 2839, Ap
C 34	13.8	81.2	152740	5	US-09-543-679A-2840	Sequence 2840, Ap
C 35	13.8	81.2	153238	6	US-60-248-505-73	Sequence 73, App1
C 36	13.8	81.2	202491	5	US-09-739-449-201	Sequence 201, App
C 37	13.8	81.2	334854	6	US-60-248-505-28	Sequence 28, App1
C 38	13.8	81.2	340602	6	US-60-248-505-114	Sequence 114, App
C 39	13.8	81.2	370156	6	US-60-248-505-162	Sequence 162, App
C 40	13.8	81.2	443925	6	US-60-248-505-299	Sequence 299, App
C 41	13.8	81.2	479874	6	US-60-248-505-72	Sequence 72, App1
C 42	13.4	78.8	216	5	US-09-533-077-369	Sequence 369, App
C 43	13.4	78.8	646	5	US-09-813-206-81	Sequence 81, App1
C 44	13.4	78.8	651	5	US-09-739-449-2292	Sequence 2292, Ap
C 45	13.4	78.8	1083	5	US-09-813-206-849	Sequence 849, App

ALIGNMENTS

RESULT 1
US-09-543-679A-1000
; Sequence 1000, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NINCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPITGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1000:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1000:
US-09-543-679A-1000
Query Match 100.0%; Score 17; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGCTTCC 17
Db 1 TTTCCCTGGGCTTCC 17

RESULT 2

US-09-543-679A-1694

Sequence 1694, Application US/09543679A

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH "B"
BRONCHOCONSTRICTION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1694:

SEQUENCE CHARACTERISTICS:

LENGTH: 133 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1694:

US-09-543-679A-1694

Query Match 100.0%; Score 17; DB 5; Length 133;

Best Local Similarity 100.0%; Pred. No. 4.1;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGCTTCC 17
Db 1 TTTCCCTGGGCTTCC 17

RESULT 3

US-09-543-679A-2503/C

Sequence 2503, Application US/09543679A

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

US-09-543-679A-2503

Sequence 2503, Application US/09543679A

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 2503:

SEQUENCE CHARACTERISTICS:

LENGTH: 894 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2503:

US-09-543-679A-2503

Query Match 100.0%; Score 17; DB 5; Length 894;

Best Local Similarity 100.0%; Pred. No. 4.4;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCCCTGGGCTTCC 17
Db 762 TTTCCCTGGGCTTCC 746

RESULT 4

US-09-543-679A-2409

Sequence 2409, Application US/09543679A

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2409:
SEQUENCE CHARACTERISTICS:
LENGTH: 7800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2409:
US-09-543-679A-2409

Query Match
Best Local Similarity 100.0%; Score 17; DB 5; Length 7800;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGCTGCTTCC 17
DB 898 TTTCCTGCTGCTTCC 914

RESULT 5
US-09-543-679A-2504/c
Sequence 2504, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2504:
SEQUENCE CHARACTERISTICS:
LENGTH: 11298 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2504:
US-09-543-679A-2504

Query Match
Best Local Similarity 100.0%; Score 17; DB 5; Length 11298;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGCTGCTTCC 17
DB 7299 TTTCCTGCTGCTTCC 7283

RESULT 6
US-09-543-679A-2505/c
Sequence 2505, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2505:
SEQUENCE CHARACTERISTICS:
LENGTH: 21742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2505:
US-09-543-679A-2505

Query Match
Best Local Similarity 100.0%; Score 17; DB 5; Length 21742;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGCTGCTTCC 17
DB 17743 TTTCCTGCTGCTTCC 17727

RESULT 7
US-09-543-679A-3002
Sequence 3002, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
US-09-543-679A-3002

COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3002:
SEQUENCE CHARACTERISTICS:
LENGTH: 117608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3002:
US-09-543-679A-3002

Query Match 100.0%; Score 17; DB 5; Length 117608;^
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTTCC 17
|||||
Db 898 TTTCCTGGGCTTCC 914

RESULT 8
US-09-543-679A-3002/c
Sequence 3002, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: Ntce, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3002:
SEQUENCE CHARACTERISTICS:
LENGTH: 117608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3002:
US-09-543-679A-3002

Query Match 100.0%; Score 17; DB 5; Length 117608;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTTCC 17
|||||
Db 110145 TTTCCTGGGCTTCC 110129

RESULT 9
US-08-276-163D-1882
Sequence 1882, Application US/08276163D
GENERAL INFORMATION:
APPLICANT: Adams, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
FILE REFERENCE: P014
CURRENT APPLICATION NUMBER: US/08/276,163D
CURRENT FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 15314
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1882
LENGTH: 507
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (248)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (305)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (310)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (341)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (346)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (357)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (390)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (394)
OTHER INFORMATION: n equals a,t,g, or c

```
NAME/KEY: misc feature
LOCATION: (401)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (409)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (411)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (430)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (475)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (482)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (486)
OTHER INFORMATION: n equals a,t,g, or c
US-08-276-163D-1882
```

```
Query Match          90.6%; Score 15.4; DB 4; Length 507;
Best Local Similarity 94.1%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCCTGGGCTTCC 17
    ||||||| |||||
Db 212 ttccctgtctctcc 228
```

```
RESULT 10
US-60-248-505-577
; Sequence 577, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 577
; TYPE: DNA
; LENGTH: 33059
; ORGANISM: human
US-60-248-505-577
```

```
Query Match          88.2%; Score 15; DB 6; Length 33059;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTTCCTGGGCTT 15
    ||||||| |||||
Db 20066 ttccctgtctct 20080
```

```
RESULT 11
US-09-543-679A-2955
; Sequence 2955, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2955:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2955:
US-09-543-679A-2955
```

```
Query Match          84.7%; Score 14.4; DB 5; Length 278;
Best Local Similarity 93.8%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 TTTCCTGGGCTTCC 17
    ||||||| |||||
Db 218 TTCCCTGAGCTTCC 233
```

```
RESULT 12
US-08-276-163D-13925
; Sequence 13925, Application US/08276163D
; GENERAL INFORMATION:
; APPLICANT: Adams, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
; FILE REFERENCE: P014
; CURRENT APPLICATION NUMBER: US/08/276,163D
; CURRENT FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 15314
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 13925
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
LOCATION: (52)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (154)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (178)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (321)
OTHER INFORMATION: n equals a,t,g, or c
```

```
; NAME/KEY: misc feature
; LOCATION: (350)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (383)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (390)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (395)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (397)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (425)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (432)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (444)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (458)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (460)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (462)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (466)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (470)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (473)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (484)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (491)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (494)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (497)
; OTHER INFORMATION: n equals a,t,g, or c
; US-08-276-163D-13925

Query Match      84.7%; Score 14.4; DB 4; Length 504;
Best Local Similarity 93.8%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 2 TTCCCTGGGCTTCC 17
    ||| ||| ||| ||| |||
Db 366 ttccctgggcttcc 381
```

```
RESULT 13
US-08-276-163D-11729/c
; Sequence 11729, Application US/08276163D
; GENERAL INFORMATION:
; APPLICANT: Adams, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
; FILE REFERENCE: PO14
```

```
; CURRENT APPLICATION NUMBER: US/08/276.163D
; CURRENT FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 15314
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11729
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (33)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (38)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (101)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (121)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (133)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (301)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (345)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (368)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (370)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (380)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (410)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (416)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (417)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (420)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (434)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (437)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (469)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (487)
; OTHER INFORMATION: n equals a,t,g, or c
; US-08-276-163D-11729

Query Match      84.7%; Score 14.4; DB 4; Length 509;
Best Local Similarity 93.8%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 2 TTCCCTGGGCTTCC 17
    ||| ||| ||| ||| |||
Db 244 TTCTCCTGGGCTTCC 229
```



```

RESULT 14
US-09-543-679A-2965
; Sequence 2965, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2965:
; LENGTH: 7368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2965:
US-09-543-679A-2965

Query Match      84.7%; Score 14.4; DB 5; Length 7368;
Best Local Similarity 93.8%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TTCCCTGGGCTCTCC 17
        |||||
Db      6103 TTCCCTGAGCTCTCC 6118

RESULT 15
US-08-276-163D-13330/C
; Sequence 13330, Application US/08276163D
; GENERAL INFORMATION:
; APPLICANT: Adams, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
; FILE REFERENCE: P014
; CURRENT APPLICATION NUMBER: US/08/276,163D
; CURRENT FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 15314
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13330
; LENGTH: 186
; TYPE: DNA
; ORGANISM: Homo sapiens

```

```

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (83)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (156)
; OTHER INFORMATION: n equals a,t,g, or c
US-08-276-163D-13330

Query Match      81.2%; Score 13.8; DB 4; Length 186;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTTCCTGGGCTCTCC 17
        | |||||
Db      154 TCTCCCTGCTCTCC 138

```

Search completed: April 20, 2001, 00:14:55
Job time: 9432 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:59:03 ; Search time 2028.86 Seconds
(without alignments)
54.633 Million cell updates/sec

Title: US-09-016-464-10

Perfect score: 18

Sequence: 1 GCCGTGTCCTCTCCTCCT 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1283235 segs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba1:*

2: gb_ba2:*

3: gb_ba3:*

4: gb_in1:*

5: gb_in2:*

6: gb_in3:*

7: gb_om:*

8: gb_ov:*

9: gb_pat1:*

10: gb_pat2:*

11: gb_ph:*

12: gb_pl1:*

13: gb_pl2:*

14: gb_pl3:*

15: gb_pl4:*

16: gb_ba1:*

17: gb_ba2:*

18: gb_fun:*

19: gb_htgo_hum:*

20: gb_htgo_inv:*

21: gb_htgo_rdd:*

22: gb_htg_hum1:*

23: gb_htg_hum2:*

24: gb_htg_hum3:*

25: gb_htg_hum4:*

26: gb_htg_hum5:*

27: gb_htg_hum6:*

28: gb_htg_hum7:*

29: gb_htg_hum8:*

30: gb_htg_inv1:*

31: gb_htg_inv2:*

32: gb_htg_other:*

33: gb_htg_rdd:*

34: gb_hum1:*

35: gb_hum2:*

36: gb_hum3:*

37: gb_hum4:*

38: gb_hum5:*

39: gb_hum6:*

40: gb_hum7:*

41: gb_in:*

42: gb_om:*

43: gb_or:*

44: gb_ov:*

45: gb_pat:*

46: gb_ph:*

47: gb_pl:*

48: gb_ro:*

49: gb_sts:*

50: gb_sy:*

51: gb_un:*

52: gb_v1:*

53: gb_sts1:*

54: gb_sts2:*

55: gb_sts3:*

56: gb_sy:*

57: gb_un:*

58: gb_v1:*

59: gb_v12:*

60: gb_htg1:*

61: gb_htg2:*

62: gb_htg3:*

63: gb_htg4:*

64: gb_htg5:*

65: gb_htg6:*

66: gb_htg7:*

67: gb_htg8:*

68: gb_htg9:*

69: gb_htg10:*

70: gb_htg11:*

71: gb_htg12:*

72: gb_htg13:*

73: gb_htg14:*

74: gb_htg15:*

75: gb_htg16:*

76: gb_htg17:*

77: gb_htg18:*

78: gb_htg19:*

79: gb_htg20:*

80: gb_htg21:*

81: gb_htg22:*

82: gb_htg23:*

83: gb_htg24:*

84: gb_htg25:*

85: gb_pr1:*

86: gb_pr2:*

87: gb_pr3:*

88: gb_pr4:*

89: gb_pr5:*

90: gb_pr6:*

91: gb_pr7:*

92: gb_pr8:*

93: gb_pr9:*

94: gb_pr1:*

95: gb_ro2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	94.4	62109	90	AL359984 Human DNA
2	17	94.4	99766	79	AL353702 Homo sapi
3	17	94.4	141204	87	AC020914 Homo sapi
4	17	94.4	164273	82	AP001542 Homo sapi
5	17	94.4	168380	69	AC024543 Homo sapi
6	17	94.4	173654	82	AP001269 Homo sapi
7	17	94.4	179993	64	AC015879 Homo sapi
8	17	94.4	186549	79	AL158847 Homo sapi
9	16.4	91.1	1036	94	AR075859 Rattus no
10	16.4	91.1	1127	9	AR075859 Sequence
11	16.4	91.1	1127	92	HSFCRG5 Human lymph

C 12	16.4	91.1	1334	8	AF155829	Gallus ga
C 13	16.4	91.1	1460	9	AF07098	Artificial
C 14	16.4	91.1	1503	9	AX026812	Sequence
C 15	16.4	91.1	1503	93	M14786	Human FC-ep
C 16	16.4	91.1	1504	9	A05303	Artificial
C 17	16.4	91.1	1504	9	A06297	Artificial
C 18	16.4	91.1	1504	9	A10540	Artificial
C 19	16.4	91.1	1504	9	A10542	H.sapiens 1
C 20	16.4	91.1	1504	9	A10995	Artificial
C 21	16.4	91.1	1504	9	A10996	Artificial
C 22	16.4	91.1	1515	9	A11841	Nucleotide
C 23	16.4	91.1	1515	9	A13365	pre-epsilon
C 24	16.4	91.1	1515	9	A13484	pre-epsilon
C 25	16.4	91.1	1515	9	A14649	pre-epsilon
C 26	16.4	91.1	1524	9	A10869	Recombinant
C 27	16.4	91.1	1529	92	HSJGBFR	X04772 Human mRNA
C 28	16.4	91.1	1530	92	HUMFCER	M15059 Human FC-ep
C 29	16.4	91.1	1532	10	E01646	CDNA encodi
C 30	16.4	91.1	1540	94	RATMHCRA	M31038 Rat MHC cla
C 31	16.4	91.1	2989	89	AK027133	Homo sapi
C 32	16.4	91.1	3108	93	HUMLYRE	M30447 Human lymph
C 33	16.4	91.1	3213	14	S0U52048	US2048 Spinaclia ol
C 34	16.4	91.1	3895	92	HSMB01474	AL133659 Homo sapi
C 35	16.4	91.1	7887	8	AF173015	AF173015 Gallus ga
C 36	16.4	91.1	7892	8	AF173014	AF173014 Gallus ga
C 37	16.4	91.1	7920	8	AF173019	AF173019 Gallus ga
C 38	16.4	91.1	7925	8	AF173018	AF173018 Gallus ga
C 39	16.4	91.1	7962	8	AF173017	AF173017 Gallus ga
C 40	16.4	91.1	7967	8	AF173016	AF173016 Gallus ga
C 41	16.4	91.1	7995	8	AF173013	AF173013 Gallus ga
C 42	16.4	91.1	8000	8	AF173012	AF173012 Gallus ga
C 43	16.4	91.1	10793	94	MUSGPD	M25558 Mouse glyce
C 44	16.4	91.1	17410	9	AR075477	AR075477 Sequence
C 45	16.4	91.1	17410	10	I15549	I15549 Sequence 3

ALIGNMENTS

RESULT 1
LOCUS AL359984 62109 bp DNA PRI 08-SEP-2000
DEFINITION Human DNA sequence from clone RP11-179J15 on chromosome 20.
ACCESSION AL359984
VERSION AL359984.5 GI:9368226
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 62109)

REFERENCE 1
AUTHORS Parker,A.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

COMMENT

On Jul 22, 2000 this sequence version replaced gi:8960202.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information

FEATURES

source	
repeat_region	on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C.elegans/wormep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20 RP11-179J15 is from the library RPCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pBAC3.6 IMPORTANT: This sequence is not the entire insert of clone RP11-179J15 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-128017 is at 62010 in this sequence. The true right end of clone RP5-1167E19 is at 100 in this sequence. Location/Qualifiers 1..62109 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="20" /clone="RP11-179J15" /clone_1lb="RPCI-11.1" 2..1163 /note="LMD repeat: matches 916..2057 of consensus" 1184..1498 /note="Alusx repeat: matches 1..310 of consensus" 1499..1876 /note="LMD repeat: matches 2057..2184 of consensus" 1877..2360 /note="LMD repeat: matches 1..495 of consensus" 2361..2599 /note="LMD repeat: matches 2184..2414 of consensus" 2689..3198 /note="LMD repeat: matches 5589..6103 of consensus" 3199..3495 /note="Alusx repeat: matches 1..297 of consensus" 3496..3540 /note="LMD repeat: matches 6103..6146 of consensus" 4955..5008 /note="MIR repeat: matches 48..102 of consensus" 6128..6413 /note="Alusg repeat: matches 1..286 of consensus" 6871..7480 /note="match: GSS: Em:B90645" 7500..7590 /note="MIR repeat: matches 157..252 of consensus" 7674..7906 /note="MIR repeat: matches 26..250 of consensus" 8136..8219 /note="L2 repeat: matches 2606..2696 of consensus" 9560..9848 /note="Alusx repeat: matches 2..291 of consensus" 10104..10526 /note="match: GSS: Em:A0681718" 10113..10499 /note="match: GSS: Em:B80029" 11084..11287 /note="Alusg/x repeat: matches 90..293 of consensus" 11864..12165 /note="match: GSS: Em:AQ102011" 12119..12264 /note="MIR17 repeat: matches 8..178 of consensus" 12287..12375 /note="MIR repeat: matches 57..146 of consensus" 12407..12602 /note="MER3A repeat: matches 12..203 of consensus" 13047..13177 /note="Charlie2 repeat: matches 2764..2898 of consensus" 13194..13360 /note="LMD2 repeat: matches 6168..6340 of consensus" 13475..14429 /note="LMD3 repeat: matches 5306..6304 of consensus" 14430..14729 repeat_region

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repeat_region /note="AluSp repeat: matches 1. .312 of consensus"
14730. .15130
/note="L1MA3 repeat: matches 4912. .5306 of consensus"
misc_feature complement(14758. .15387)
/note="match: GSS: Em:AQ051475"
repeat_region 15284. .15438
/note="MER5A repeat: matches 7. .183 of consensus"
repeat_region 15448. .15820
/note="L1MA5A repeat: matches 5909. .6292 of consensus"
repeat_region 16016. .16076
/note="L2 repeat: matches 2549. .2616 of consensus"
repeat_region 16320. .16492
/note="MIR repeat: matches 83. .262 of consensus"
repeat_region 16510. .17003
/note="MER54A repeat: matches 7. .507 of consensus"
repeat_region 16979. .17233
/note="MER73 repeat: matches 387. .636 of consensus"
repeat_region 17397. .17533
/note="MIR repeat: matches 81. .214 of consensus"
repeat_region 17548. .17812
/note="L1MB8 repeat: matches 5452. .5720 of consensus"
repeat_region 17815. .17936
/note="L1R28 repeat: matches 1. .775 of consensus"
repeat_region 17922. .18146
/note="MER52A repeat: matches 1262. .1474 of consensus"
repeat_region 18147. .18304
/note="MER52A repeat: matches 1598. .1755 of consensus"
repeat_region 18395. .18834
/note="L1MB8 repeat: matches 5716. .6171 of consensus"
misc_feature 18900. .19388
/note="match: GSS: Em:AQ085072"
repeat_region 18987. .19088
/note="MER5B repeat: matches 54. .162 of consensus"
repeat_region 19769. .20265
/note="MIR1J repeat: matches 5. .516 of consensus"
repeat_region 20496. .20591
/note="MIR repeat: matches 79. .181 of consensus"
repeat_region 20751. .20994
/note="L2 repeat: matches 2140. .2419 of consensus"
repeat_region 22123. .22155
/note="MIR repeat: matches 63. .95 of consensus"
misc_feature complement(22777. .23176)
/note="match: GSS: Em:AQ092310"
repeat_region 22847. .22940
/note="MIR repeat: matches 169. .262 of consensus"
repeat_region 23729. .23992
/note="L2 repeat: matches 2403. .2745 of consensus"
repeat_region 25283. .25502
/note="L1R33 repeat: matches 25. .250 of consensus"
repeat_region 25651. .26012
/note="L1MB5 repeat: matches 5814. .6175 of consensus"
repeat_region 26013. .26073
/note="Alu repeat: matches 224. .284 of consensus"
repeat_region 26074. .26258
/note="AluSp repeat: matches 3. .284 of consensus"
repeat_region 26260. .26323
/note="L1MB5 repeat: matches 5765. .5827 of consensus"
repeat_region 26340. .26516
/note="MER5A repeat: matches 3. .188 of consensus"
repeat_region 26521. .26598
/note="L1R33 repeat: matches 440. .519 of consensus"
misc_feature 26601. .27053
/note="match: GSS: Em:AQ070871"
repeat_region 26706. .26961
/note="L1R16C repeat: matches 165. .387 of consensus"
repeat_region 27970. .28164
/note="L1R16C repeat: matches 27. .226 of consensus"
repeat_region 28224. .28370
/note="L1R16A repeat: matches 301. .448 of consensus"
repeat_region 28575. .29089
/note="MIR2CB repeat: matches 6. .501 of consensus"
misc_feature 29438. .29853
/note="match: GSS: Em:B48715"

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misc_feature 29441. .30166
/note="match: GSS: Em:AQ080993"
repeat_region 29790. .30227
/note="L2 repeat: matches 2038. .2491 of consensus"
repeat_region 30290. .30647
/note="L179 copies 2 mer ct 66% conserved"
repeat_region 30707. .31065
/note="L1ME3 repeat: matches 5664. .6055 of consensus"
repeat_region 31066. .31444
/note="MST1A repeat: matches 1. .426 of consensus"
repeat_region 31445. .31457
/note="L1ME3 repeat: matches 5653. .5664 of consensus"
repeat_region 31474. .31784
/note="Alu repeat: matches 1. .311 of consensus"
repeat_region 31855. .32007
/note="MIR1I repeat: matches 59. .218 of consensus"
repeat_region 32023. .33272
/note="L1MA3 repeat: matches 4936. .6277 of consensus"
repeat_region 33601. .33708
/note="L2 repeat: matches 2602. .2708 of consensus"
repeat_region 33787. .33870
/note="L1MC repeat: matches 1628. .1714 of consensus"

Query Match 94.4%; Score 17; DB 90; Length 62109;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CCTGTCTCTCTCTCT 18
Db 51014 CCTGTCTCTCTCT 51030

RESULT 2
AL353702
LOCUS AL353702 99766 bp DNA 23-JAN-2001
DEFINITION Homo sapiens chromosome 1 clone RP4-768112 map p13.3-21.1, ***
SEQUENCING IN PROGRESS ***, 8 unordered pieces.
ACCESSION AL353702
VERSION AL353702.8 GI:9930873
KEYWORDS HMG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 99766)
AUTHORS Pavitt,R.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:9863656.

COMMENT ----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: d1768112
----- Summary Statistics
Assembly program: XGAP; version 4.5
Sequencing vector: M13; M77815; 3% of reads
Chemistry: Dye-terminator ET-amersham; 24% of reads
Dye-terminator Big Dye; 75% of reads
Consensus quality: 96251 bases at least Q40
Consensus quality: 97539 bases at least Q30
Consensus quality: 98295 bases at least Q20
Insert size: 99066; sum-of-contigs
Insert size: 116736; 2.3% error; agarose-tp
Quality coverage: 5.91x in Q20 bases; sum-of-contigs quality
coverage: 5.07x in Q20 bases; agarose-tp
-----
* NOTE: This is a 'working draft' sequence. It currently

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* consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 9384: contig of 9384 bp in length
 * 9385 9484: gap of 100 bp
 * 9485 12714: contig of 3230 bp in length
 * 12715 12814: gap of 100 bp
 * 12815 17769: contig of 4955 bp in length
 * 17770 17869: gap of 100 bp
 * 17870 28080: contig of 10211 bp in length
 * 28081 28180: gap of 100 bp
 * 28181 48542: contig of 20362 bp in length
 * 48543 48642: gap of 100 bp
 * 48643 70662: contig of 22020 bp in length
 * 70663 70762: gap of 100 bp
 * 70763 75605: contig of 4843 bp in length
 * 75606 75705: gap of 100 bp
 * 75706 99766: contig of 24061 bp in length.

FEATURES
 source
 Location/Qualifiers
 1. .99766
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="1"
 /map="p13.3-21.1"
 /clone="RP4-768112"
 /clone_id="RPC1-4"
 1. .9384
 /note="assembly_fragment:00866
 fragment_chain:1"
 9485. 12714
 /note="assembly_fragment:00213
 fragment_chain:1"
 12815. 17769
 /note="assembly_fragment:00307
 fragment_chain:1"
 17870. 28080
 /note="assembly_fragment:00259
 fragment_chain:1"
 28181. 48542
 /note="assembly_fragment:00895
 fragment_chain:2"
 48643. 70662
 /note="assembly_fragment:00349
 fragment_chain:2"
 70763. 75605
 /note="assembly_fragment:00793"
 75706. 99766
 /note="assembly_fragment:01377"

BASE COUNT 25973 a 23690 c 23922 g 25472 t 709 others
 ORIGIN

misc_feature
 /note="assembly_fragment:00213
 fragment_chain:1"
 12815. 17769
 /note="assembly_fragment:00307
 fragment_chain:1"
 17870. 28080
 /note="assembly_fragment:00259
 fragment_chain:1"
 28181. 48542
 /note="assembly_fragment:00895
 fragment_chain:2"
 48643. 70662
 /note="assembly_fragment:00349
 fragment_chain:2"
 70763. 75605
 /note="assembly_fragment:00793"
 75706. 99766
 /note="assembly_fragment:01377"

Query Match 94.4%: Score 17; DB 79; Length 99766;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCC 17
 |||
 Db 74538 GCCTGTCTCTCTCTCC 74554

RESULT 3
 AC020914/C AC020914 141204 bp DNA PRI 30-SEP-2000
 LOCUS Homo sapiens chromosome 19 clone CTD-3073N11, complete sequence.
 DEFINITION AC020914
 ACCESSION AC020914.7 GI:10440603
 VERSION HTG.
 KEYWORDS human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 141204)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE
 Direct Submission
 JOURNAL
 Unpublished
 REFERENCE
 2 (bases 1 to 141204)
 DOE Joint Genome Institute.
 AUTHORS
 TITLE
 Direct Submission
 JOURNAL
 Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE
 3 (bases 1 to 141204)
 DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (30-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 On Sep 30, 2000 this sequence version replaced g1:7711622.
 COMMENT
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40 99.6% of Sequence;
 Estimated Total Number of Errors is 0.5.

FEATURES
 source
 Location/Qualifiers
 1. 141204
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="19"
 /clone="CVD-3073N11"

BASE COUNT 37678 a 33210 c 31770 g 38546 t
 ORIGIN

Query Match 94.4%: Score 17; DB 87; Length 141204;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTGTCTCTCTCTCT 18
 |||
 Db 20915 CCTGTCTCTCTCTCT 20899

RESULT 4
 AP001542 AP001542 164273 bp DNA HTG 30-MAY-2000
 LOCUS Homo sapiens chromosome 18 clone RP11-703116 map 18p11.2, WORKING
 DEFINITION DRAFT SEQUENCE, 39 unordered pieces.
 ACCESSION AP001542
 VERSION AP001542.2 GI:8117380
 KEYWORDS HTG: HTGS PHASE1; HTGS DRAFT.
 SOURCE
 Homo sapiens DNA, clone:RP11-703116.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 164273)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Homo sapiens 164,273 genomic DNA of 18p11.2
 Published Only in Database (2000) In press
 REFERENCE
 2 (bases 1 to 164273)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Direct Submission
 JOURNAL
 Submitted (24-MAR-2000) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
 Japan (E-mail:hattori@gsc.riken.go.jp,
 url:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
 Fax:81-42-778-9924)
 On May 30, 2000 this sequence version replaced g1:7340841.

COMMENT
 ----- Genome Center
 Center: RIKEN Genomic Sciences Center(GSC)

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Center code: RIKEN
Web site: http://hnp.gsc.riken.go.jp/
Contact: hatori@gsc.riken.go.jp
-----
Project Information
Center project name: HumDrift18
Center clone name: RP11-703116
-----
Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 142924 bases at least Q40
Consensus quality: 152892 bases at least Q30
Consensus quality: 157278 bases at least Q20
Insert size: 160473; sum-of-ctrls
Quality coverage: 4.28x in Q20 bases; sum-of-ctrls
-----
NOTE: This is a 'working draft' sequence. It currently consists of
39 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs 'N', but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

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FEATURES	* 163052	163151:	gap of	100 bp
	* 163152	164273:	contly of	1122 bp in length.
source	Location/Qualifiers			
	1. .164273			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/chromosome="18"			
	/map="18p11.2"			
	/clone="RP11-703116"			
	1. .19160			
misc_feature	/note="assembly_fragment"			
	19261. .31174			
misc_feature	/note="assembly_fragment"			
	31275. .40412			
misc_feature	/note="assembly_fragment"			
	40513. .51441			
misc_feature	/note="assembly_fragment"			
	51542. .60747			
misc_feature	/note="assembly_fragment"			
	60848. .68811			
misc_feature	/note="assembly_fragment"			
	68912. .75960			
misc_feature	/note="assembly_fragment"			
	76061. .84207			
misc_feature	/note="assembly_fragment"			
	84308. .90247			
Query Match	94.4%;	Score 17;	DB 82;	Length 164273;
Best Local Similarity	100.0%;	Pred. No. 65;		
Matches	17;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	GCCTGTCTCTCTCTCC	17	
Db	68099	GCCTGTCTCTCTCTCC	68115	
LOCUS	AC024543/C			
DEFINITION	Homo sapiens chromosome 4 clone RP11-556114 map 4, WORKING DRAFT			
ACCESSION	AC024543			
VERSION	AC024543.2			
KEYWORDS	HTG; HTGS-PHASE1; HTGS-DRAFT.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	1 (bases 1 to 168380)			
JOURNAL	Birren,B., Linton,L., Nusbaum,C. and Lander,E.			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 168380)			
	Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,			
	Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,			
	Boukhalil,B., Brown,A., Burkett,G., Campolongo,A., Castle,A.,			
	Chapel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,			
	DeRavello,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M.,			
	Fenster,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,			
	Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,			
	Grand-Pierre,N., Grant,G., Hagos,B., Hesford,A., Horton,L.,			
	Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,			
	Klein,J., Lander,T., Laroque,K., Lehotzky,J., Levine,R.,			
	Lieu,C., Liu,G., Locke,K., MacDonald,P., Margus,N., McCarthy,M.,			
	McEwan,P., McGurt,A., McKernan,K., McPheters,R., Meldrum,J.,			
	Menus,L., Mihova,T., Miranda,C., Mianga,V., Morrow,J., Naylor,J.,			
	Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M.,			
	Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C.,			
	Riley,P., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,			
	Severy,R., Spencer,B., Stange-Thomann,N., Stojanovic,N.,			
	Sudramanlan,A., Talamas,J., Tesfaye,S., Theodore,J., Tittell,A.,			
	Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,			
	Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and			

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TITLE      Direct Submission
JOURNAL    Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT    On Apr 11, 2000 this sequence version replaced gi:7108374.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information
Center project name: L7402
Center clone name: 556_I_14
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 157924 bases at least Q40
Consensus quality: 162668 bases at least Q30
Consensus quality: 164801 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 166680; sum-of-ctrls
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-ctrls

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1      2419: contig of 2419 bp in length
*
*      2420 2519: gap of 100 bp
*
*      2520      4792: contig of 2273 bp in length
*
*      4793 4892: gap of 100 bp
*
*      4893      7922: contig of 3030 bp in length
*
*      7923 8022: gap of 100 bp
*
*      8023 10921: contig of 2899 bp in length
*
*      10922 11021: gap of 100 bp
*
*      11022 14376: contig of 3355 bp in length
*
*      14377 14476: gap of 100 bp
*
*      14477 19314: contig of 4838 bp in length
*
*      19315 19414: gap of 100 bp
*
*      19415 25446: contig of 6032 bp in length
*
*      25447 25546: gap of 100 bp
*
*      25547 31755: contig of 6209 bp in length
*
*      31756 31855: gap of 100 bp
*
*      31856 38149: contig of 6294 bp in length
*
*      38150 38249: gap of 100 bp
*
*      38250 46588: contig of 8339 bp in length
*
*      46589 46688: gap of 100 bp
*
*      46689 56323: contig of 9635 bp in length
*
*      56324 56423: gap of 100 bp
*
*      56424 70104: contig of 13681 bp in length
*
*      70105 70204: gap of 100 bp
*
*      70205 85003: contig of 12799 bp in length
*
*      85004 83103: gap of 100 bp
*
*      83104 94048: contig of 10945 bp in length
*
*      94049 94148: gap of 100 bp
*
*      94149 108827: contig of 14679 bp in length
*
*      108828 108927: gap of 100 bp
*
*      108928 126811: contig of 17864 bp in length
*
*      126812 126911: gap of 100 bp
*
*      126912 143238: contig of 16337 bp in length
*
*      143239 143338: gap of 100 bp
*
*      143339 168380: contig of 25042 bp in length.

Location/Qualifiers
1. 168380

```



```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-556114"
/clone_lib="RPC1-11 Human Male BAC"
1. 2419
misc_feature
  /note="assembly_fragment"
  2520..4792
  /note="assembly_fragment"
  4893..7922
  /note="assembly_fragment"
  8023..10921
  /note="assembly_fragment"
  11022..14376
  /note="assembly_fragment"
  14477..19314
  /note="assembly_fragment"
  19415..25446
  /note="assembly_fragment"
  25547..31755
  /note="assembly_fragment"
  clone_end:SP6
  vector_side:left"
  31856..38149
  /note="assembly_fragment"
  38250..46588
  /note="assembly_fragment"
  46689..56323
  /note="assembly_fragment"
  56424..70104
  /note="assembly_fragment"
  70205..83003
  /note="assembly_fragment"
  83104..94048
  /note="assembly_fragment"
  94149..108827
  /note="assembly_fragment"
  108928..126811
  /note="assembly_fragment"
  126912..143238
  /note="assembly_fragment"
  14339..168380
  /note="assembly_fragment"
  clone_end:T7
  vector_side:left"
BASE COUNT  52721 a 31064 c 30784 g 52101 t 1710 others
ORIGIN
Query Match          94.4%; Score 17; DB 69; Length 168380;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 CCGTGTCTCTCTCTCT 18
      11111111111111111111
Db 57802 CCGTGTCTCTCTCTCT 57786

RESULT  6
LOCUS   AP001269 173654 bp DNA HTG 30-MAY-2000
DEFINITION Homo sapiens chromosome 18 clone RP11-820116 map 18p11.2, WORKING
DRAFT SEQUENCE, 36 unordered pieces.
ACCESSION AP001269.2 GI:8117661
VERSION   AP001269.2
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    Homo sapiens DNA, clone:RP11-820116.
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 173654)
AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

```

```

TITLE      Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
JOURNAL    Homo sapiens 173,654 genomic DNA of 18p11.2
REFERENCE  2 (bases 1 to 173654) In press
AUTHORS    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
          Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL    Submitted (23-FEB-2000) Masahira Hattori, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
          Kitasato Univ., 1-15-1 Kitasato, Sagamiara, Kanagawa 228-8555,
          Japan (E-mail:hattori@gsc.riken.go.jp,
          URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
          Fax:81-42-778-9924)
          On May 31, 2000 this sequence version replaced gi:7106137.
COMMENT    ----- Genome Center
          Center: RIKEN Genomic Sciences Center(GSC)
          Center code: RIKEN
          Web site: http://hgp.gsc.riken.go.jp/
          Contact: hattori@gsc.riken.go.jp
          ----- Project Information
          Center project name: Humdraft18
          Center clone name: RP11-820116
          ----- Summary Statistics
          Sequencing vector: PCR products; 100% of reads
          Chemistry: Dye-terminator ET-amersham; 100% of reads
          Assembly program: Phrap; version 0.990329
          Consensus quality: 150290 bases at least Q40
          Consensus quality: 161033 bases at least Q30
          Consensus quality: 166450 bases at least Q20
          Insert size: 170154; sum-of-ctrls
          Quality coverage: 4.39x in Q20 bases; sum-of-ctrls
          -----
NOTE: This is a 'working draft' sequence. It currently consists of
36 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1 13180 contig of 13180 bp in length
13281 25135 contig of 11855 bp in length
25236 38657 contig of 13422 bp in length
38758 51908 contig of 13151 bp in length
52009 63693 contig of 11685 bp in length
63794 73269 contig of 9476 bp in length
73370 82158 contig of 8789 bp in length
82259 90203 contig of 7945 bp in length
90304 96577 contig of 6274 bp in length
96678 101230 contig of 4553 bp in length
101331 106415 contig of 5085 bp in length
106516 111092 contig of 4577 bp in length
111193 115716 contig of 4524 bp in length
115817 120498 contig of 4682 bp in length
120599 123521 contig of 2923 bp in length
123622 127552 contig of 3931 bp in length
127653 130319 contig of 2667 bp in length
130420 133308 contig of 2889 bp in length
133409 136102 contig of 2694 bp in length
136203 138988 contig of 2786 bp in length
139089 142390 contig of 3302 bp in length
142491 144891 contig of 2401 bp in length
144992 148017 contig of 3026 bp in length
148118 151187 contig of 3070 bp in length
151288 153575 contig of 2288 bp in length
153676 155740 contig of 2065 bp in length
155841 159041 contig of 3201 bp in length
159142 161518 contig of 2377 bp in length
161619 163255 contig of 1637 bp in length
163356 164468 contig of 1113 bp in length
164569 166270 contig of 1702 bp in length
166371 168052 contig of 1682 bp in length
168153 169766 contig of 1614 bp in length
169867 171153 contig of 1287 bp in length

```

171254 172536 contig of 1283 bp in length
172637 173654 contig of 1018 bp in length
Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 36 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 13180: contig of 13180 bp in length
13181 13280: gap of 100 bp
13281 25135: contig of 11855 bp in length
25136 25235: gap of 100 bp
25236 38657: contig of 13422 bp in length
38658 38737: gap of 100 bp
38738 51908: contig of 13151 bp in length
51909 52008: gap of 100 bp
52009 63693: contig of 11685 bp in length
63694 63793: gap of 100 bp
63794 73269: contig of 9476 bp in length
73270 73369: gap of 100 bp
73370 82158: contig of 8789 bp in length
82159 82258: gap of 100 bp
82259 90203: contig of 7945 bp in length
90204 90303: gap of 100 bp
90304 96577: contig of 6274 bp in length
96578 96677: gap of 100 bp
96678 101230: contig of 4553 bp in length
101231 101330: gap of 100 bp
101331 106415: contig of 5085 bp in length
106416 106515: gap of 100 bp
106516 111092: contig of 4577 bp in length
111093 111192: gap of 100 bp
111193 115716: contig of 4524 bp in length
115717 115816: gap of 100 bp
115817 120498: contig of 4682 bp in length
120499 120598: gap of 100 bp
120599 123521: contig of 2823 bp in length
123522 123621: gap of 100 bp
123622 127552: contig of 3931 bp in length
127553 127652: gap of 100 bp
127653 130319: contig of 2667 bp in length
130320 130419: gap of 100 bp
130420 133308: contig of 2889 bp in length
133309 133408: gap of 100 bp
133409 136102: contig of 2694 bp in length
136103 136202: gap of 100 bp
136203 138988: contig of 2786 bp in length
138989 139088: gap of 100 bp
139089 142390: contig of 3302 bp in length
142391 142490: gap of 100 bp
142491 144891: contig of 2401 bp in length
144892 144991: gap of 100 bp
144992 148017: contig of 3026 bp in length
148018 148117: gap of 100 bp
148118 151187: contig of 3070 bp in length
151188 151287: gap of 100 bp
151288 153575: contig of 2288 bp in length
153576 153675: gap of 100 bp
153676 155740: contig of 2065 bp in length
155741 155840: gap of 100 bp
155841 159041: contig of 3201 bp in length
159042 159141: gap of 100 bp
159142 161518: contig of 2377 bp in length
161519 161618: gap of 100 bp
161619 163255: contig of 1637 bp in length
163256 163355: gap of 100 bp
163356 164468: contig of 1113 bp in length
164469 164568: gap of 100 bp
164569 166270: contig of 1702 bp in length
166271 166370: gap of 100 bp

* 166371 168052: contig of 1682 bp in length
* 168053 168152: gap of 100 bp
* 168153 169766: contig of 1614 bp in length
* 169767 169866: gap of 100 bp
* 169867 171153: contig of 1287 bp in length
* 171154 171253: gap of 100 bp
* 171254 172536: contig of 1283 bp in length
* 172537 172636: gap of 100 bp
* 172637 173654: contig of 1018 bp in length.

FEATURES

SOURCE

1. 173654
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
/map="18p11.2"
/clone="RP11-820116"
1. 13180
/note="assembly-fragment"
13281. 25135
/note="assembly-fragment clone_end:SP6 vector_side:left"
25236. 38657
/note="assembly-fragment"
38758. 51908
/note="assembly-fragment"
52009. 63693
/note="assembly-fragment"
63794. 73269
/note="assembly-fragment"
73370. 82158
/note="assembly-fragment"
82259. 90203
/note="assembly-fragment"
90304. 96577
/note="assembly-fragment"
96678. 101230
/note="assembly-fragment"
101331. 106415
/note="assembly-fragment clone_end:T7 vector_side:right"
106516. 111092
/note="assembly-fragment"
111193. 115716
/note="assembly-fragment"

Query Match

Best Local Similarity 100.0%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCCTGTCTCTCTCTCC 17

DB 136337 GCCTGTCTCTCTCTCC 136353

RESULT 7

AC015879/c

LOCUS AC015879 179993 bp DNA HTG 07-SEP-2000
DEFINITION Homo sapiens chromosome 18 clone RP11-31607 map 18, WORKING DRAFT

SEQUENCE, 20 unordered pieces.

AC015879

VERSION AC015879.4 GI:9966981

KEYWORDS HTG; HTGS-PHASE1; HTGS-DRAFT.

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 179993)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens chromosome 18, clone RP11-31607

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 179993)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Bouknight,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domiano,M., Donegan,L., Doyle,M.,

TITLE
JOURNAL
COMMENT

Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardy, S., Grant, G., Hagos, B., Heatord, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczy, J., Lieu, C., Locke, K., Macdonald, P., Margis, N., McEwan, P., McGuirk, A., McKernan, K., McLaughlin, J., Meltrin, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Tirrell, A., Vassilev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 5, 2000 this sequence version replaced g1:7283209.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence-submissions@genome.wi.mit.edu

Project Information

Center project name: L685

Center clone name: 316_O_7

Summary Statistics

Sequencing vector: M13; M77815: 90% of reads

Sequencing vector: plasmid; 108752: 10% of reads

Chemistry: Dye-primer-amersham; 20% of reads

Chemistry: Dye-terminator Big Dye; 80% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 168712 bases at least Q40

Consensus quality: 173598 bases at least Q30

Consensus quality: 176241 bases at least Q20

Insert size: 16900; agarose-ftp

Insert size: 178093; sum-of-ctrls

Quality coverage: 6.2 in Q20 bas.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

1 18393: contig of 18393 bp in length
18394 18493: gap of 100 bp
18494 19505: contig of 1012 bp in length
19506 19605: gap of 100 bp
19606 20680: contig of 1075 bp in length
20681 20780: gap of 100 bp
20781 22403: contig of 1623 bp in length
22404 22503: gap of 100 bp
22504 24501: contig of 1998 bp in length
24502 24601: gap of 100 bp
24602 26656: contig of 2055 bp in length
26657 26756: gap of 100 bp
26757 29340: contig of 2584 bp in length
29341 29440: gap of 100 bp
29441 32230: contig of 2790 bp in length
32231 32330: gap of 100 bp
32331 35045: contig of 2715 bp in length
35046 35145: gap of 100 bp
35146 37809: contig of 2664 bp in length
37810 37909: gap of 100 bp
37910 44700: contig of 6791 bp in length
44701 44800: gap of 100 bp
44801 51023: contig of 6223 bp in length
51024 51123: gap of 100 bp
51124 57645: contig of 6522 bp in length
57646 57745: gap of 100 bp
57746 67800: contig of 10055 bp in length
67801 67900: gap of 100 bp

```

```

* 67901 76820: contig of 8920 bp in length
* 76821 76920: gap of 100 bp
* 76921 105604: contig of 28684 bp in length
* 105605 105704: gap of 100 bp
* 105705 124555: contig of 18851 bp in length
* 124556 124655: gap of 100 bp
* 124656 145741: contig of 21086 bp in length
* 145742 145841: gap of 100 bp
* 145842 170251: contig of 24410 bp in length
* 170252 170351: gap of 100 bp
* 170352 179993: contig of 9642 bp in length.
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/db_xref="taxon:9606"
/chromosome="18"
/map="18"
/clone="RP11-31607"
/clone_1lb="RP11 Human Male BAC"
1. .18393
/clone="assembly-fragment"
vector_end:SP6
vector_side:left"

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FEATURES

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  /note="assembly-fragment"
  1. .18393
misc_feature
  /note="assembly-fragment"
  18494. .19505
misc_feature
  /note="assembly-fragment"
  19606. .20680
misc_feature
  /note="assembly-fragment"
  20781. .22403
misc_feature
  /note="assembly-fragment"
  22504. .24501
misc_feature
  /note="assembly-fragment"
  24602. .26656
misc_feature
  /note="assembly-fragment"
  26757. .29340
misc_feature
  /note="assembly-fragment"
  29441. .32230
misc_feature
  /note="assembly-fragment"
  32331. .35045
misc_feature
  /note="assembly-fragment"
  35146. .37809
misc_feature
  /note="assembly-fragment"
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  44801. .51023
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  51124. .57645
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  /note="assembly-fragment"
  57746. .67800
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  /note="assembly-fragment"
  67901. .76820
misc_feature
  /note="assembly-fragment"
  76921. .103604
misc_feature
  /note="assembly-fragment"
  105705. .124555
misc_feature
  /note="assembly-fragment"
  124656. .145741
misc_feature
  /note="assembly-fragment"
  145842. .170251
misc_feature
  /note="assembly-fragment"
  170352. .179993
misc_feature
  /note="assembly-fragment"
  clone_end:17
  vector_side:right"
BASE COUNT 46743 a 42919 c 41781 g 46643 t 1907 others
ORIGIN

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Query Match          94.4%: Score 17; DB 64; Length 179993;
Best Local Similarity 100.0%: Pred. No. 65;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTGTCTCTCTCC 17
|||||

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Db 105505 GCCTGTCTCTCTCC 105489

RESULT 8
 AL158847/c
 LOCUS
 DEFINITION Homo sapiens chromosome 1 clone RP4-735C1, ** SEQUENCING IN
 PROGRESS ***, 11 unordered pieces.
 ACCESSION AL158847
 VERSION AL158847.9 GI:12539527
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 186549)
 Direct Submission
 Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Jan 25, 2001 this sequence version replaced gi:12189825.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk
 ----- Project Information
 Center project name: dJ735C1
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: M13; M77815; 16% of reads
 Sequencing vector: plasmid; L08752; 83% of reads
 Chemistry: Dye-terminator ET-amersham; 6% of reads Chemistry:
 Dye-terminator Big Dye; 93% of reads
 Consensus quality: 183619 bases at least Q40
 Consensus quality: 184456 bases at least Q30
 Consensus quality: 184942 bases at least Q20
 Insert size: 185549; sum-of-contigs
 Insert size: 171686; 3.8% error; agarose-fp
 Quality coverage: 8.20x in Q20 bases; sum-of-contigs Quality
 coverage: 9.02x in Q20 bases; agarose-fp

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 11 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 52703: contig of 52703 bp in length
 * 52704 52803: gap of 100 bp
 * 52804 62659: contig of 9856 bp in length
 * 62660 62759: gap of 100 bp
 * 62760 70504: contig of 7745 bp in length
 * 70505 70604: gap of 100 bp
 * 70605 77682: contig of 7078 bp in length
 * 77683 77782: gap of 100 bp
 * 77783 90089: contig of 12307 bp in length
 * 90090 90189: gap of 100 bp
 * 90190 121154: contig of 30965 bp in length
 * 121155 121254: gap of 100 bp
 * 121255 157989: contig of 36735 bp in length
 * 157990 158089: gap of 100 bp
 * 158090 172619: contig of 14530 bp in length
 * 172620 172719: gap of 100 bp
 * 172720 176012: contig of 3293 bp in length
 * 176013 176112: gap of 100 bp
 * 176113 181203: contig of 5091 bp in length
 * 181204 181303: gap of 100 bp
 * 181304 186549: contig of 5246 bp in length.
 Location/Qualifiers

source 1..186549
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 /db_xref="taxon:9606"
 /chromosome="1"
 /clone="RP4-735C1"
 /clone_1lb="RPC1-4"
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 /note="assembly-fragment:00005
 fragment_chain:1"
 52804..62659
 /note="assembly-fragment:03701
 fragment_chain:1"
 62760..70504
 /note="assembly-fragment:01536
 fragment_chain:1"
 70605..77682
 /note="assembly-fragment:00798
 fragment_chain:1"
 77783..90089
 /note="assembly-fragment:00223
 fragment_chain:1"
 90190..121154
 /note="assembly-fragment:02379
 fragment_chain:2"
 121255..157989
 /note="assembly-fragment:02199
 fragment_chain:2"
 158090..172619
 /note="assembly-fragment:02260
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 /note="assembly-fragment:00079"
 176113..181203
 /note="assembly-fragment:02303"
 181304..186549
 /note="assembly-fragment:03340"
 BASE COUNT 50139 a 44539 c 44230 g 46603 t 1038 others
 ORIGIN

Query Match 94.4%; Score 17; DB 79; Length 186549;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCC 17
 Db 103697 GCCTGTCTCTCTCC 103681

RESULT 9
 RNAJ5024/c
 LOCUS
 DEFINITION Rattus norvegicus mRNA for mature MHC class Ib alpha chain, clone
 CG22.
 ACCESSION AJ005024
 VERSION AJ005024.1 GI:3006075
 KEYWORDS alpha chain; major histocompatibility complex.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 1 (bases 1 to 1036)
 Leong,L.Y.W., Le Rolle,A.F., Deverson,E.V., Powis,S.J.,
 Larkins,A.P., Vaage,J.T., Stokland,A., Lambrecht-Washing,D.,
 Rolstad,B., Joly,E. and Butcher,G.W.
 RTI-U: Identification of a novel, active, class Ib alloantigen of
 the rat MHC
 J. Immunol. 162 (2), 743-752 (1999)
 JOURNAL 99113732
 MEDLINE
 REFERENCE 2 (bases 1 to 1036)
 Leong,L.Y.W., Le Rolle,A.F., Deverson,E.V., Larkins,A.P.,
 Vaage,J.T., Stokland,A., Lambrecht,D., Wontgeitl,K., Rolstad,B.,
 Joly,E. and Butcher,G.W.

TITLE Expression cloning of novel, expressed MHC class Ib alloantigens of the rat MHC: RT1-U

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1036)

AUTHORS Leong,L.Y.W.

TITLE Direct Submission

JOURNAL Submitted (26-MAR-1998) Leong L.Y.W., The Babraham Institute, Immunology, Cambridge, CB2 4AT, UK

FEATURES

source

1..1036

/organism="Rattus norvegicus"

/strain="PVG.R19"

/db_xref="taxon:10116"

/chromosome="20"

/haplotype="Aav1 B/Dav1 Cc"

/sex="female"

/dev_stage="adult"

/tissue_type="spleen"

/clone="Cc22"

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<1..888

/codon_start=1

/product="MHC class Ib alpha chain"

/protein_id="CAA06297.1"

/db_xref="GI:3006076"

/db_xref="SPTREMBL:O62935"

/translation="GSHSLRPHYTAVSRRGLGEPRIYGVYDDNQFVYPSDAENPK YEPRAWMREGEPEYWEBOETRYAKGOEDYRSLRNLSYINQSEGSHTTORMGCD VSDSDSLRGYEQHAYDGRDYIALNEDLKTWAVADPAAMITTSKMQORNAERSRAYV ECTGEWMLRYLERGETLDRSDPEAHVHTLRREGDVTLCMALGFYPADITLTWO LNGEDLTOMLEVTETRPAGDGTFFQKWSVVPDLGKEQNTYTCHEHGLPEPLSQRWEP SPSTSNLLFLFLMOFL"

BASE COUNT 218 a 271 c 346 g 201 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 94; Length 1036;

Best local Similarity 94.4%; Pred. No. 1.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCCT 18

|||||||

Db 947 GCCTGTCTCTCCT 930

RESULT 10

AR075859/c 1127 bp DNA PAT 30-AUG-2000

LOCUS AR075859

DEFINITION Sequence 1 from patent US 5958707.

ACCESSION AR075859

VERSION AR075859.1 GI:10002605

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1127)

AUTHORS de Vries,J.E., Jenh,C., Narula,S.K. and Zavodny,P.J.

TITLE Human Interleukin-4 antagonist/agonist screens

JOURNAL Patent: US 5958707-A 1 28-SEP-1999;

FEATURES

source

1..1127

/organism="unknown"

BASE COUNT 231 a 309 c 306 g 281 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 1127;

Best local Similarity 94.4%; Pred. No. 1.6e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCCT 18

|||||||

Db 663 GCCTGTCTCTCTCCT 646

RESULT 11

HSFCERG5/c 1127 bp DNA PRI 13-NOV-1998

LOCUS HSFCERG5

DEFINITION Human lymphocyte IgE receptor gene 5'-region (Fc-epsilon R)

ACCESSION X06049

VERSION X06049.1 GI:31316

KEYWORDS alternate splicing; antigen; CD23 antigen; Fc receptor; Fc-epsilon receptor; IgE receptor.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1127)

AUTHORS Suter,U., Bastos,R. and Hofstetter,H.

TITLE Molecular structure of the gene and the 5'-flanking region of the human lymphocyte immunoglobulin E receptor

JOURNAL Nucleic Acids Res. 15 (18), 7295-7308 (1987)

MEDLINE 88015596

COMMENT Data kindly reviewed (8 July 1988) by HOFSTETTER H.

FEATURES

source

1..1127

/organism="Homo sapiens"

/db_xref="taxon:9606"

/tissue_type="placenta"

/clone_11b="lambda Charon 4A"

/clone="lambda 4A.1."

121..308

/note="inverted repeat A"

415..419

/evidence=not_experimental

441..450

/evidence=not_experimental

521..527

/evidence=not_experimental

536..541

/note="putative alternative TATA-box"

/evidence=not_experimental

551

/note="5' end of cDNA"

<551..678

/number=1

566

/note="5' end of cDNA"

679..>1127

/note="intron 1"

820..830

GC_signal

932..1119

/note="inverted repeat A"

BASE COUNT 231 a 309 c 306 g 281 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 92; Length 1127;

Best local Similarity 94.4%; Pred. No. 1.6e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCCT 18

|||||||

Db 663 GCCTGTCTCTCTCCT 646

RESULT 12

AF155829/c 1334 bp mRNA VRT 01-JAN-2000

LOCUS AF155829

DEFINITION Gallus gallus N-type calcium channel alpha-1B subunit mRNA, partial

ACCESSION AF155829

VERSION AF155829.1 GI:6651246

KEYWORDS

SOURCE ORGANISM chicken.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
REFERENCE 1 (bases 1 to 1334)
AUTHORS Schliff, M., Siderovski, D., Jordan, J.D., Brothers, G., Snow, B.,
Dho, S., Wolting, C., McGlade, J., De Vries, L., Ortiz, D. and
Diverse-Plerluisi, M.
TITLE GABA B receptor-induced N-type calcium channel modulation is
mediated by interactions of the P7B domain of RGS12 with the
lysosine-phosphorylated channel
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1334)
AUTHORS Schliff, M., Siderovski, D., Jordan, J.D., Brothers, G., Snow, B.,
Dho, S., Wolting, C., McGlade, J., De Vries, L., Ortiz, D. and
Diverse-Plerluisi, M.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-1999) Pharmacology, Mount Sinai School of
Medicine, 1425 Madison Ave. Rm. 1252, New York, NY 10029, USA
FEATURES
source
1. 1334
Location/Qualifiers
/organism="Gallus gallus"
/db_xref="taxon:9031"
CDS
<1..>1334
/note="pore-forming Ca2+ channel subunit"
/product="N-type calcium channel alpha-1B subunit"
/protein_id="AF22237.1"
/db_xref="GI:651247"
/translation="KDEEMEEATNQKLALQKAKEVAEVSPTSANISIAKQONSSK
SKSWERTSOIRMHNFASCEALYNELDPERVRYATLHIRPMKTHLDRLVYEP
RGEGNINNEERHROHRSRKEGSKGKSDRSOGSGGCHHRGSGVEGFEHR
RHRTIRHAEKQKSGKCTINGANSEKERTIRHGRSSNRREPSKENGDEPHRRH
KFRSAUSTYDSEKENEKGEETAEKHQNHQENECETASVSIPVHTLPSTY
LQKYPEQEDADQENVTIRMIOPLDKTTVNIPTVITAPGETTVIPMNNVEFSKT
EEKVDIDLTNGPKPIPNYSMFLSPTNIRLFIHYIVLRYPEVMIKMI"
BASE COUNT 392 a 336 c 428 g 178 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 1334;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCCT 18
||||| |||||||
Db 520 GCCTGTCTCTCTCCT 503

RESULT 13
LOCUS A07098 1460 bp mRNA PAT 23-AUG-1993
DEFINITION Artificial sequence mRNA for human B-cell Ige-BF related protein.
ACCESSION A07098
VERSION A07098.1 GI:412977
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 1460)
AUTHORS Hofstetter, H., Kluchherr, E. and Schmitz, A.
TITLE Preparation of binding factor related polypeptides
JOURNAL Patent: EP 0254249-A 2 27-JAN-1988;
CIBA-GEIGY AG
FEATURES
source
1. 1460
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
146..1111
/note="human B-cell Ige-BF related protein"
/codon_start=1

/transl_table=1
/protein_id="CAA00609.1"
/db_xref="GI:412978"
/translation="MEEQVSEIEIPRRRCRGTQIVLGLVTAAIMAGLLILL
WMIDTOSLKQLEERAAHNVQSKNLEHNGDDMAQCSOSTQISQLEELRAQORL
KSQDELSTWNLNGLOADLSSPSKOLEHNRNASDLERLREVTKLMEELQVSSGFC
NTCEKWINFORKCYEFGKGTQWVHAYACDDMEGQVLSIHSPEEDFLTKHSHSG
SWIGLRNLDLGEFTWDSHVDSNNAPEPTSRSGQEDCVMMRSGSRWMDAFCDRK
LGAWCDLATCTPPASGSAESMGPPSRPDRPLPTPSAPLHS"
BASE COUNT 340 a 439 c 424 g 257 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 1460;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCCT 18
||||| |||||||
Db 45 GCCTGTCTCTCTCCT 28

RESULT 14
LOCUS AX026812/C 1503 bp DNA PAT 16-SEP-2000
DEFINITION Sequence 18 from Patent EP1006183.
ACCESSION AX026812
VERSION AX026812.1 GI:10187945
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1503)
AUTHORS
TITLE Recombinant soluble fc receptors
JOURNAL Patent: EP 1006183-A 18 07-JUN-2000;
MAX PLANCK GEBELTSCHAFT (DE)
FEATURES
source
1. 1503
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 345 a 456 c 431 g 271 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 1503;
Best Local Similarity 94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCCT 18
||||| |||||||
Db 81 GCCTGTCTCTCTCCT 64

RESULT 15
LOCUS HUMPCERA/C 1503 bp mRNA PRI 08-NOV-1994
DEFINITION Human Fc-epsilon receptor CD23 antigen (Ige receptor) mRNA complete
cds.
ACCESSION M14766
VERSION M14766.1 GI:182449
KEYWORDS Fc-epsilon receptor; Ige receptor; cell surface receptor;
glycoprotein.
SOURCE Human EBV transformed B-cell line RPMI-8866, cDNA to mRNA, clone
pFC-epsilon-R-1.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1503)
AUTHORS Kikutani, H., Inui, S., Sato, R., Barsumian, E.L., Owaki, H.,
Yamasaki, K., Kaisho, T., Uchibayashi, N., Hardy, R.R., Hirano, T.,
Tsunasawa, S., Sakiyama, F., Suemura, M. and Kishimoto, T.

TITLE Molecular structure of human lymphocyte receptor for immunoglobulin E

JOURNAL Cell 47 (5), 657-665 (1986)

MEDLINE 87051737

COMMENT Draft entry and clean copy of sequence [1] kindly provided by H.Kikutani, 05-MAR-1987.

FEATURES

SOURCE 1. .1503
Location/Qualifiers

organism="Homo sapiens"
db_xref="taxon:9606"
map="1q21-q23"
<1. .1503
note="Fce mRNA"
186. .1148
gene="CRP1"
note="Fc-epsilon receptor membrane bound form"
186. .1151
gene="CRP1"
186. .1151
gene="CRP1"
note="Fc-epsilon receptor old gene name 'FCE1A'"
/codon_start=1
/db_xref="GDB:600-119-072"
/protein_id="AA52435.1"
/db_xref="GI:182450"
translation="MEEGQYSEIEELPRRCRRGTQIVLGLVYALMAGILTLILL
MHMDTOSLKOLEERAARNAVSOVKNSLESHHGDMAOKSOSTOISOELEELRAEQRL
KSQLELSWNRNGQADLSFKSQELNERNASDLERLREYTKLRNLELYSSGFVC
NTCEKWINFQKCTYFGKTKQWHAFTACDDMGQLVSIHSPEDDLTKHASHTG
SWIGLRNLDLGEFTWDSHVDYSNMAYGEPTSRSGEDCVMMRGSGRWMDAFCDRK
LGAWVCDRLATCTPPASGSAESMGPDSPDPDGRPLTPPSAPLHS"
633. .1148
mat_peptide
/gene="CRP1"
/note="Fc-epsilon receptor soluble form"

BASE COUNT 345 a 456 c 431 g 271 t

ORIGIN 47 bp upstream of SalI site.

Query Match 91.1%; Score 16.4; DB 93; Length 1503;
Best Local Similarity -94.4%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCCTGTGCTCTCTCTCT 18
|||||

Db 81 GCCTGTGCTCTCTCTCT 64

Search completed: April 19, 2001, 23:59:20
Job time: 9437 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:46 ; Search time 547.68 Seconds
(without alignments)
19,187 Million cell updates/sec

Title: US-09-016-464-10
Perfect score: 18
Sequence: 1 GCCTGCTCTCTCTCTCT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0401.*

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- 2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT.*
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- 4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT.*
- 6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT.*
- 8: /SIDS2/gcgdata/geneseq/geneseqn/NA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT.*
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- 19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	91.1	18	18	Human IGF receptor
2	16.4	91.1	18	18	Human FC-epsilon r
3	16.4	91.1	18	20	Human IGF receptor
4	16.4	91.1	18	20	Human FC-epsilon C
5	16.4	91.1	18	21	Human IGF receptor
6	16.4	91.1	18	21	Human IGF receptor
7	16.4	91.1	18	21	Human IGF receptor
8	16.4	91.1	18	21	Human IGF receptor
9	16.4	91.1	279	20	Human IGF receptor
10	16.4	91.1	279	21	Human IGF receptor
11	16.4	91.1	279	21	Human adenosine re

12	16.4	91.1	291	21	F20143	Human low adenosin
13	16.4	91.1	291	21	A34021	Human adenosine re
14	16.4	91.1	299	20	X54562	Human FC-epsilon C
15	16.4	91.1	299	21	F20131	Human IGF receptor
16	16.4	91.1	299	21	A34009	Human adenosine re
17	16.4	91.1	402	21	C26766	Human secreted pro
18	16.4	91.1	1127	20	Z09902	Human FC-epsilon R
19	16.4	91.1	1465	9	N81437	pL1-2 cDNA insert
20	16.4	91.1	1503	10	N90344	Plasmid pFC-epsilo
21	16.4	91.1	1503	21	F21303	Human low adenosin
22	16.4	91.1	1503	21	A35181	Human adenosine re
23	16.4	91.1	1504	9	N81485	ECORI insert from
24	16.4	91.1	1504	9	N81367	Sequence of a gene
25	16.4	91.1	1504	9	N81512	FC epsilon recepto
26	16.4	91.1	1515	10	N90134	DNA encoding FC ga
27	16.4	91.1	1529	9	N81612	Human low adenosin
28	16.4	91.1	1530	21	F21304	Human low adenosin
29	16.4	91.1	1530	21	A35182	Human adenosine re
30	16.4	91.1	1531	8	N70107	DNA encoding IGF b
31	16.4	91.1	1549	9	N82252	Human low affinity
32	16.4	91.1	3108	21	F21302	Human low adenosin
33	16.4	91.1	3108	21	A35180	Human adenosine re
34	16.4	91.1	6532	21	F21305	Human low adenosin
35	16.4	91.1	6532	21	A35183	Human adenosine re
36	16.4	91.1	7800	21	F20842	Human multiple tar
37	16.4	91.1	7803	20	X55272	Human adenosine re
38	16.4	91.1	7803	20	X55272	Human receptor-rel
39	16.4	91.1	17350	15	O72708	hOPI human osteoge
40	16.4	91.1	17410	14	O53142	Sequence encoding
41	16.4	91.1	17410	17	T18381	hOP-1 genomic DNA.
42	16.4	91.1	17410	19	V15205	Human osteogenic p
43	16.4	91.1	17410	20	Z27575	Human osteogenic p
44	16.4	91.1	17410	20	X00230	Human osteogenic p
45	16.4	91.1	17415	17	T11639	Human osteogenic p

ALIGNMENTS

RESULT	ID	1	ALIGNMENTS
T76087	T76087	standard; DNA; 18 BP.	
AC	T76087;		
XX	12-SEP-1997	(first entry)	
DE	Human IGE receptor Fc epsilon R antisense oligonucleotide HSJGBFRA31.		
XX	Asthma; airway epithelium; adenosine free; cystic fibrosis;		
KW	chronic obstructive pulmonary disease; bronchitis; immunoglobulin; ss.		
OS	Synthetic.		
XX	WO9640162-A1.		
PN	19-DEC-1996.		
PD	06-JUN-1996;	96WO-US09306.	
PF	07-JUN-1995;	95US-0474497.	
PR	(UYEC-) UNIV EAST CAROLINA.		
XX	Metzger WJ, Nyce JW;		
XX	WPI; 1997-051871/05.		
DR	Treatment of airway diseases such as asthma - by topically applying		
XX	adenosine-free antisense oligo:nucleotide to airway epithelium of		
PT	subject		
XX	Example 5; Page 25; 71pp; English.		

XX A method for treating airway disease in a subject has been produced.
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide
 CC HSGGFRCD23AS1 specific for the human IGE receptor FC epsilon R. The
 CC method can be used to treat airway diseases such as cystic fibrosis,
 CC asthma, chronic obstructive pulmonary disease, bronchitis and other
 CC airway diseases characterised by an inflammatory response. By
 CC eliminating adenosine from the antisense ON, its liberation upon
 CC antisense degradation is prevented, thereby preventing adenosine-
 CC induced bronchoconstriction in patients with hyper-reactive airways.

XX Sequence 18 BP: 0 A: 7 C: 4 G: 7 T: 0 other:

Query Match 91.1%; Score 16.4; DB 18; Length 18;
 Best Local Similarity 94.4%; Pred. No. 84;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCGTGTCCTCTCCTCC 18
 ||||||||| |||||
 Db 1 gccctgtctgtctctcct 18

RESULT 2
 T76073
 ID T76073 standard; DNA: 18 BP.
 AC T76073;
 XX
 XX
 DT 11-SEP-1997 (first entry)
 XX

DE Human FC-epsilon receptor antisense oligonucleotide HUMIGERC23AS1.
 XX
 XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
 KW chronic obstructive pulmonary disease; bronchitis; immunoglobulin; ss.
 KM
 OS Synthetic.

XX MO9640162-A1.

XX 19-DEC-1996.

XX 06-JUN-1996: 96WO-US09306.

XX 07-JUN-1995: 95US-0474497.

XX (UYEC-) UNIV EAST CAROLINA.

XX Metzger WJ, Nyce JW;

XX WPI: 1997-051871/05.

PT Treatment of airway diseases such as asthma - by topically applying
 PT adenosine-free antisense oligo:nucleotide to airway epithelium of
 PT subject

XX Claim 5; Page 25; 71pp: English.

XX A method for treating airway disease in a subject has been produced,
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide
 CC HUMIGERC23AS1 specific for the human FC-epsilon receptor CD23
 CC antigen (IGE receptor). The method can be used to treat airway diseases
 CC such as cystic fibrosis, asthma, chronic obstructive pulmonary disease,
 CC bronchitis and other airway diseases characterised by an inflammatory
 CC response. By eliminating adenosine from the antisense ON, its liberation
 CC upon antisense degradation is prevented, thereby preventing adenosine-
 CC induced bronchoconstriction in patients with hyper-reactive airways.

XX Sequence 18 BP: 0 A: 7 C: 4 G: 7 T: 0 other:

Query Match 91.1%; Score 16.4; DB 18; Length 18;
 Best Local Similarity 94.4%; Pred. No. 84;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCGTGTCCTCTCCTCC 18
 ||||||||| |||||
 Db 1 gccctgtctgtctctcct 18

RESULT 3
 X53892
 ID X53892 standard; DNA: 18 BP.
 AC X53892;
 XX
 XX
 DT 05-JUL-1999 (first entry)
 XX

DE Human IGE receptor antisense oligonucleotide fragment.
 XX
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.

XX Synthetic.

XX MO9913886-A1.

XX 25-MAR-1999.

XX 17-SEP-1998: 98WO-US19419.

XX 09-JUN-1998: 98US-0093972.

XX 17-SEP-1997: 97US-0059160.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI: 1999-229400/19.

PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 XX
 XX Disclosure: Page 44; 120pp: English.

XX The specification describes antisense oligonucleotides (X52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'universal' or alternative base, (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antihasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and

CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system peptide
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
CC
CC
SQ Sequence 18 BP: 0 A; 7 C; 4 G; 7 T; 0 other;

Query Match 91.1%; Score 16.4; DB 21; Length 18;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGTGTCTCTCTCTCT 18
DB 1 gctgtgtctgtctctct 18
|||||

RESULT 6
F19457
ID F19457 standard; DNA: 18 BP.
AC F19457;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human IGE receptor polynucleotide fragment #1024.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antilastmatic; analgesic; hypotensive; cyostatic;
XX respiratory obstruction; pulmonary obstruction; impeded respiration;
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX cancer; ss.
XX
XX
XX OS Homo sapiens.
XX
XX WO200062736-A2.
XX
XX PD 26-OCT-2000.
XX
XX PE 24-MAR-2000; 2000WO-US08020.
XX
XX PR 06-APR-1999; 99US-0127958.
XX
XX PA (UYEC-) UNIV EAST CAROLINA.
XX
XX PI (NYCE/) NYCE J W.
XX
XX NYCE JW;
XX
XX MPI: 2000-679539/66.
XX
XX DR
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
XX trigger adenosine receptors during metabolism, useful e.g. for treating
XX cancers and respiratory obstructions -
XX
XX PS Claim 14; Page 131; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antilastmatic, hypotensive and cyostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
CC
CC
SQ Sequence 18 BP: 0 A; 7 C; 4 G; 7 T; 0 other;

Query Match 91.1%; Score 16.4; DB 21; Length 18;
Best Local Similarity 94.4%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGTGTCTCTCTCTCT 18
DB 1 gctgtgtctgtctctct 18
|||||

RESULT 7
A33315
ID A33315 standard; DNA: 18 BP.
AC A33315;
XX
XX DT 28-JUL-2000 (first entry)
XX
XX DE Low adenosine antisense oligonucleotide SEQ ID NO:1004.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antilastmatic; cyostatic; analgesic; impeded airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
XX
XX OS Homo sapiens.
XX
XX WO200009525-A2.
XX
XX PD 24-FEB-2000.
XX
XX PE 03-AUG-1999; 99WO-US17712.
XX
XX PR 03-AUG-1998; 98US-0095212.
XX
XX PA (UYEC-) UNIV EAST CAROLINA.

XX NYce JW;
 PI
 XX
 DR WPI: 2000-205971/18.
 XX
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 PS
 XX
 PS Claim 18; Page 391; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A32313 to A35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, and the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
 CC to A33992) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 CC
 CC Sequence 18 BP: 0 A; 7 C; 4 G; 7 T; 0 other;
 XX
 XX

Query Match 91.1%; Score 16.4; DB 21; Length 18;
 Best Local Similarity 94.4%; Pred. No. 84;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCCTGTCTCTCCTCCT 18
 Db 1 gctgtgtctgtctcct 18
 A33335
 ID A33335 standard; DNA; 18 BP.
 AC A33335;
 XX
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Low adenosine antisense oligonucleotide SEQ ID NO:1024.
 XX
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 KM
 XX
 OS Homo sapiens.
 XX
 XX WO200009525-A2.
 XX
 XX

PD 24-FEB-2000.
 XX
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI NYce JW;
 XX
 XX
 DR WPI: 2000-205971/18.
 XX
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 PS
 XX
 PS Claim 18; Page 393; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A32313 to A35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, and the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
 CC to A33992) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 CC
 CC Sequence 18 BP: 0 A; 7 C; 4 G; 7 T; 0 other;
 XX
 XX

Query Match 91.1%; Score 16.4; DB 21; Length 18;
 Best Local Similarity 94.4%; Pred. No. 84;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCCTGTCTCTCCTCCT 18
 Db 1 gctgtgtctgtctcct 18
 X54573
 ID X54573 standard; DNA; 279 BP.
 AC X54573;
 XX
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human IGE receptor antisense oligonucleotide fragment.
 XX
 XX Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impaired respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW

KM	immunosuppressive; antialsthmatic; analgesic; hypotensive; cytostatic;
KM	respiratory obstruction; pulmonary obstruction; impeded respiration;
KM	respiratory hypoproduction; pulmonary vasoconstriction; asthma; ROS;
KM	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM	pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM	cancer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200062736-A2.
XX	
PD	26-OCT-2000.
XX	
PF	24-MAR-2000; 2000WO-US08020.
XX	
XX	06-APR-1999; 99US-0127958.
PR	
XX	(UYEC-) UNIV EAST CAROLINA.
PA	(NYCE/) NYCE J W.
XX	
PI	Nyce JW;
XX	
DR	WPI: 2000-679539/66.
XX	
PT	Low adenosine (A) content antisense oligonucleotides which do not
PT	trigger adenosine receptors during metabolism, useful e.g. for treating
PT	cancers and respiratory obstructions -
XX	
PS	Claim 14; Page 131; 1592pp: English.
XX	
CC	The present invention describes low adenosine (A) content antisense
CC	oligonucleotides and compositions (I) comprising them. In the antisense
CC	oligonucleotides the A is replaced by a 'universal' or alternative base.
CC	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC	immunosuppressive, antialsthmatic, hypotensive and cytostatic activities.
CC	The antisense oligonucleotides and (I) can be used to down-regulate the
CC	expression and or activity of target polypeptides associated with
CC	lung/respiratory disorders and malignancies, such as stimulating and
CC	activating peptide factors and transmitters, transcription factors,
CC	immunoglobulins and antibodies, antibody receptors, cytokines and
CC	chemokines, endogenously produced specific and non-specific enzymes,
CC	binding proteins, adhesion molecules and their receptors, cytokine and
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central
CC	nervous system (CNS) and peripheral nervous and non-nervous system
CC	receptors, CNS and peripheral nervous and non-nervous system peptide
CC	transmitters, defensins, growth factors, vasoactive peptides and
CC	receptors, binding proteins and malignancy associated proteins. The
CC	antisense oligonucleotides may be used in this way to treat disorders
CC	including respiratory obstruction (especially pulmonary obstruction
CC	and/or bronchoconstriction) and/or lung inflammation, allergy(es)
CC	and/or surfactant hypoproduction which are associated with a disease or
CC	condition selected from pulmonary vasoconstriction, inflammation,
CC	allergies, asthma, impeded respiration, respiratory distress syndrome
CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC	and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC	and antisense oligonucleotides used in the exemplification of the
CC	present invention.
XX	
XX	
SQ	Sequence 279 BP; 7 A; 92 C; 87 G; 78 T; 15 other;
Query Match 91.1%; Score 16.4; DB 21; Length 279;	
Best Local Similarity 94.4%; Pred. No. 88;	
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 GCGTGTGCTCTCCNCT 18
DB	18
	1 gcctgtgtcctccct 18

RESULT 11
 A34020 standard; DNA: 279 BP.
 AC A34020;
 DT 28-JUL-2000 (first entry)
 DE Human adenosine receptor related polynucleotide SEQ ID NO:1709.
 KM Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KM phosphorothioate; impaired respiration; inflammation; allergy;
 KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KM antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
 KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 KM Homo sapiens.
 OS
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PF 03-AUG-1999; 99WO-US17712.
 PR 03-AUG-1998; 98US-0095212.
 PA (UYEC-) UNIV EAST CAROLINA.
 PI Nyce JW;
 DR WPI: 2000-205971/18.
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 PS Disclosure: Page 477; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cyostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A32313 to A33312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
 CC to A33992) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 XX
 SQ Sequence 279 BP; 7 A; 92 C; 87 G; 78 T; 15 other;

Query Match 91.1%; Score 16.4; DB 21; Length 279;
 Best Local Similarity 94.4%; Pred. No. 88;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCCTGTCTCTCCCT 18
 Db 1 gccctgtctgtctccct 18
 RESULT 12
 F20143
 ID F20143 standard; DNA: 291 BP.
 XX
 AC F20143;
 DT 14-MAR-2001 (first entry)
 DE Human low adenosine antisense oligonucleotide #1710.
 KM
 KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
 KM respiratory obstruction; pulmonary obstruction; impaired respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 KM
 OS Homo sapiens.
 PN WO200062736-A2.
 PD 26-OCT-2000.
 PF 24-MAR-2000; 2000WO-US08020.
 PR 06-APR-1999; 99US-0127958.
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 PI Nyce JW;
 DR WPI: 2000-679539/66.
 XX
 CC Low adenosine (A) content antisense oligonucleotides which do not
 CC trigger adenosine receptors during metabolism, useful e.g. for treating
 CC cancers and respiratory obstructions -
 PS Claim 14; Page 543; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,

CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.

XX
SQ Sequence 291 BP; 7 A; 97 C; 89 G; 83 T; 15 other;

Query Match 91.1%; Score 16.4; DB 21; Length 291;
Best Local Similarity 94.4%; Pred. No. 88;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCTCT 18
Db 1 gccctgtctctctctct 18

RESULT 13

ID A34021 standard; DNA: 291 BP.

XX A34021;

DT 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide SEQ ID NO:1710.

XX Human: adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS WO200009525-A2.

XX 24-FEB-2000.

PD 03-AUG-1999; 99WO-US17712.

XX 03-AUG-1998; 98US-0095212.

PR (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

PI WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -

XX Disclosure: Page 477; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive

CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A3313 to A33312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A33233
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.

XX SQ Sequence 291 BP; 7 A; 97 C; 89 G; 83 T; 15 other;

Query Match 91.1%; Score 16.4; DB 21; Length 291;
Best Local Similarity 94.4%; Pred. No. 88;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCTCT 18
Db 1 gccctgtctctctctct 18

RESULT 14

ID X54562 standard; DNA: 299 BP.

XX X54562;

DT 05-JUL-1999 (first entry)

XX Human Fc-epsilon CD23 antigen antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.

XX Synthetic.

OS WO9913886-A1.

XX 25-MAR-1999.

PD 17-SEP-1998; 98WO-US19419.

XX 09-JUN-1998; 98US-0093972.

PR 17-SEP-1997; 97US-0059160.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

PI WPI; 1999-229400/19.

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
XX Disclosure: Page 43; 120pp; English.

XX The specification describes antisense oligonucleotides (X52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene

CC Initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences X55272-74. These multiple target
CC oligonucleotides (specifically X55180-271) can be used for the antisense
CC treatment of diseases and conditions. Typical diseases and conditions
CC are those associated with impaired respiration and inflammation,
CC including lung diseases, pulmonary vasoconstriction, inflammation,
CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC metastases, as well as all types of cancers which may metastasize or have
CC metastasized to the lungs, including breast and prostate cancer.

SQ Sequence 299 BP; 7 A; 98 C; 93 G; 94 T; 7 other;

Query Match 91.1%; Score 16.4; DB 20; Length 299;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCTCT 18
|||||||
Db 1 gcctgtctctctctct 18

RESULT 15

F20131
ID F20131 standard; DNA; 299 BP.

AC F20131;

DT 14-MAR-2001 (first entry)

DE Human IGE receptor polynucleotide fragment #1698.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antisthmatic; analgesic; hypotensive; cytoskeletal;
XX respiratory obstruction; pulmonary obstruction; impeded respiration;
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX cancer; ss.

OS Homo sapiens.

PN WO200062736-A2.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US08020.

PR 06-APR-1999; 99US-0127958.

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PI Nyce JW;

DR WPI; 2000-679539/66.

PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
PS Claim 14; Page 130; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antisthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasocactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.

SQ Sequence 299 BP; 7 A; 98 C; 93 G; 94 T; 7 other;

Query Match 91.1%; Score 16.4; DB 21; Length 299;
Best Local Similarity 94.4%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCTCT 18
|||||||
Db 1 gcctgtctctctctct 18

Search completed: April 20, 2001, 00:12:47
Job time: 10009 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:24:37 ; Search time 7150.85 Seconds
(without alignments)
0.368 Million cell updates/sec

Title: US-09-016-464-10

Perfect score: 18

Sequence: 1 GCCTGTCCTCTCCTCCT 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

10: gb_est10:*

11: gb_est11:*

12: gb_est12:*

13: gb_est13:*

14: gb_est14:*

15: gb_est15:*

16: gb_est16:*

17: gb_est17:*

18: gb_est18:*

19: gb_est19:*

20: gb_est20:*

21: gb_est21:*

22: gb_est22:*

23: gb_est23:*

24: gb_est24:*

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27: gb_est27:*

28: gb_est28:*

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287: gb_est287:*

288: gb_est288:*

289: gb_est


```

19 16.4 91.1 442 22 A1607542 mr88h04.y
20 16.4 91.1 448 147 BE376729 RC6-TN007
21 16.4 91.1 497 19 A1374636 ta60b04.x
22 16.4 91.1 502 215 A2069851 RPCT-23-3
23 16.4 91.1 532 201 A0062291 CIT-HSP-2
24 16.4 91.1 541 223 A2560763 RPCT-23-2
25 16.4 91.1 567 223 A2505366 A2505366
26 16.4 91.1 567 216 A2102825 RPCT-23-4
27 16.4 91.1 574 172 BG010142 MR3-GN018
28 16.4 91.1 590 140 BE872658 601451396
29 16.4 91.1 617 145 BE247873 601858211
30 16.4 91.1 617 122 A2497500 1M0334E19
31 16.4 91.1 653 170 BE878744 MR0-ET010
32 16.4 91.1 776 210 A0738613 HS-5381-B
33 16.4 91.1 865 138 BE731702 601568109
34 16.4 91.1 884 142 BE960443 601653176
35 16.4 91.1 886 145 BE208627 601871955
36 16.4 91.1 972 139 BE746998 601580740
37 16.4 91.1 993 230 CENS037PB Tetradon
38 16.4 91.1 1091 230 CENS02QMF Tetradon
39 16.4 91.1 1374 142 BE963819 601657470
40 16.4 91.1 1576 150 BE569091 602184467
41 16.4 91.1 1717 171 BE974279 602243933
42 16.4 91.1 1802 147 BE345584 602019178
43 16.4 91.1 251 220 A2390475 1M0151B21
44 16.4 91.1 387 17 A1239748 qh32f02.x
45 16.4 91.1 417 213 A0937147 NBI-669R

```

ALIGNMENTS

RESULT 1

```

LOCUS A0822796 520 bp DNA GSS 26-AUG-1999
DEFINITION HS_2205-B2.D01_MR CIT Approved Human Genomic Sperm Library D Homo
ACCESSION A0822796
VERSION A0822796.1 GI:5785189
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

```

```

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,D., Zhao,S., Adams,M.D. and
Hood,L.

```

```

TITLE Sequence-tagged connectors: A sequence approach to mapping and
JOURNAL scanning the human genome
MEDLINE Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
COMMENT 99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

```

```

BAC end Web Server: http://www.htsc.washington.edu
Plate: 2205 row: H column: 2
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 520.
Location/Qualifiers
1..520

```

```

FEATURES
source

```

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2205 Col=2 Row=H"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelOBAC1; BAC Clones in

```

```

BASE COUNT 158 a 123 c 96 g 132 t 11 others
ORIGIN

```

```

Query Match 100.0%; Score 18; DB 212; Length 520;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 GCCTGTCTCTCTCTCTCT 18
Db 355 GCCTGTCTCTCTCTCTCT 372

```

RESULT 2

```

LOCUS BE779902 1276 bp mRNA EST 20-OCT-2000
DEFINITION BE779902 601467924F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871325 5',
mrna sequence.
ACCESSION BE779902
VERSION BE779902.1 GI:10201100
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

```

```

REFERENCE NIH-MGC http://mgc.ncl.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

```

```

Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M9623 row: o column: 06
High quality sequence start: 5
High quality sequence stop: 10.
Location/Qualifiers
1..1276

```

```

FEATURES
source

```

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3871325"
/clone_lib="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pMW-SPORT6; Site:1: Not;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
BASP COUNT 430 a 257 c 368 g 220 t 1 others
ORIGIN

```

```

Query Match 100.0%; Score 18; DB 139; Length 1276;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 GCCTGTCTCTCTCTCTCT 18
Db 1148 GCCTGTCTCTCTCTCTCT 1131

```

```

RESULT 3
LOCUS F14993 329 bp mRNA EST 09-SEP-1996
DEFINITION SSC9811 Porcine small intestine cDNA library sus scrofa cDNA clone
c9b11, mRNA sequence.

```

ACCESSION F14993
 VERSION F14993.1 GI:972330
 KEYWORDS EST.
 SOURCE P19.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 REFERENCE 1 (bases 1 to 329)
 AUTHORS Winters, A.K., Fredholm, M., and Davies, W.
 TITLE Evaluation and characterization of a porcine small intestine cDNA library: analysis of 839 clones
 JOURNAL Mamm. Genome 7 (7), 509-517 (1996)
 MEDLINE 96337607
 COMMENT Contact: A.K. Winters
 Department of Animal Science and Animal Health, Division of Animal Genetics, The Royal Veterinary and Agricultural University
 Bulowvej 13, 1870 Frederiksberg C, Denmark.
 Location/Oualifiers
 FEATURES
 source 1..329
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /clone="c9b11"
 /clone_lib="Porcine small intestine cDNA library"
 /note="directionally cloned cDNA in X1-blue MRF"
 BASE COUNT 59 a 77 c 77 g 113 t 3 others
 ORIGIN
 Query Match 94.4%; Score 17; DB 152; Length 329;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CCTGTCTCTCTCTCT 18
 DB 48 CCTGTCTCTCTCTCT 64
 RESULT 4
 A1626763 444 bp mRNA EST 23-APR-1999
 LOCUS fc03b01.y1 zebrafish wshu MPIMG EST Danio rerio cDNA 5', mRNA
 DEFINITION sequence.
 ACCESSION A1626763
 VERSION A1626763.1 GI:4663563
 KEYWORDS EST.
 SOURCE zebrafish.
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Rasbortinae; Danio.
 1 (bases 1 to 444)
 Clark, M., Johnson, S.L., Lehnach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Rittler, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
 Wshu zebrafish EST Project 1998
 Unpublished (1998)
 TITLE JOURNAL
 COMMENT Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrafish@wustl.edu
 CDNA Library Preparation: Matthew Clark. CDNA library Arrayed by:
 Matthew Clark. DNA Sequencing by: Washington University Genome
 Sequencing Center Clone Distribution: Genome Systems, St. Louis,
 Missouri (web address: www.genomesystems.com) (email contact:
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 Resourcezentrum für Primatendatenbank, Berlin, Germany (web address:
 www.rzpd.de)

FEATURES
 source Seq primer: T3 ET from Amersham.
 Location/Oualifiers
 1..444
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone_lib="Zebrafish Wshu MPIMG EST"
 /sex="mixed"
 /tissue_type="26 somite embryos, adult livers, shield
 stage embryos"
 /lab_host="X1-blue MRF"
 /note="vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
 strand cDNA was primed with a Not I - oligo(dT)15 primer
 15'GACATGATCTTCATGCGCGCGCCCTTTTCTTTT3';
 double-stranded cDNA was ligated into the Not I and Sal I
 sites of the pSPORT1 vector (BRL). Library was constructed
 by Matthew Clark (Lehnach lab; ICRF, London and Max Planck
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
 analysis were selected following oligonucleotide
 hybridization fingerprinting of arrayed clones from
 zebrafish late somitogenesis (26 ss), adult liver or
 embryonic shield stage (5.6 h) libraries. Fingerprint
 data were used to computationally cluster cDNAs, and a
 single cDNA from each cluster was chosen for sequencing.
 In some cases multiple members of the same cluster were
 sequenced to assess clustering parameters or single clones
 were sequenced additional times to assess quality
 control."
 BASE COUNT 120 a 97 c 64 g 162 t 1 others
 ORIGIN
 Query Match 94.4%; Score 17; DB 22; Length 444;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CCTGTCTCTCTCTCT 18
 DB 232 CCTGTCTCTCTCTCT 248
 RESULT 5
 BF956039 137 bp mRNA EST 22-JAN-2001
 LOCUS RC4-NN1178-201100-012-a09 NN1178 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF956039
 ACCESSION BF956039.1 GI:12373314
 VERSION EST.
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 137)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 TITLE JOURNAL
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC4&cl2=RC4~NN1178-201100-012-a09&cl3=2000-11-20&cl4=1>)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 136.

FEATURES

Location/Qualifiers

1..137

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NN1178"

/dev_stage="Adult"

/note="Organ: nervous, normal. Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT

38 a 27 c 53 g 19 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 171; Length 137;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCGTGCTCTCTCTCTCT 18

Db 79 GCCGTGCTCTCTCTCTCT 62

RESULT 6

LOCUS

BF515114 139 bp mRNA EST 07-DEC-2000

UI-H-BM1-anv-e-03-0-UI-S1 NCI_CGAP_Sub7 Homo sapiens cDNA clone

IMAGE:3083620 3', mRNA sequence.

ACCESSION

BF515114

BF515114.1 GI:11600293

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 139)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:

NCI-CGAP clone distribution information can be found through the

I.M.A.G.E. Consortium/ILMIL at:

www.bio.lilil.gov/birp/image/image.html The following repetitive

elements were found in this cDNA sequence: 13-51, >(CACA

)n#Simple_repeat

Seg primer: M13 Forward

FEATURES

SOURCE

Location/Qualifiers

1..139

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NCI_CGAP_Sub7"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub7

is a subcloned library derived from NCI_CGAP_Sub6. The

NCI_CGAP_Sub7 library had 12 million recombinants. A

single-stranded DNA preparation of NCI_CGAP_Sub6 was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LHM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clones 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LHM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clones 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LHM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991, 1520904-1522439); NCI_CGAP_G4 pool 1 LHM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI_CGAP_P122 pool 1 LHM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones 985608-986759, 1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1 LHM 2644-2653, 2871-2872 (IMAGE Clones 1057416-1061255, 1144584-1145351). (6% of the driver population), plus a pool of 3,840 arrayed clones from NCI_CGAP_Sub1 (IMAGE Clones 2708616-2710535) and NCI_CGAP_Sub2 (IMAGE Clones 2710536-2712455) (4% of the driver population), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE Clones 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE Clones 2723592-2729326) (40% of the driver population), plus a pool of 4032 clones from NCI_CGAP_Sub6 (IMAGE Clones 2728969-2733190) (40% of the driver population). Subtraction was performed as previously described [Bonaldo and Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

Research 6, 791-806.
TAG_L1B=NCI_CGAP-Lu13
TAG_TISSUE=Lung
TAG_SEQ=GCCGG"

BASE COUNT

20 a 32 c 42 g 45 t

Query Match 91.1%; Score 16.4; DB 149; Length 139;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCGTGCTCTCTCTCTCT 18

Db 40 GCCGTGCTCTCTCTCTCT 57

RESULT 7

LOCUS

BF737550 223 bp mRNA EST 10-JAN-2001

CM4-KT0035-091200-583.f06 KT0035 Homo sapiens cDNA, mRNA sequence.

ACCESSION

VERSION

BF737550.1 GI:12064226

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 223)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2704922

Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=C57BL/6J-CM4&C2=CM4-KT0035-091200-005-901&C3=2000-12-15&C4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 223.

FEATURES

Location/Qualifiers

1..223
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1lb="KT0035"
 /dev_stage="Adult"

/note="Organ: bladder tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 57 a 58 c 59 g 49 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 168; Length 223;
 Best Local Similarity 94.4%; Pred. No. 1.1e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
 ||||||||| |||||
 Db 172 GCCTGTCTCTCTCTCT 189

RESULT 8 283 bp DNA GSS 09-MAY-2000
 A2098171/c LOCUS
 DEFINITION RPCI-23-462B18.TV RPCI-23 Mus musculus genomic clone RPCI-23-462B18
 , DNA sequence.
 ACCESSION A2098171
 A2098171.1 GI:7751227
 GSS.
 KEYWORDS house muscle.
 SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 283)
 Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S., Akınret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)

TITLE

Unpublished (1999)

Other_GSSs: RPCI-23-462B18.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: szhao@ligr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@edlong.med.bufileo.edu). Clones may be purchased from BACAC Resources (http://bacpac.med.bufileo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.ligr.org/ldb/bac_ends/mouse/bac_end_intro.html
 Plate: 462 row: B column: 18
 Seq primer: 17
 Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1..283
 /organism="Mus musculus"
 /strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="RPCI-23-462B18"
 /clone_1lb="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 118 a 99 c 66 g 0 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 216; Length 283;
 Best Local Similarity 94.4%; Pred. No. 1.1e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
 ||||||||| |||||
 Db 271 GCCTGTCTCTCTCTCT 254

RESULT 9 315 bp mRNA EST 13-JAN-2001
 BF823056/c LOCUS
 DEFINITION MRI-RT0038-151200-005-901 RT0038 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF823056
 BF823056.1 GI:12163527
 EST.
 KEYWORDS human.
 SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 315)
 Dias Neto, E., Garcia Correia, R., Verjowski-Almeida, S., Britones, M.R., Nagai, M.A., da Silva, M.Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Medline
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR1&C2=MR1-RT0038-151200-005-901&C3=2000-12-15&C4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 244.

FEATURES

source

Location/Qualifiers
 1..315
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1lb="RT0038"
 /dev_stage="Adult"
 /note="Organ: Kidney_tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under

BASE COUNT 67 a 86 c 88 g 74 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 169; Length 315;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
|||||

Db 119 GCCTGTCTCTCTCTCT 102

RESULT 10
BF872714 320 bp mRNA EST 17-JAN-2001
LOCUS IL3-ET0114-011100-333-F09 ET0114 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF872714
ACCESSION
VERSION BF872714.1 GI:12262844
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
AUTHORS 1 (bases 1 to 320)
Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Simpson,A.J.
Sequence tagging of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&ct=IL3-ET0114-011100-333-F09&ct3=2000-11-01<4=1)
Seq primer: puc 18 forward
High quality sequence stop: 320.
Location/Qualifiers
1..320
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0114"
/dev_stage="Adult"
/note="Organ: lung,tumor; Vector: puc18; Site:1: Smal; Site:2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 66 a 106 c 48 g 100 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 170; Length 320;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
|||||

Db 114 GCCTGTCTCTCTCTCT 131

RESULT 11
BE768406/c 338 bp mRNA EST 20-SEP-2000
LOCUS QV4-FT0005-070600-248-g02 FT0005 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE768406
ACCESSION BE768406
VERSION BE768406.1 GI:10222064
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
AUTHORS 1 (bases 1 to 338)
Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Simpson,A.J.
Sequence tagging of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=6t2-QV4-FT0005-070600-248-g02&ct3=2000-06-07<4=1)
Seq primer: puc 18 forward
High quality sequence stop: 338.
Location/Qualifiers
1..338
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FT0005"
/dev_stage="Adult"
/note="Organ: prostate,tumor; Vector: puc18; Site:1: Smal; Site:2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 84 a 81 c 96 g 77 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 139; Length 338;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
|||||

Db 69 GCCTGTCTCTCTCTCT 52

RESULT 12
AO564843 367 bp DNA GSS 29-MAY-1999
LOCUS HS_5361.A2.H04.SPEE.RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION AO564843
ACCESSION AO564843
VERSION AO564843.1 GI:4924314
KEYWORDS GSS.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia; Eutheria: Primates: Catarrhini; Hominoidea: Homo. 1 (bases 1 to 367)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end web Server: http://www.htsc.washington.edu
Plate: 937 row: 0 column: 8
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 367.
Location/Qualifiers
1..367
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

BASE COUNT 76 a 108 c 97 g 86 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 208; Length 367;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
IIIIIIIIIIIIIIIIIIII
Db 328 GCCTGTCTCTCTCTCT 345

RESULT 13
LOCUS AL118677 380 bp mRNA EST 29-FEB-2000
DEFINITION DKFZp761J0210.r1.761 (synonym: hamy2) Homo sapiens cDNA clone
ACCESSION AL118677
VERSION AL118677.1 GI:5924576
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia; Eutheria: Primates; Catarrhini; Hominoidea: Homo. 1 (bases 1 to 380)
AUTHORS Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Blum H
MIPS
Am Klopfersplitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de; sequenced by LMU (Ludwig Maximilians University, Munich/Germany) within the cDNA sequencing consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp761J0210) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp761J0210"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT 61 a 97 c 126 g 96 t
ORIGIN

Query Match 91.1%; Score 16.4; DB 105; Length 380;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
IIIIIIIIIIIIIIIIIIII
Db 201 GCCTGTCTCTCTCTCT 218

RESULT 14
LOCUS AAI54566 393 bp mRNA EST 11-FEB-1997
DEFINITION mr88h04.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
ACCESSION AAI54566
VERSION AAI54566.1 GI:1725602
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 393)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LIND; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:369999
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 347.
Location/Qualifiers
1..393
/organism="Mus musculus"
/strain="NIH/Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:604567"
/clone_lib="Stratagene mouse heart (#937316)"
/sex="pooled"

```

/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/notes="Organ: heart; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT, 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGACTTTTCTTTTCTTTT 3'"

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BASE COUNT

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112 a 116 c 85 g 80 t

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ORIGIN

```

Query Match          91.1%; Score 16.4; DB 3; Length 393;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GCCTGTCTCTCTCTCT 18
    ||||| ||||| |||||

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Db 309 GCCTGTCTCTCTCTCT 326

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RESULT 15

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A2287043

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LOCUS

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DEFINITION

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```

A2287043 406 bp DNA GSS 27-JUL-2000
RPCI-23-142C10.TJ RPCI-23 Mus musculus genomic clone RPCI-23-142C10
, DNA sequence.

```

```

ACCESSION A2287043

```

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VERSION A2287043.1 GI:9528829

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KEYWORDS

```

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SOURCE

```

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ORGANISM

```

```

MUS MUSCULUS

```

```

EUKARYOTA;

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```

MAMMALIA;

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EUTHERIA;

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RODENTIA;

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SCIUROGNATHI;

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MURIDAE;

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MURINAE;

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MUS.

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1 (bases 1 to 406)

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Zhao,S.,

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Nierman,W.,

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Feidblyum,T.,

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Malek,J.,

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Shatsman,S.,

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Akinret

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,B.,

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Levins,M.,

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McGann,S.,

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Tsegaye,G.,

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Geer,K.,

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Krol,M.,

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de Jong,P.

```

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and Fraser,C.M.

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```

Mouse BAC End Sequences from library RPCI-23

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```

Unpublished (1999)

```

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Other_GSSs: RPCI-23-142C10.TJ

```

```

Contact: Shaying Zhao

```

```

Department of Eukaryotic Genomics

```

```

The Institute for Genomic Research

```

```

9712 Medical Center Dr.,

```

```

Rockville, MD 20850, USA

```

```

Tel: 301 838 0200

```

```

Fax: 301 838 0208

```

```

Email: szhao@tigr.org

```

```

Clones are derived from the mouse BAC library RPCI-23. For BAC

```

```

library availability, please contact Pieter de Jong

```

```

(pleter@dejong.med.bufileo.edu). Clones may be purchased from

```

```

BACPAC Resources (http://bacpac.med.bufileo.edu/orderingframe.htm)

```

```

or from Resea ch Genetics (info@resgen.com). BAC end page:

```

```

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

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Plate: 142 row: C column: 10

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Seq primer: SP6

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Class: BAC ends.

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FEATURES

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Source

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Location/Qualifiers

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1..406

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/organism="Mus musculus"

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/strain="C57BL/6J"

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/db_xref="taxon:10090"

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/clone="RPCI-23-142C10"

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/clone_lib="RPCI-23"

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/sex="female"

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/lab_host="DH10B"

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/notes="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:

```

```

EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or

```

```

brain genomic DNA was isolated and partially digested

```

```

with a combination of EcoRI and EcoRI Methylase. Size

```

```

selected DNA was cloned into the pBACe3.6 vector at the

```

```

EcoRI sites. The ligation products were transformed into

```

```

DH10B electrocompetent cells (BRL Life Technologies)."

```

```

BASE COUNT          94 a 101 c 89 g 122 t
ORIGIN

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Query Match

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Best Local Similarity 91.1%; Score 16.4; DB 219; Length 406;
Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GCCTGTCTCTCTCTCT 18
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Db 25 GTCTGTCTCTCTCTCT 42

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Search completed: April 19, 2001, 23:24:40
Job time: 8157 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:27 ; Search time 280.46 Seconds
(without alignments)
11.206 Million cell updates/sec

Title: US-09-016-464-10

Perfect score: 18
Sequence: 1 GCCTGTCTCTCTCTCTCT 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2.6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2.6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2.6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2.6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2.6/ptodata/2/ina/PTCUTS.COMB.seq:*
6: /cgn2.6/ptodata/2/ina/Backfill1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16.4	91.1	1127	2	US-08-453-024-1
C 2	16.4	91.1	1127	4	US-08-070-162-1
C 3	16.4	91.1	17410	1	US-07-841-646-3
C 4	16.4	91.1	17410	1	US-08-147-023-3
C 5	16.4	91.1	17410	1	US-08-447-570-3
C 6	16.4	91.1	17410	2	US-08-449-700-3
C 7	16.4	91.1	17410	2	US-08-449-699A-3
C 8	16.4	91.1	17415	3	US-08-486-343A-1
C 9	16.4	91.1	17415	5	PCT-US95-07349-1
C 10	15.4	85.6	1183	3	US-09-029-045-11
C 11	14.8	82.2	151	1	US-08-337-268A-50
C 12	14.8	82.2	151	1	US-08-484-570A-50
C 13	14.8	82.2	397	1	US-08-330-108-8
C 14	14.8	82.2	397	5	PCT-US92-10087-8
C 15	14.8	82.2	1356	3	US-08-997-803-13
C 16	14.8	82.2	1523	3	US-08-997-803-12
C 17	14.8	82.2	1869	2	US-08-811-897A-40
C 18	14.8	82.2	1869	2	US-08-855-213-40
C 19	14.8	82.2	1960	2	US-08-463-081B-9
C 20	14.8	82.2	1960	2	US-08-461-379A-9
C 21	14.8	82.2	1960	2	US-08-462-390B-9
C 22	14.8	82.2	1960	3	US-08-463-074B-9
C 23	14.8	82.2	1960	3	US-08-465-585C-9
C 24	14.8	82.2	1960	3	US-08-652-446-9
C 25	14.8	82.2	2548	2	US-08-811-897A-41
C 26	14.8	82.2	2548	2	US-08-855-213-41
C 27	14.8	82.2	3369	2	US-08-619-198-2

C 28	14.8	82.2	4170	2	US-08-619-198-4	Sequence 4, Appli
C 29	14.8	82.2	5192	2	US-08-619-198-8	Sequence 8, Appli
C 30	14.8	82.2	5198	2	US-08-619-198-1	Sequence 1, Appli
C 31	14.4	80.0	304	1	US-08-189-199A-2	Sequence 2, Appli
C 32	14.4	80.0	1673	4	US-08-294-143-4	Sequence 4, Appli
C 33	14.4	80.0	1673	4	US-09-256-331-4	Sequence 4, Appli
C 34	14.4	80.0	2760	1	US-08-026-138E-18	Sequence 18, Appli
C 35	14.4	80.0	2760	1	US-08-026-138E-19	Sequence 19, Appli
C 36	14.4	80.0	3530	4	US-08-704-711A-10	Sequence 10, Appli
C 37	14	77.8	20303	1	US-08-370-975B-6	Sequence 6, Appli
C 38	14	77.8	26764	1	US-08-370-975B-1	Sequence 1, Appli
C 39	13.8	76.7	120	1	US-07-666-719-21	Sequence 21, Appli
C 40	13.8	76.7	120	6	5191064-1	Patent No. 5191064
C 41	13.8	76.7	153	2	US-08-611-757-12	Sequence 12, Appli
C 42	13.8	76.7	153	5	PCT-US95-05980-12	Sequence 19, Appli
C 43	13.8	76.7	213	2	US-08-332-766A-38	Sequence 38, Appli
C 44	13.8	76.7	544	2	US-08-890-980-17	Sequence 17, Appli
C 45	13.8	76.7	544	3	US-08-890-979-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-453-024-1/c
; Sequence 1, Application US/08453024
; Patent No. 5958707
; GENERAL INFORMATION:
; APPLICANT: de Vries, Jan
; APPLICANT: Jenh, Chung-Her
; APPLICANT: Narula, Satwant
; APPLICANT: Zavadny, Paul
; TITLE OF INVENTION: Human Interleukin-4 Antagonist/Agonist Screens
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Schering-Plough Corporation
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,024
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,162
; FILING DATE: 28-MAY-1993
; APPLICATION NUMBER: US07/869914
; FILING DATE: 16-APR-1992
; APPLICATION NUMBER: US07/770081
; FILING DATE: 03-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Dulak, No. 5958707/man C.
; REGISTRATION NUMBER: 31,608
; REFERENCE/DOCKET NUMBER: JBO214K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 822 7375
; TELEFAX: 201 822 7039
; TELEX: 219165
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1127 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-453-024-1

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Best Local Similarity 94.4%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCCTGTCTCTCTCTCT 18
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Db 663 GCCTGTCTCTCTCTCT 646

RESULT 2
US-08-070-162-1/c

; Sequence 1, Application US/08070162
; Patent No. 6200805

; GENERAL INFORMATION:

; APPLICANT: de Vries, Jan
; APPLICANT: Jenh, Chung-Her
; APPLICANT: Narula, Salwant
; APPLICANT: Zavadny, Paul

; TITLE OF INVENTION: Human Interleukin-4 Antagonist/Agonist Screens
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070.162
; FILING DATE: 19930528
; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US07/869914
; FILING DATE: 16-APR-1992
; APPLICATION NUMBER: US07/770081
; FILING DATE: 03-OCT-1991

; ATTORNEY/AGENT INFORMATION:
; NAME: Dulak, No. 6200805man C.
; REGISTRATION NUMBER: 31,608
; REFERENCE/DOCKET NUMBER: JB0214K

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 822 7375
; TELEFAX: 201 822 7039
; TELEX: 219165

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1127 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear

US-08-070-162-1

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Best Local Similarity 94.4%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCCTGTCTCTCTCTCT 18
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Db 663 GCCTGTCTCTCTCTCT 646

RESULT 3
US-07-841-646-3

; Sequence 3, Application US/07841646
; Patent No. 5266683

; GENERAL INFORMATION:

; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, KOY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/841.646
; FILING DATE: 19920221
; CLASSIFICATION: 530

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/248-7000
 TELEFAX: 617/248-7100
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17410 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: homo sapiens
 FEATURE:
 NAME/KEY: exon
 LOCATION: 3192..3730
 OTHER INFORMATION: /label= EXON-1
 OTHER INFORMATION: /note= "START CODON BEGINS AT POSITION 3313"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 10413..10414
 OTHER INFORMATION: /label= GAP-1
 OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
 OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 10413 AND 10414 IN
 OTHER INFORMATION: THIS SEQUENCE."
 FEATURE:
 NAME/KEY: exon
 LOCATION: 10696..10891
 OTHER INFORMATION: /label= EXON-2
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 10960..10961
 OTHER INFORMATION: /label= GAP-2
 OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
 OTHER INFORMATION: BE MISSING BETWEEN POSITION 10960 AND 10961 IN
 OTHER INFORMATION: THIS SEQUENCE."
 FEATURE:
 NAME/KEY: exon
 LOCATION: 11059..11211
 OTHER INFORMATION: /label= EXON-3
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 11351..11352
 OTHER INFORMATION: /label= GAP-3
 OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
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 OTHER INFORMATION: THIS SEQUENCE."
 FEATURE:
 NAME/KEY: exon
 LOCATION: 11420..11617
 OTHER INFORMATION: /label= EXON-4
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 NAME/KEY: misc_feature
 LOCATION: 11721..11722
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 OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 11721 AND 11722 IN
 OTHER INFORMATION: THIS SEQUENCE."
 FEATURE:
 NAME/KEY: exon
 LOCATION: 13354..13436
 OTHER INFORMATION: /label= EXON-5
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 LOCATION: 15044..15160
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 LOCATION: 17245..17410
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 US-07-841-646-3

Query Match 91.1%; Score 16.4; DB 1; Length 17410;
 Best Local Similarity 94.4%; Pred. No. 18;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GCGTGTGTCTCTCCTCT 18
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 Db 11036 GCCGTGTCTCTCCTCT 11053
 RESULT 4
 US-08-147-023-3
 ; Sequence 3, Application US/08147023
 ; Patent No. 5468845
 ; GENERAL INFORMATION:
 ; APPLICANT: OPPERMANN, HERMANN
 ; APPLICANT: OZKAYNAK, ENGİN
 ; APPLICANT: KUBERASAMPATH, THANCAVEL
 ; APPLICANT: RUEGER, DAVID C.
 ; APPLICANT: PANG, ROY H.L.
 ; TITLE OF INVENTION: OSTEOGENIC DEVICES
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
 ; STREET: 53 STATE STREET
 ; CITY: BOSTON
 ; STATE: MASSACHUSETTS
 ; COUNTRY: U.S.A.
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/147,023
 ; FILING DATE: 21-FEB-1992
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 810,560
 ; FILING DATE: 20-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 827,052
 ; FILING DATE: 28-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 660,162
 ; FILING DATE: 22-FEB-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 621,988
 ; FILING DATE: 04-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 621,849
 ; FILING DATE: 04-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 616,374
 ; FILING DATE: 21-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 600,024
 ; FILING DATE: 18-OCT-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 599,543
 ; FILING DATE: 18-OCT-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 579,865
 ; FILING DATE: 07-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 569,920
 ; FILING DATE: 20-AUG-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 483,913
 ; FILING DATE: 22-FEB-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 422,613
 ; FILING DATE: 17-OCT-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 315,342

FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 3192..3730
OTHER INFORMATION: /label= EXON-1
OTHER INFORMATION: /note= "START CODON BEGINS AT POSITION 3313"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10413..10414
OTHER INFORMATION: /label= GAP-1
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 10413 AND 10414 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 10696..10891
OTHER INFORMATION: /label= EXON-2
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10960..10961
OTHER INFORMATION: /label= GAP-2
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OTHER INFORMATION: BE MISSING BETWEEN POSITION 10960 AND 10961 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11059..11211
OTHER INFORMATION: /label= EXON-3
FEATURE:
NAME/KEY: misc_feature
LOCATION: 11351..11352
OTHER INFORMATION: /label= GAP-3
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 11351 AND 11352 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11420..11617
OTHER INFORMATION: /label= EXON-4
FEATURE:
NAME/KEY: misc_feature
LOCATION: 11721..11722
OTHER INFORMATION: /label= GAP-4
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 11721 AND 11722 IN
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FEATURE:
NAME/KEY: exon
LOCATION: 13354..13436
OTHER INFORMATION: /label= EXON-5
FEATURE:

NAME/KEY: exon
LOCATION: 15044..15160
OTHER INFORMATION: /label= EXON-6
FEATURE:
NAME/KEY: exon
LOCATION: 17245..17410
OTHER INFORMATION: /label= EXON-7
US-08-147-023-3
Query Match 91.18; Score 16.4; DB 1; Length 17410;
Best Local Similarity 94.48; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCGGTGTCCTCCTCCT 18
Db 11036 GCCCGTCTCTCCTCCT 11053
RESULT 5
US-08-447-570-3
Sequence 3, Application US/08447570
Patent No. 5714589
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,570
FILING DATE: 21-FEB-1992
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865

FILED DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 3192..3730
OTHER INFORMATION: /label= EXON-1
FEATURE:
NAME/KEY: misc-feature
LOCATION: 10413..10414
OTHER INFORMATION: /label= GAP-1
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 10413 AND 10414 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 10696..10891
OTHER INFORMATION: /label= EXON-2
FEATURE:
NAME/KEY: misc-feature
LOCATION: 10960..10961
OTHER INFORMATION: /label= GAP-2
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITION 10960 AND 10961 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11059..11211
OTHER INFORMATION: /label= EXON-3
FEATURE:
NAME/KEY: misc-feature
LOCATION: 11351..11352
OTHER INFORMATION: /label= GAP-3
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FEATURE:
NAME/KEY: exon
LOCATION: 11420..11617
OTHER INFORMATION: /label= EXON-4

FEATURE:
NAME/KEY: misc-feature
LOCATION: 11721..11722
OTHER INFORMATION: /label= GAP-4
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FEATURE:
NAME/KEY: exon
LOCATION: 13354..13436
OTHER INFORMATION: /label= EXON-5
FEATURE:
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LOCATION: 15044..15160
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LOCATION: 17245..17410
OTHER INFORMATION: /label= EXON-7
US-08-447-570-3
Query Match 91.1%; Score 16.4; DB 1; Length 17410;
Best Local Similarity 94.4%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCTGTGCTCTCTCTCT 18
DB 11036 GCCCGTGTCTCTCTCT 11053
RESULT 6
US-08-449-700-3
Sequence 3, Application US/08449700
Patent No. 5863758
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGİN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,700
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849

FILED DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 3192..3730
OTHER INFORMATION: /label= EXON-1
OTHER INFORMATION: /note= "START CODON BEGINS AT POSITION 3313"
FEATURE:
NAME/KEY: misc-feature
LOCATION: 10413..10414
OTHER INFORMATION: /label= GAP-1
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
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OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 10696..10891
OTHER INFORMATION: /label= EXON-2
FEATURE:
NAME/KEY: misc-feature
LOCATION: 10960..10961
OTHER INFORMATION: /label= GAP-2
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITION 10960 AND 10961 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11059..11211

OTHER INFORMATION: /label= EXON-3
FEATURE:
NAME/KEY: misc-feature
LOCATION: 11351..11352
OTHER INFORMATION: /label= GAP-3
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 11351 AND 11352 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11420..11617
OTHER INFORMATION: /label= EXON-4
FEATURE:
NAME/KEY: misc-feature
LOCATION: 11721..11722
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FEATURE:
NAME/KEY: exon
LOCATION: 13354..13436
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LOCATION: 15044..15160
OTHER INFORMATION: /label= EXON-6
FEATURE:
NAME/KEY: exon
LOCATION: 17245..17410
OTHER INFORMATION: /label= EXON-7
US-08-449-700-3

Query Match 91.1%; Score 16.4; DB 2; Length 17410;
Best Local Similarity 94.4%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCGTGTCCTCCTCCT 18
Db 11036 GCCGTGTCCTCCTCCT 11053

RESULT 7
US-08-449-699A-3
Sequence 3, Application US/08449699A
Patent No. 5958441
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OKAYANAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,699A
FILING DATE: 24-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023

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; FILING DATE: 01-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27, 829
; REFERENCE/DOCKET NUMBER: STK-001CP6CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7100
; TELEFAX: 617/248-7000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
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; FEATURE:
; NAME/KEY: exon
; LOCATION: 3192..3730
; OTHER INFORMATION: /label= EXON-1
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10413..10414
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; FEATURE:
; NAME/KEY: exon
; LOCATION: 10696..10891
; OTHER INFORMATION: /label= EXON-2
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; FEATURE:
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; LOCATION: 10960..10961
; OTHER INFORMATION: /label= GAP-2
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; NAME/KEY: exon
; LOCATION: 11059..11211
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; OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
; OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 11351 AND 11352 IN
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; FEATURE:
; NAME/KEY: exon
; LOCATION: 11420..11617
; OTHER INFORMATION: /label= EXON-4
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11721..11722
; OTHER INFORMATION: /label= GAP-4
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; FEATURE:
; NAME/KEY: exon
; LOCATION: 13354..13436
; OTHER INFORMATION: /label= EXON-5
;
; FEATURE:
; NAME/KEY: exon
; LOCATION: 15044..15160
; OTHER INFORMATION: /label= EXON-6
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; FEATURE:
; NAME/KEY: exon
; LOCATION: 17245..17410

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; OTHER INFORMATION: /label= EXON-7
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; US-08-449-699A-3
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; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; QY 1 GCCTGTCTCTCTCTCT 18
; DB 11036 GCCCGTCTCTCTCTCT 11053
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; RESULT 8
; US-08-486-343A-1
; Sequence 1, Application US/08486343A
; Patent No. 6071695
;
; GENERAL INFORMATION:
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: OPPERMANN, HERMANN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; TITLE OF INVENTION: MORPHOGENIC PROTEIN EXPRESSION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSER: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; ADDRESSER: INC.
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,343A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: A35
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; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, Edmund R
; REGISTRATION NUMBER: 27, 829
; REFERENCE/DOCKET NUMBER: CRP-091CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17415 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
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; US-08-486-343A-1
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; Query Match
; Best Local Similarity 91.1%; Score 16.4; DB 3; Length 17415;
; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; QY 1 GCCTGTCTCTCTCTCT 18
; DB 11041 GCCCGTCTCTCTCTCT 11058
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; RESULT 9
; PCT-US95-07349-1
; Sequence 1, Application PC/TUS9507349
; GENERAL INFORMATION:
; APPLICANT:

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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
MORPHOGEN EXPRESSION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
ADDRESS: INC.
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 07148
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07349
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,021
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-091PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)-435-9001
TELEFAX: (508)-435-0992
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17415 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-07349-1

Query Match 91.1%; Score 16.4; DB 5; Length 17415;
Best Local Similarity 94.4%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCCT 18
Db 11041 GCCCGTCTCTCTCCT 11058

RESULT 10
US-09-029-045-11/C
Sequence 11, Application US/09029045
Patent No. 6056952
GENERAL INFORMATION:
APPLICANT: Rosenberg, Amy Sonya
TITLE OF INVENTION: Selective Elimination of T Cells That
TITLE OF INVENTION: Recognize Specific Preselected Targets
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,045
FILING DATE: 02-JUN-1998

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,964
FILING DATE: 30-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/13873
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-236100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 82..1107
OTHER INFORMATION: /product="d-D MHC"
OTHER INFORMATION: /note="nucleic acid encoding d-D MHC"
US-09-029-045-11

Query Match 85.6%; Score 15.4; DB 3; Length 1183;
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Db 1031 CCTGTCTCTCTCCT 1015

RESULT 11
US-08-337-268A-50/C
Sequence 50, Application US/08337268A
Patent No. 5589336
GENERAL INFORMATION:
APPLICANT: Lee, Soohye
TITLE OF INVENTION: Diagnostic Method and Kit for
TITLE OF INVENTION: Determining Kell Blood Group
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ronald J. Baron, Esq.
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: USA
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,268A
FILING DATE: 11-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: No. 5589336e
ATTORNEY/AGENT INFORMATION:
NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 454-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550

TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
US-08-337-268A-50

Query Match 82.2%; Score 14.8; DB 1; Length 151;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCCCT 18
Db 151 GCCTGTCTCTCCCT 134

RESULT 12

US-08-484-570A-50/C
; Sequence 50, Application US/08484570A
; Patent No. 5804379
; GENERAL INFORMATION:
; APPLICANT: Lee, Soohae
; APPLICANT: Redman, Colvin L.
; TITLE OF INVENTION: Diagnostic Method and Kit for
; TITLE OF INVENTION: Determining Kell Blood Group
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ronald J. Baron, Esq.
; ADDRESS: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,570A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/337,268
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 454-3 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
US-08-484-570A-50

Query Match 82.2%; Score 14.8; DB 1; Length 151;
Best Local Similarity 88.9%; Pred. No. 77;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCTGTCTCTCCCT 18
Db 151 GCCTGTCTCTCCCT 134

RESULT 13

US-08-330-108-8
; Sequence 8, Application US/08330108
; Patent No. 5795752
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A.
; TITLE OF INVENTION: IL-2-Stimulated Gene
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,108
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,736
; FILING DATE:
; APPLICATION NUMBER: US/07/796,066
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: human
; CELL TYPE: T-cell blast
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: 10F9-T3
US-08-330-108-8

Query Match 82.2%; Score 14.8; DB 1; Length 397;
Best Local Similarity 88.9%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCCCT 18
Db 58 GCCTGTCTCTCCCT 75

RESULT 14

PCT-US92-10087-8
; Sequence 8, Application PC/TUS9210087
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A.
; TITLE OF INVENTION: IL-2-Stimulated Gene
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Title: US-09-016-464-10

Perfect score: 18

Sequence: 1 GCCTGTCTCTCTCTCTCT 18

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Post-processing: Minimum Match 0%

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24: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
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26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
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38: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
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40: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
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42: /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US6011_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	18	100.0	18	US-08-474-497-10	Sequence 10, Appl
2	18	100.0	18	US-09-016-464-10	Sequence 182, Appl
3	17	94.4	179024	US-60-212-664-182	Sequence 12, Appl
4	16.4	91.1	18	US-08-474-497-12	Sequence 104, Ap
5	16.4	91.1	18	US-09-016-464-12	Sequence 1024, Ap
6	16.4	91.1	18	US-09-509-152A-1004	Sequence 4340, Ap
7	16.4	91.1	18	US-09-509-152A-1024	Sequence 18066, A
8	16.4	91.1	18	US-09-509-152A-1709	Sequence 4340, Ap
9	16.4	91.1	275	US-09-535-897-18066	Sequence 1709, Ap
10	16.4	91.1	275	US-60-044-029-4340	Sequence 427, App
11	16.4	91.1	279	US-09-509-152A-1709	Sequence 18077, A
12	16.4	91.1	291	US-08-917-947-427	Sequence 427, App
13	16.4	91.1	291	US-09-509-152A-1710	Sequence 18077, A
14	16.4	91.1	291	US-09-535-897-18077	Sequence 427, App
15	16.4	91.1	291	US-60-025-203-427	Sequence 1698, Ap
16	16.4	91.1	299	US-09-509-152A-1698	Sequence 1509, Ap
17	16.4	91.1	323	US-09-338-425-1509	Sequence 1509, Ap
18	16.4	91.1	323	US-09-726-790-1509	Sequence 2838, Ap
19	16.4	91.1	366	US-08-971-050-2838	Sequence 2838, Ap
20	16.4	91.1	366	US-08-971-050-2838	Sequence 2838, Ap
21	16.4	91.1	366	US-08-971-050-2838	Sequence 2838, Ap
22	16.4	91.1	399	US-09-359-067-22856	Sequence 22856, A
23	16.4	91.1	407	US-09-411-999-10764	Sequence 10764, A
24	16.4	91.1	412	US-09-489-036-3385	Sequence 3385, Ap
25	16.4	91.1	415	US-09-528-409-65909	Sequence 65909, A
26	16.4	91.1	415	US-09-528-409-65909	Sequence 76266, A
27	16.4	91.1	417	US-09-293-872-26723	Sequence 76266, A
28	16.4	91.1	427	US-09-240-371-7981	Sequence 7981, Ap
29	16.4	91.1	427	US-09-277-227-20780	Sequence 20780, A
30	16.4	91.1	429	US-09-338-425-921	Sequence 921, App
31	16.4	91.1	429	US-09-726-790-921	Sequence 6800, Ap
32	16.4	91.1	432	US-09-515-026-6800	Sequence 6800, Ap
33	16.4	91.1	432	US-09-577-409-6800	Sequence 4340, Ap
34	16.4	91.1	436	US-09-234-611-4340	Sequence 4340, Ap
35	16.4	91.1	456	US-09-248-797-39141	Sequence 39141, A
36	16.4	91.1	462	US-09-489-036-30213	Sequence 30213, A
37	16.4	91.1	483	US-09-396-970-5396	Sequence 5396, Ap
38	16.4	91.1	556	US-09-620-392-27842	Sequence 27842, A
39	16.4	91.1	556	US-09-620-392-27842	Sequence 3155, Ap
40	16.4	91.1	605	US-09-432-241A-1290	Sequence 1290, Ap
41	16.4	91.1	605	US-09-637-890-4466	Sequence 4466, Ap
42	16.4	91.1	623	US-09-396-885-2489	Sequence 2489, Ap
43	16.4	91.1	642	US-09-396-885-2489	Sequence 2489, Ap
44	16.4	91.1	715	US-60-194-243-831	Sequence 831, App
45	16.4	91.1	715	US-09-396-870-8695	Sequence 8695, Ap

ALIGNMENTS

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RESULT 1
US-08-474-497-10
: Sequence 10, Application US/08474497
: GENERAL INFORMATION:
: APPLICANT: Nyce, Jonathan W.
: TITLE OF INVENTION: Method of Treatment of Lung Diseases
: TITLE OF INVENTION: Using Antisense Oligonucleotides
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth D. Sibley
: STREET: Post Office Drawer 34009
: CITY: Charlotte
: STATE: NC
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/474,497
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5218-32
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 881-3140
: TELEFAX: (919) 881-3175
: TELEX: 575102
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-474-497-10

Query Match      100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTGTCCTCCCT 18
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Db 1 GCCTGTGTCCTCCCT 18

RESULT 2
US-09-016-464-10
: Sequence 10, Application US/09016464
: GENERAL INFORMATION:
: APPLICANT: Nyce, Jonathan W.
: TITLE OF INVENTION: Method of Treatment of Lung Diseases
: TITLE OF INVENTION: Using Antisense Oligonucleotides
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth D. Sibley
: STREET: Post Office Drawer 34009
: CITY: Charlotte
: STATE: NC
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,464
FILING DATE: 30-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,497
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-016-464-10

Query Match      100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTGTCCTCCCT 18
    |||
Db 1 GCCTGTGTCCTCCCT 18

RESULT 3
US-60-212-664-182
: Sequence 182, Application US/60212664
: GENERAL INFORMATION:
: APPLICANT: Ladunga, Steve
: APPLICANT: Spier, Gene
: APPLICANT: Greenberg, Simon
: APPLICANT: Rabkin, Steven
: APPLICANT: Wang, Yu
: TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
: FILE REFERENCE: CL000687
: CURRENT APPLICATION NUMBER: US/60/212,664
: CURRENT FILING DATE: 2000-06-20
: NUMBER OF SEQ ID NOS: 636
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 182
: LENGTH: 179024
: TYPE: DNA
: ORGANISM: HUMAN
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(179024)
: OTHER INFORMATION: n = A,T,C or G
US-60-212-664-182

Query Match      94.4%; Score 17; DB 53; Length 179024;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTGTCCTCCCT 17
    |||
Db 109503 gccctgtctctccctc 109519
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RESULT 4
US-08-474-497-12
: Sequence 12, Application US/08474497
: GENERAL INFORMATION:
: APPLICANT: NYCE, Jonathan W.
: TITLE OF INVENTION: Method of Treatment of Lung Diseases
: TITLE OF INVENTION: Using Antisense Oligonucleotides
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth D. Sibley
: STREET: Post Office Drawer 34009
: CITY: Charlotte
: STATE: NC
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/474,497
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5218-32
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 881-3140
: TELEFAX: (919) 881-3175
: TELEX: 575102
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-474-497-12

Query Match          91.1%; Score 16.4; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCCTCCT 18
    |||||
Db 1 GCCTGTCTCTCCTCCT 18

RESULT 5
US-09-016-464-12
: Sequence 12, Application US/09016464
: GENERAL INFORMATION:
: APPLICANT: NYCE, Jonathan W.
: TITLE OF INVENTION: Method of Treatment of Lung Diseases
: USING ANTISENSE OLIGONUCLEOTIDES
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth D. Sibley
: STREET: Post Office Drawer 34009
: CITY: Charlotte
: STATE: NC
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/016,464
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: FILING DATE: 30-Jan-1998
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/474,497
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5218-32
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919) 881-3140
: TELEFAX: (919) 881-3175
: TELEX: 575102
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-016-464-12

Query Match          91.1%; Score 16.4; DB 14; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCCTCCT 18
    |||||
Db 1 GCCTGTCTCTCCTCCT 18

RESULT 6
US-09-509-152A-1004
: Sequence 1004, Application US/09509152A
: GENERAL INFORMATION:
: APPLICANT: NYCE, JONATHAN W.
: TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
: FORMULATIONS, KITS & APPLICATIONS
: NUMBER OF SEQUENCES: 2419
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: EPGENESIS PHARMACEUTICALS, INC.
: STREET: 7 CLARKE DRIVE
: CITY: CRANBURY
: STATE: NJ
: COUNTRY: USA
: ZIP: 08512
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: ASCII
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/509,152A
: FILING DATE: 17-Mar-2000
: CLASSIFICATION: UNKNOWN
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/059,160
: FILING DATE: 1997-09-17
: ATTORNEY/AGENT INFORMATION:
: NAME: Amzel, Viviana
: REGISTRATION NUMBER: 30,930
: REFERENCE/DOCKET NUMBER: EPI-00991
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 609-409-3035
: TELEFAX: 413-254-9245
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 1004:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1004
US-09-509-152A-1004

Query Match 91.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCCCT 18
|||||
Db 1 GCCTGTCTCTCTCCCT 18

RESULT 7
US-09-509-152A-1024
Sequence 1024, Application US/09509152A

GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509.152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059.160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30.930
REFERENCE/DOCKET NUMBER: EPI-00991
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1024:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1024:
US-09-509-152A-1024

Query Match 91.1%; Score 16.4; DB 19; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCCCT 18
|||||
Db 1 GCCTGTCTCTCTCCCT 18

RESULT 8
US-09-070-693-4340
Sequence 4340, Application US/09070693
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.

APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Aketblom, Ingrid E.
APPLICANT: Deleageane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: TNP-1 CELL LINE
NUMBER OF SEQUENCES: 5375
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070.693
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0362P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166

INFORMATION FOR SEQ ID NO: 4340:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 2757972H1
US-09-070-693-4340

Query Match 91.1%; Score 16.4; DB 14; Length 275;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCCCT 18
|||||
Db 2 GCCTGTCTCTCTCCCT 19

RESULT 9
US-09-535-897-18066
Sequence 18066, Application US/09535897

GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleageane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING TRANSCRIPTION FACTORS
FILE REFERENCE: PD-1008 CIP
CURRENT FILING DATE: 2000-03-24
CURRENT APPLICATION NUMBER: US/09/535.897
PRIOR APPLICATION DATA removed - refer to PALM or File Wrapper
NUMBER OF SEQ ID NOS: 46364
SOFTWARE: PERL Program
SEQ ID NO 18066

LENGTH: 275
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu00386202
NAME/KEY: unsure
LOCATION: 78
OTHER INFORMATION: a, t, c, g, or other
US-09-535-897-18066

Query Match 91.1%; Score 16.4; DB 20; Length 275;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
DB 2 gcctgtctctctctctct 19

RESULT 10
US-60-044-029-4340

Sequence 4340, Application US/60044029
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Aketdiom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: THP-1 CELL LINE
NUMBER OF SEQUENCES: 3375
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/044.029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0362P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 4340:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 2757972H1
US-60-044-029-4340

Query Match 91.1%; Score 16.4; DB 36; Length 275;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCTGTCTCTCTCTCT 18
DB 2 gcctgtctctctctctct 19

RESULT 11
US-09-509-152A-1709
Sequence 1709, Application US/09509152A
GENERAL INFORMATION:

APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESS:
ADDRESS: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1709:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1709:
US-09-509-152A-1709

Query Match 91.1%; Score 16.4; DB 19; Length 279;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
DB 1 gcctgtctctctctctct 18

RESULT 12
US-08-917-047-427

Sequence 427, Application US/08917047
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Aketdiom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.

```
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; NUMBER OF SEQUENCES: 2077
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/917,047
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C., Ph.D.
; REGISTRATION NUMBER: 39132
; REFERENCE/DOCKET NUMBER: PD-0230P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 845-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 427:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 1849535
; US-08-917-047-427

Query Match          91.1%; Score 16.4; DB 13; Length 291;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCTGTGTCCTCCTCCT 18
        ||||| ||||| |||||
Db      5 GCCTGTCTCTCTCCTCCT 22

RESULT 13
US-09-509-152A-1710
; Sequence 1710, Application US/09509152A
; GENERAL INFORMATION:
; APPLICANT: NYCE, JONATHAN W.
; TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
; FORMULATIONS, KITS & APPLICATIONS
; NUMBER OF SEQUENCES: 2419
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIDERMIS PHARMACEUTICALS, INC.
; STREET: 7 CLARKE DRIVE
; CITY: CRANBURY
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/509,152A
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: 60/059,160
; FILING DATE: 1997-09-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1710:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1710:
US-09-509-152A-1710

Query Match          91.1%; Score 16.4; DB 19; Length 291;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCTGTGTCCTCCTCCT 18
        ||||| ||||| |||||
Db      1 GCCTGTGTCCTCCTCCT 18

RESULT 14
US-09-535-897-18077
; Sequence 18077, Application US/09535897
; GENERAL INFORMATION:
; APPLICANT: Sellhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING TRANSCRIPTION FACTORS
; FILE REFERENCE: PD-1008 CIP
; CURRENT APPLICATION NUMBER: US/09/535,897
; CURRENT FILING DATE: 2000-03-24
; PRIOR APPLICATION DATA removed - refer to PALM or File Wrapper
; NUMBER OF SEQ ID NOS: 46364
; SOFTWARE: PERL Program
; SEQ ID NO 18077
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00284471
US-09-535-897-18077

Query Match          91.1%; Score 16.4; DB 20; Length 291;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCCTGTGTCCTCCTCCT 18
        ||||| ||||| |||||
Db      5 gccgtctctctctctcct 22

RESULT 15
US-60-025-203-427
; Sequence 427, Application US/60025203
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
```

APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Rod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: HUMAN FETAL LUNG
NUMBER OF SEQUENCES: 2077
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/025,203
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C., Ph.D.
REGISTRATION NUMBER: 39132
REFERENCE/DOCKET NUMBER: PD-0230P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 427:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 1849535
US-60-025-203-427

Query Match 91.1%; Score 16.4; DB 34; Length 291;
Best local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCTGTCCTCTCTCTCT 18
||||| |||||||||
DB 5 GCCTGTCCTCTCTCTCT 22

Search completed: April 20, 2001, 03:21:14
Job time: 14161 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:14:55 ; Search time 101.94 Seconds
(without alignments)
24.434 Million cell updates/sec

Title: US-09-016-464-10
Perfect score: 18
Sequence: 1 GCCTGTCCTCTCTCTCT 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 46985 segs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_MA_New.*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	18	US-09-543-679A-1004	Sequence 1004, Ap
2	16.4	91.1	18	US-09-543-679A-1024	Sequence 1024, Ap
3	16.4	91.1	279	US-09-543-679A-1709	Sequence 1709, Ap
4	16.4	91.1	291	US-09-543-679A-1710	Sequence 1710, Ap
5	16.4	91.1	299	US-09-543-679A-1698	Sequence 1698, Ap
6	16.4	91.1	1503	US-09-543-679A-2870	Sequence 2870, Ap
7	16.4	91.1	1530	US-09-543-679A-2871	Sequence 2871, Ap
8	16.4	91.1	3108	US-09-543-679A-2869	Sequence 2869, Ap
9	16.4	91.1	6532	US-09-543-679A-2872	Sequence 2872, Ap
10	16.4	91.1	7800	US-09-543-679A-2409	Sequence 2409, Ap
11	16.4	91.1	117608	US-09-543-679A-3002	Sequence 3002, Ap
12	15.4	85.6	504	US-60-248-505-1627	Sequence 1627, Ap
13	15.4	85.6	6401	US-60-248-505-295	Sequence 295, Ap
14	15.4	85.6	46465	US-60-248-505-318	Sequence 318, Ap
15	15.4	85.6	47614	US-60-248-505-75	Sequence 75, App1
16	15	83.3	782	US-09-739-449-1514	Sequence 1514, Ap
17	14.8	82.2	1015	US-09-739-449-1283	Sequence 1283, Ap
18	14.8	82.2	12084	US-60-248-505-239	Sequence 239, App
19	14.8	82.2	16901	US-60-248-505-259	Sequence 259, App
20	14.8	82.2	28770	US-09-817-198-3	Sequence 3, App1
21	14.8	82.2	84638	US-60-248-505-576	Sequence 576, App
22	14.8	82.2	84633	US-60-248-505-177	Sequence 177, App
23	14.8	82.2	122715	US-60-248-505-46	Sequence 46, App1
24	14.8	82.2	122716	US-60-248-505-507	Sequence 507, App
25	14.8	82.2	145803	US-60-248-505-394	Sequence 394, App
26	14.8	82.2	479674	US-60-248-505-72	Sequence 72, App1
27	14.4	80.0	428	US-09-487-566A-3275	Sequence 3275, Ap

c 28	14.4	80.0	499	4	US-08-276-163D-2516	Sequence 2516, Ap
c 29	14.4	80.0	6381	6	US-60-248-505-1593	Sequence 1593, Ap
c 30	14.4	80.0	25423	1	PCR-US01-01550-193	Sequence 193, App
c 31	14.4	80.0	25424	1	PCR-US01-01350-194	Sequence 194, App
c 32	14.4	80.0	50911	6	US-60-248-505-18	Sequence 18, App1
c 33	14.4	80.0	60442	6	US-60-248-505-261	Sequence 261, App
c 34	14.4	80.0	62078	6	US-60-248-505-439	Sequence 439, App
c 35	14.4	80.0	71885	6	US-60-248-505-661	Sequence 661, App
c 36	14.4	80.0	82150	6	US-60-248-505-268	Sequence 268, App
c 37	14.4	80.0	582670	6	US-60-248-505-4	Sequence 4, App1
c 38	14	77.8	1088	5	US-09-739-449-1512	Sequence 1512, Ap
c 39	14	77.8	104299	6	US-60-248-505-108	Sequence 108, App
c 40	13.8	76.7	25	5	US-09-543-679A-1153	Sequence 1153, App
c 41	13.8	76.7	269	5	US-09-487-566A-3822	Sequence 3822, App
c 42	13.8	76.7	327	4	US-08-276-163D-3577	Sequence 3577, App
c 43	13.8	76.7	333	4	US-08-276-163D-4472	Sequence 4472, App
c 44	13.8	76.7	380	4	US-08-276-163D-13773	Sequence 13773, A
c 45	13.8	76.7	496	4	US-08-276-163D-11198	Sequence 11198, A

ALIGNMENTS

RESULT 1
US-09-543-679A-1004
Sequence 1004, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT & METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED WITH BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSER: EPICENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1004:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1004:
US-09-543-679A-1004
Query Match 91.1%; Score 16.4; DB 5; Length 18;
Best Local Similarity 94.4%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCCT 18
 |||||
 Db 1 GCCTGTCTCTCTCCT 18

RESULT 2

US-09-543-679A-1024
 ; Sequence 1024, Application US/09543679A

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
 COMPOSITIONS, KIT & METHOD FOR TREATMENT

OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESSES:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <UNKNOWN>

INFORMATION FOR SEQ ID NO: 1024:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1024:

US-09-543-679A-1024

Query Match 91.1%; Score 16.4; DB 5; Length 18;

Best Local Similarity 94.4%; Pred. No. 18;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCCT 18

|||||

Db 1 GCCTGTCTCTCTCCT 18

RESULT 3

US-09-543-679A-1709

; Sequence 1709, Application US/09543679A

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
 COMPOSITIONS, KIT & METHOD FOR TREATMENT

OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESSES:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <UNKNOWN>

INFORMATION FOR SEQ ID NO: 1709:

SEQUENCE CHARACTERISTICS:

LENGTH: 279 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1709:

US-09-543-679A-1709

Query Match 91.1%; Score 16.4; DB 5; Length 279;

Best Local Similarity 94.4%; Pred. No. 20;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTCTCTCCT 18

|||||

Db 1 GCCTGTCTCTCTCCT 18

RESULT 4

US-09-543-679A-1710

; Sequence 1710, Application US/09543679A

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
 COMPOSITIONS, KIT & METHOD FOR TREATMENT

OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESSES:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1710:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1710:
US-09-543-679A-1710

Query Match 91.1%; Score 16.4; DB 5; Length 291;
Best Local Similarity 94.4%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
|||||
DB 1 GCCTGTCTCTCTCTCT 18

RESULT 5
US-09-543-679A-1698
Sequence 1698, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1698:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1698:

US-09-543-679A-1698

Query Match 91.1%; Score 16.4; DB 5; Length 299;
Best Local Similarity 94.4%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
|||||
DB 1 GCCTGTCTCTCTCTCT 18

RESULT 6
US-09-543-679A-2870/C
Sequence 2870, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2870:
SEQUENCE CHARACTERISTICS:
LENGTH: 1503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2870:
US-09-543-679A-2870

Query Match 91.1%; Score 16.4; DB 5; Length 1503;
Best Local Similarity 94.4%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
|||||
DB 81 GCCTGTCTCTCTCTCT 64

RESULT 7
US-09-543-679A-2871/C
Sequence 2871, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
SEQUENCE CHARACTERISTICS:
LENGTH: 1530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2871:
US-09-543-679A-2871

Query Match 91.1%; Score 16.4; DB 5; Length 1530;
Best Local Similarity 94.4%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
|||||
DB 113 GCCTGTCTCTCTCTCT 96

RESULT 8
US-09-543-679A-2869/c
Sequence 2869, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
OPERATING SYSTEM: DOS
SOFTWARE: N/A

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
SEQUENCE CHARACTERISTICS:
LENGTH: 3108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2869:
US-09-543-679A-2869

Query Match 91.1%; Score 16.4; DB 5; Length 3108;
Best Local Similarity 94.4%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCTCT 18
|||||
DB 1401 GCCTGTCTCTCTCTCTCT 1384

RESULT 9
US-09-543-679A-2872/c
Sequence 2872, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
SEQUENCE CHARACTERISTICS:
SEQUENCE DESCRIPTION: SEQ ID NO: 2872:
US-09-543-679A-2872

LENGTH: 6532 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2872:
US-09-543-679A-2872

Query Match 91.1%; Score 16.4; DB 5; Length 6532;
Best Local Similarity 94.4%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCCTCCT 18
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Db 5115 GCCTGTCTCTCCTCCT 5098

RESULT 10
US-09-543-679A-2409
Sequence 2409, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIDENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2409:
SEQUENCE CHARACTERISTICS:
LENGTH: 7800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2409:
US-09-543-679A-2409

Query Match 91.1%; Score 16.4; DB 5; Length 7800;
Best Local Similarity 94.4%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCCTCCT 18
|||||
Db 1031 GCCTGTCTCTCCTCCT 1048

RESULT 11
US-09-543-679A-3002
Sequence 3002, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIDENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 3002:
SEQUENCE CHARACTERISTICS:
LENGTH: 117608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3002:
US-09-543-679A-3002

Query Match 91.1%; Score 16.4; DB 5; Length 117608;
Best Local Similarity 94.4%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCCTCCT 18
|||||
Db 1031 GCCTGTCTCTCCTCCT 1048

RESULT 12
US-60-248-505-1627/c
Sequence 1627, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: c1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1627
LENGTH: 504
TYPE: DNA
ORGANISM: Human

US-60-248-505-1627

Query Match

85.6%: Score 15.4; DB 6; Length 504;
Best Local Similarity 94.1%: Pred. No. 58;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCTGTCTCTCTCTCT 18
|||
Db 154 CCGGTCTCTCTCTCT 138

RESULT 13

US-60-248-505-295/c
; Sequence 295, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 6401
; TYPE: DNA
; ORGANISM: human
US-60-248-505-295

Query Match

85.6%: Score 15.4; DB 6; Length 6401;
Best Local Similarity 94.1%: Pred. No. 65;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCTGTCTCTCTCTCT 18
|||
Db 2987 CCGGTCTCTCTCTCT 2971

RESULT 14

US-60-248-505-318/c
; Sequence 318, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 318
; LENGTH: 46465
; TYPE: DNA
; ORGANISM: human
US-60-248-505-318

Query Match

85.6%: Score 15.4; DB 6; Length 46465;
Best Local Similarity 94.1%: Pred. No. 71;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCTGTCTCTCTCTCT 18
|||
Db 45051 CCGGTCTCTCTCTCT 45035

RESULT 15

US-60-248-505-75
; Sequence 75, Application US/60248505

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
FILE REFERENCE: c1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75
LENGTH: 47614
TYPE: DNA
ORGANISM: human
US-60-248-505-75

Query Match

85.6%: Score 15.4; DB 6; Length 47614;
Best Local Similarity 94.1%: Pred. No. 71;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCTGTCTCTCTCTCT 18
|||
Db 6398 cctgtctctctctct 6414

Search completed: April 20, 2001, 00:15:00
Job time: 9437 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:59:20 ; Search time 2028.86 Seconds
(without alignments)
54.633 Million cell updates/sec

Title: US-09-016-464-11

Perfect score: 18
Sequence: 1 GCCCTTCCTGGTCTCTT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_bal:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
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13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
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17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
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91: gb_vl34:*
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93: gb_vl36:*
94: gb_vl37:*
95: gb_vl38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	696	10	AX074290 Sequence
2	18	100.0	696	10	AX074292 Sequence
3	18	100.0	1068	9	A21606 human FC ep
4	18	100.0	1068	9	AX026808 Sequence
5	18	100.0	1081	93	HUMMC1AA
6	18	100.0	1198	10	AX074287 Sequence
7	18	100.0	1198	10	AX074289 Sequence
8	18	100.0	1198	92	HSFCERT
9	18	100.0	7659	93	AB045365 Homo sapien
10	18	100.0	126549	85	AB045365 Homo sapi
11	18	100.0	184997	82	AL513323 Homo sapi

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c 12 18 100.0 239684 90 AP002535 Homo sapi
13 17 94.4 126091 60 AC008420 Homo sapi
14 16.4 1010 54 CDS078AN
15 16.4 1198 10 109686
16 16.4 3508 5 AF053538
17 16.4 47274 78 AC087391 Alvinella
18 16.4 58009 78 AC087383 AC087383 Homo sapi
19 16.4 67870 77 AC083787 AC083787 Homo sapi
20 16.4 67870 77 AC083787 AC083787 Homo sapi
21 16.4 110000 60 AC008653_2 Continuation (3 of
22 16.4 91.1 124764 60 AC008377 Homo sapi
23 16.4 91.1 136411 79 AL157904 Homo sapi
24 16.4 91.1 136411 79 AL157904 Homo sapi
25 16.4 91.1 142942 62 AC010501 AC010501 Homo sapi
26 16.4 91.1 146691 83 AP002402 AP002402 Homo sapi
27 16.4 91.1 147366 64 AC015920 AC015920 Homo sapi
28 16.4 91.1 150762 70 AC026246 AC026246 Homo sapi
29 16.4 91.1 158665 80 AL356138 AL356138 Homo sapi
30 16.4 91.1 159577 77 AC080060 AC080060 Homo sapi
31 16.4 91.1 161222 64 AC016037 AC016037 Homo sapi
32 16.4 91.1 162349 81 AL445231 AL445231 Homo sapi
33 16.4 91.1 163082 67 AC022142 AC022142 Homo sapi
34 16.4 91.1 167477 67 AC022529 AC022529 Homo sapi
35 16.4 91.1 168318 68 AC024042 AC024042 Homo sapi
36 16.4 91.1 170864 77 AC087057 AC087057 Homo sapi
37 16.4 91.1 171092 68 AC023232 AC023232 Homo sapi
38 16.4 91.1 173426 62 AC011960 AC011960 Homo sapi
39 16.4 91.1 174957 71 AC034131 AC034131 Homo sapi
40 16.4 91.1 175601 65 AC016712 AC016712 Homo sapi
41 16.4 91.1 176291 87 AC024610 AC024610 Homo sapi
42 16.4 91.1 176742 86 AC007386 AC007386 Homo sapi
43 16.4 91.1 178097 65 AC016704 AC016704 Homo sapi
44 16.4 91.1 181524 73 AC064872 AC064872 Homo sapi
45 16.4 91.1 183171 67 AC022176 AC022176 Homo sapi
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ALIGNMENTS

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RESULT 1
AX074290/c 696 bp DNA PAT 06-FEB-2001
LOCUS AX074290
DEFINITION Sequence 4 from Patent WO0104310.
ACCESSION AX074290
VERSION AX074290.1 GI:12710477
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS Weber,E.R., Wood,K.V. and Hall,M.P.
TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic
JOURNAL acid molecules, fusion proteins and uses thereof
PATENT: WO 0104310-A 4 18-JAN-2001;
Heska Corporation (US) ; PROMEGA CORPORATION (US)
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FEATURES
SOURCE location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="unnamed protein product"
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/protein_id="CAC28464.1"
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/translation="VPOKPKVSLNPMNRIRKGENVTLTGNGNFEVSSTKWPHNGS
LSEETNSLNIIVNAKFEDESGEYKCOHQVNSSEPYLLEFDMILQASAEVWGCP
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BASE COUNT 208 a 150 c 159 g 179 t
ORIGIN
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Query Match 100.0% Score 18; DB 10; Length 696;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCCTTCCGTCGTTCTCTT 18
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Db 651 GCCTTCCGTCGTTCTCTT 634
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RESULT 2

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AX074292 696 bp DNA PAT 06-FEB-2001
LOCUS AX074292
DEFINITION Sequence 6 from Patent WO0104310.
ACCESSION AX074292
VERSION AX074292.1 GI:12710479
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 696)
AUTHORS Weber,E.R., Wood,K.V. and Hall,M.P.
TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic
JOURNAL acid molecules, fusion proteins and uses thereof
PATENT: WO 0104310-A 6 18-JAN-2001;
Heska Corporation (US) ; PROMEGA CORPORATION (US)
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FEATURES
SOURCE location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 179 a 159 c 150 g 208 t
ORIGIN
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Query Match 100.0% Score 18; DB 10; Length 696;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GCCTTCCGTCGTTCTCTT 18
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Db 46 GCCTTCCGTCGTTCTCTT 63
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RESULT 3
A21606/c 1068 bp DNA PAT 21-JUL-1994
LOCUS A21606
DEFINITION human Fc epsilon RIIa.
ACCESSION A21606
VERSION A21606.1 GI:579605
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1068)
AUTHORS HYBRID Fc RECEPTOR MOLECULES
JOURNAL Patent: WO 9106570-A 29 16-MAY-1991;
TITLE Location/Qualifiers
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/db_xref="SWISS-PROT:P12319"
/translation="MAPAMESPTLTCVALLFFAPDGVLAVPQKPKVSLNPMNRIFKGE
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FEATURES
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/db_xref="taxon:9606"
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gene
CDS
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BASE COUNT 208 a 150 c 159 g 179 t
ORIGIN
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DTGLFISTQOOVTFLLIKRTKRGRLLNPHKPPKNN"

BASE COUNT 330 a 215 c 229 g 294 t

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 1068;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTT 18
|||||

Db 765 GCCTTCTGCTGTTCTT 748

RESULT 4
AX026808/c 1068 bp DNA PAT 16-SEP-2000
LOCUS AX026808
DEFINITION Sequence 14 from Patent EP1006183.
ACCESSION AX026808
VERSION AX026808.1 GI:10187941
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1068)

AUTHORS Recombinant soluble fc receptors
TITLE Patent: EP 1006183-A 14 07-JUN-2000;
JOURNAL MAX PLANCK GESELLSCHAFT (DE)

FEATURES
SOURCE location/Qualifiers
1..1068
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 330 a 215 c 229 g 294 t

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 1068;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTT 18
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Db 765 GCCTTCTGCTGTTCTT 748

RESULT 5
HUMNCIAA/c 1081 bp mRNA PRI 11-JUN-1993
LOCUS HUMNCIAA
DEFINITION Human mast cell Ige receptor alpha-chain.
ACCESSION J03605
VERSION J03605.1 GI:187449
KEYWORDS immunoglobulin-like sequence; receptor.
SOURCE Human mast cell line KU812, cDNA to mRNA, clone pAS-h-IgE-110B.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1081)

AUTHORS Shimizu,A., Tepler,I., Benfey,P.N., Berenstein,E.H.,
Sizargian,A.R.P. and Leder,P.
TITLE Human and rat mast cell high-affinity immunoglobulin E receptors:
JOURNAL Characterization of putative alpha-chain gene products
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911 (1988)
COMMENT 8818102

Computer-readable copy of sequence in [1] kindly provided by
P.Leder, 08-FEB-1988.
FEATURES
SOURCE location/Qualifiers
1..1081
/organism="Homo sapiens"
/db_xref="taxon:9606"

mRNA
/note="mast cell Ige receptor alpha-chain mRNA"
35..808
CDS
/note="mast cell Ige receptor alpha-chain"
/codon_start=1
/protein_id="AAA36204.1"
/db_xref="GI:307164"

Query Match 100.0%; Score 18; DB 93; Length 1081;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTT 18
|||||

Db 760 GCCTTCTGCTGTTCTT 743

RESULT 6

AX074287/c 1198 bp DNA PAT 06-FEB-2001
LOCUS AX074287
DEFINITION Sequence 1 from Patent WO0104310.
ACCESSION AX074287
VERSION AX074287.1 GI:12710474
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1198)

AUTHORS Weber,E.R., Wood,K.V. and Hall,M.P.
TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic
JOURNAL acid molecules, fusion proteins and uses thereof
Heska Corporation (US) ; PROMEGA CORPORATION (US)
location/Qualifiers
1..1198
/organism="Homo sapiens"
/db_xref="taxon:9606"

FEATURES
SOURCE

CDS
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC28463.1"
/db_xref="GI:12710475"

BASE COUNT 389 a 243 c 245 g 321 t

ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 1198;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTT 18
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Db 832 GCCTTCTGCTGTTCTT 815

RESULT 7
AX074289 1198 bp DNA PAT 06-FEB-2001
LOCUS AX074289
DEFINITION Sequence 3 from Patent WO0104310.

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ACCESSION      AX074289
VERSION        AX074289.1   GI:12710476
KEYWORDS
SOURCE
ORGANISM       human.
                Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo..
REFERENCE
AUTHORS        Weber,E.R., Wood,K.V., and Hall,M.P.
TITLE          Fc epsilon receptor luminescence inducing protein chimeric nucleic
                acid molecules, fusion proteins and uses thereof
                Patent: WO 0104310-A 3 18-JAN-2001;
JOURNAL         Heska Corporation (US) : PROMEGA CORPORATION (US)
FEATURES
Source
1..1198
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT     321 a      245 c      243 g      389 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Ox             1 GCCTTCCGTGGTCCTT 18
Db             367 GCCTTCCGTGCTCTCT 384
RESULT         8
LOCUS          HSFCERI 1198 bp mRNA PRI 21-MAR-1995
DEFINITION     Human mRNA for high affinity IGE receptor alpha-subunit (FCERI).
ACCESSION      X06948
VERSION        X06948.1   GI:31317
KEYWORDS       FCERI gene; IGE receptor alpha-subunit.
SOURCE         human.
ORGANISM       Homo sapiens
                Eumaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS        Kochan,J.P.
TITLE          Direct Submission
JOURNAL         Submitted (24-FEB-1988) Kochan J. P., Hoffman-La Roche, Dept
                Molecular Genetics, 340 Kingsland, Nutley, New Jersey 07110.
                2 (bases 1 to 1198)
AUTHORS        Kochan,J., Pettine,L.F., Hakimi,J., Kishi,K. and Kinet,J.P.
TITLE          Isolation of the gene coding for the alpha subunit of the human
                high affinity Ige receptor
                Nucleic Acids Res. 16 (8), 3584 (1988)
JOURNAL         88233953
COMMENT         *source cell line=KUB12; library=lamba gt11 cDNA.
FEATURES
Source
location/Qualifiers
1..1198
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cclone="PLJ587 & PLJ663"
107..181
/product="put. signal peptide (AA -25 to -1)"
107..880
/note="precursor (AA -25 to 232)"
/codon_start=1
/protein_id="CAA30025.1"
/db_xref="GI:31318"
/db_xref="SWISS-PROT:P12319"
/translacion="MAPAMESPTLLCAVALLFPADGVLAIPQPKVISLNPWNRIEKG
ENVVLICNGNNEFEVSSTKMFNSLSLETNSSLIYNAKEDSGEKCOHQVNESSE
PVIYLEVEDSLILLOASAEEVMEGOLFIRCHIGMRMDVYKYIYYDGAALIKVENHNH
ISYNATVDSDGTYCGKVMQLDYESPLNTIVTKAPREKYMQLGFIPLVILFAVA
DTGFGITGOOVFTFLKKTRRKGRFRLNPPKRPNKN"
182..877
/product="mature IGE receptor (AA 1-232)"

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misc_feature	182..718	/note="put. extracellular domain"
misc_feature	719..778	/note="put. transmembrane region"
misc_feature	779..877	/note="put. cytoplasmic tail"
BASE COUNT	389 a 243 c 245 g 321 t	
ORIGIN		
Query Match	100.0%; Score 18; DB 92; Length 1198;	
Best Local Similarity	100.0%; Pred. No. 12;	
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 GCCTTCTGCTTCCTT 18 	
Db	832 GCCTTCTGCTTCCTT 815	
RESULT	9	
HUMIGERA/c	HUMIGERA	7659 bp DNA PRI 26-JAN-1994
LOCUS	Homo sapiens immunoglobulin receptor alpha chain gene, complete cds.	
DEFINITION	L14075	GI:410211
ACCESSION	L14075	GI:410211
VERSION	L14075.1	
KEYWORDS	Ig receptor alpha chain; Immunoglobulin.	
SOURCE	Homo sapiens DNA.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 7659)	
AUTHORS	Pang,Y., Taylor,G.R., Munroe,D.G., Ishaque,A., Fung-Leung,W.P., Lau,C.Y., Liu,F.T. and Zhou,L.	
TITLE	Characterization of the gene for the human high affinity Ige receptor (Fc epsilon RI) alpha-chain	
JOURNAL	J. Immunol. 151 (11), 6166-6174 (1993)	
MEDLINE	94065170	
FEATURES		
source	Location/Qualifiers	
	1..7659	
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	/db_xref="taxon:9606"	
	/tissue-type="placenta"	
	/tissue_lib="Clontech Cat. #L1067j"	
	1258..7146	
	1258..1341	
	/number=1	
	join(1287..1341,1776..1796,2850..3104,4910..5167,6670..6834)	
	/product="immunoglobulin receptor alpha chain"	
	/codon_start=1	
	/protein_id="AAA16115.1"	
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	/translation="MAPAMESPTLLCAVALLFFAPDGVLAVPQKPKVSLNPWNRTFKKENVLTTCGNHFEFVSSTKPFHNGSLSEITVNAKFEDEGTCQHQVNESEPVYLEVSDMLLQASAEVMEGQPLFRCHGMRMDYKVIYKDEGALYENHNHISINATVEEDSGTYCTGKVMQDYESEPLITVTKAPREKYLQFFILVLILFAVADTGFIETQDQVFTFLAKIKRTRKGFRLNPHRPKNKN"	
	1342..1775	
	/number=1	
	1776..1796	
	/number=2	
	1797..2849	
	/number=2	
	2850..3104	
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	3105..4909	
	/number=3	
	4910..5167	
	/number=4	
	5168..6669	
	/number=4	
	6670..7146	

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/number=5
polyA_signal      7044..7049
polyA_signal      7104..7109
polyA_signal      7109..7114
BASE COUNT      2270 a 1451 c 1538 g 2400 t
ORIGIN
Query Match      100.0%; Score 18; DB 93; Length 7659;
Best Local Similarity 100.0%; Pred.No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCTTCCTGCTCTCTT 18
        |||
Db      6806 GCCTTCCTGCTCTCTT 6789

RESULT 10
AB045365/c      DNA      PRI      04-JUL-2000
LOCUS      AB045365/c
DEFINITION      Homo sapiens genomic DNA, chromosome 1q22-q23, clone:622b6,
complete sequence.
ACCESSION      AB045365
VERSION      AB045365.1 GI:8918549
KEYWORDS      HTG.
SOURCE      Homo sapiens
ORGANISM      Homo sapiens DNA, clone_lib:PAC RPC14 and 5 clone:622b6.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (sites)
AUTHORS      Shimizu,T., Ando,A., Takishima,N., Kikkawa,E., Iwata,K.,
Kikumura,Y., Kuwano,Y., Yamazaki,M., Soeda,E. and Inoko,H.
TITLE      A 1,139,684 bp region encompassing CD1 genes on human chromosome
1q22-q23
JOURNAL      Unpublished (2000)
REFERENCE      2 (bases 1 to 126549)
AUTHORS      Shimizu,T.
TITLE      Direct Submission
JOURNAL      Submitted (30-JUN-2000) to the DDBJ/EMBL/GenBank databases. Takashi
Shima, Tokai University School of Medicine, Molecular Life Science
2, Bohseidai, Isehara, Kanagawa 259-1193, Japan
(E-mail:tsuhlina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121(ex.2582),
Fax:81-463-94-8884)
FEATURES
source      1. 126549
              Location/Qualifiers
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /chromosome="1"
              /clone="622b6"
              /clone_lib="PAC RPC14 and 5"
              /map="1q22-q23"
BASE COUNT      37251 a 26186 c 25055 g 38057 t
ORIGIN

Query Match      100.0%; Score 18; DB 85; Length 126549;
Best Local Similarity 100.0%; Pred.No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCTTCCTGCTCTCTT 18
        |||
Db      116930 GCCTTCCTGCTCTCTT 116913

RESULT 11
AL513323      AL513323      184997 bp      DNA      HTG      01-FEB-2001
LOCUS      Homo sapiens chromosome 1 clone RP11-550P17, *** SEQUENCING IN
DEFINITION      PROGRESS ***, 33 unordered pieces.
ACCESSION      AL513323
VERSION      AL513323.2 GI:12657242
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
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ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE      1 (bases 1 to 184997)
JOURNAL      Pavlitt,R.
Direct Submission
Submitted (31-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Feb 2, 2001 this sequence version replaced gi:12655355.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA550P17
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: l08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 170807 bases at least Q40
Consensus quality: 176835 bases at least Q30
Consensus quality: 179764 bases at least Q20
Insert size: 181797; sum-of-ctigs
Insert size: 199167; 5.4% error; agarose-fp
Quality coverage: 3.38x in Q20 bases; sum-of-ctigs Quality
Coverage: 3.35x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1      3393: contig of 3393 bp in length
*      3394 3493: gap of 100 bp
*      3494 10260: contig of 6767 bp in length
*      10261 10360: gap of 100 bp
*      10361 13496: contig of 3136 bp in length
*      13497 13596: gap of 100 bp
*      13597 20609: contig of 7013 bp in length
*      20610 20709: gap of 100 bp
*      20710 22882: contig of 2173 bp in length
*      22883 22982: gap of 100 bp
*      22983 25902: contig of 2920 bp in length
*      25903 26002: gap of 100 bp
*      26003 29694: contig of 3692 bp in length
*      29695 29794: gap of 100 bp
*      29795 31812: contig of 2018 bp in length
*      31813 31912: gap of 100 bp
*      31913 45010: contig of 13098 bp in length
*      45011 45110: gap of 100 bp
*      45111 51556: contig of 6446 bp in length
*      51557 51656: gap of 100 bp
*      51657 55646: contig of 3590 bp in length
*      55647 55746: gap of 100 bp
*      55747 62513: contig of 6767 bp in length
*      62514 62613: gap of 100 bp
*      62614 69331: contig of 6718 bp in length
*      69332 69431: gap of 100 bp
*      69432 73006: contig of 3575 bp in length
*      73007 73106: gap of 100 bp
*      73107 75678: contig of 2572 bp in length
*      75679 75778: gap of 100 bp
*      75779 94410: contig of 18632 bp in length
*      94411 94510: gap of 100 bp
*      94511 96724: contig of 2214 bp in length
*      96725 96824: gap of 100 bp
*      96825 103301: contig of 6477 bp in length
*      103302 103401: gap of 100 bp
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* 103402 106636: contig of 3235 bp in length
* 106637 106736: gap of 100 bp
* 106737 117270: contig of 10534 bp in length
* 117271 117370: gap of 100 bp
* 117371 123262: contig of 5892 bp in length
* 123263 123362: gap of 100 bp
* 123363 129797: contig of 6435 bp in length
* 129798 129897: gap of 100 bp
* 129898 133490: contig of 3593 bp in length
* 133491 133590: gap of 100 bp
* 133591 141466: contig of 7876 bp in length
* 141467 141566: gap of 100 bp
* 141567 144951: contig of 3385 bp in length
* 144952 145051: gap of 100 bp
* 145052 149403: contig of 4352 bp in length
* 149404 149503: gap of 100 bp
* 149504 151872: contig of 2369 bp in length
* 151873 151972: gap of 100 bp
* 151973 155452: contig of 3480 bp in length
* 155453 155552: gap of 100 bp
* 155453 159442: contig of 3890 bp in length
* 159443 159542: gap of 100 bp
* 159543 162257: contig of 2715 bp in length
* 162258 162357: gap of 100 bp
* 162358 166835: contig of 4478 bp in length
* 166836 166935: gap of 100 bp
* 166936 174278: contig of 7343 bp in length
* 174279 174378: gap of 100 bp
* 174379 184997: contig of 10619 bp in length.

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FEATURES
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            /db_xref="taxon:9606"
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            /clone_11b="RP11-11.2"
            1. 3393
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                fragment_chain:1"

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    fragment_chain:1"
    10361..13496
    /note="assembly-fragment:00863
    fragment_chain:1"
    13597..20609
    /note="assembly-fragment:00946
    fragment_chain:1"
    20710..22882
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    22983..25902
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    75779..94410
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    94511..96724
    /note="assembly-fragment:01062
    fragment_chain:5"
    96825..103301
    /note="assembly-fragment:01288
    fragment_chain:5"
    103402..106636
    /note="assembly-fragment:01064
    fragment_chain:6"
    106737..117270
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    117371..123262
    /note="assembly-fragment:01255
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Query Match 100.0%; Score 18; DB 82; Length 184997;
Best Local Similarity 100.0%; Pred. No. 29;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCCTGCTCTCTT 18

DB 31018 GCCTTCCTGCTCTCTT 31035

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RESULT 12
AP002535/c 239684 bp DNA PRI 17-JUN-2000
LOCUS Homo sapiens genomic DNA, chromosome 1q22-q23, CDI region, section
DEFINITION 4/4.
ACCESSION AP002535
VERSION AP002535.1 GI:8570526
KEYWORDS
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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REFERENCE 1 (sites) Shilina,T., Takishima,N. and Inoko,H.
AUTHORS DNA sequence analysis of a 1.1-Mb region on chromosome 1q22-q23
TITLE Published Only in Database (2000) In press
JOURNAL

```

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REFERENCE      2 (bases 1 to 239684)
AUTHORS        Hirakawa,M. and Yamaguchi,H.
TITLE          Direct Submission
JOURNAL        Submitted (15-JUN-2000) to the DDBJ/EMBL/GenBank databases. Mita
                Hirakawa, Japan Science and Technology Corporation (JST), Advanced
                Databases Department, 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
                Japan (E-mail:mika@tokyo.jst.go.jp,
                URL:http://www-alls.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
                Fax:81-3-5214-8470)
COMMENT        This sequence is conducted by Tokai University
                as a JST sequencing Team.
                Principal Investigator: Hidetoshi Inoko Ph.D
                Phone:+81-463-93-1121, Fax:+81-463-94-8884,
                The sequence is submitted by Human Genome Sequencing in ALIS
                project of JST
                Japan Science and Technology Corporation (JST)
                5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
                For further information about this sequences,
                please visit our sequence archive web site
                (http://www-alls.tokyo.jst.go.jp/HGS/top.html)
                or send email to webmaster@www-alls.tokyo.jst.go.jp.

FEATURES
Source         1..239684
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                /db_xref="taxon:9606"
                /map="1q22-q23"
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                RH49477:The location is between each flanking site of PCR
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                RH49671:The location is between each flanking site of PCR
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                RH42663:The location is between each flanking site of PCR
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                primers.
                RH49672:The location is between each flanking site of PCR
                primers.
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                /db_xref="GDB:4562103"
                complement(123902..124025)
                /note="RH10586:The location is between each flanking site
                of PCR primers."
                /db_xref="GDB:4563254"
                complement(124038..124168)
                /note="SHGC-16876:The location is between each flanking
                site of PCR primers."
                /db_xref="GDB:732985"
                126979..127201
                /note="P38/39:The location is between each flanking site
                of PCR primers."
                /db_xref="GDB:728415"
                127118..128676
                /gene="FY"

REFERENCE      2 (bases 1 to 239684)
AUTHORS        Hirakawa,M. and Yamaguchi,H.
TITLE          Direct Submission
JOURNAL        Submitted (15-JUN-2000) to the DDBJ/EMBL/GenBank databases. Mita
                Hirakawa, Japan Science and Technology Corporation (JST), Advanced
                Databases Department, 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
                Japan (E-mail:mika@tokyo.jst.go.jp,
                URL:http://www-alls.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
                Fax:81-3-5214-8470)
COMMENT        This sequence is conducted by Tokai University
                as a JST sequencing Team.
                Principal Investigator: Hidetoshi Inoko Ph.D
                Phone:+81-463-93-1121, Fax:+81-463-94-8884,
                The sequence is submitted by Human Genome Sequencing in ALIS
                project of JST
                Japan Science and Technology Corporation (JST)
                5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
                For further information about this sequences,
                please visit our sequence archive web site
                (http://www-alls.tokyo.jst.go.jp/HGS/top.html)
                or send email to webmaster@www-alls.tokyo.jst.go.jp.

FEATURES
Source         1..239684
                location/Qualifiers
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /map="1q22-q23"
                /chromosome="1"
                complement(29448..29598)
                /note="RH2183:The location is between each flanking site
                of PCR primers.
                RH49477:The location is between each flanking site of PCR
                primers.
                RH49671:The location is between each flanking site of PCR
                primers."
                65700..65871
                /note="RH49465:The location is between each flanking site
                of PCR primers."
                119084..119245
                /note="RH12336:The location is between each flanking site
                of PCR primers."
                /db_xref="GDB:4565482"
                122637..122787
                /note="RH30693:The location is between each flanking site
                of PCR primers.
                RH42663:The location is between each flanking site of PCR
                primers.
                RH49278:The location is between each flanking site of PCR
                primers.
                RH49672:The location is between each flanking site of PCR
                primers.
                RH85534:The location is between each flanking site of PCR
                primers."
                complement(123236..123423)
                /note="RH75337:The location is between each flanking site
                of PCR primers."
                complement(123894..124073)
                /note="STS638:The location is between each flanking site
                of PCR primers."
                /db_xref="GDB:4562103"
                complement(123902..124025)
                /note="RH10586:The location is between each flanking site
                of PCR primers."
                /db_xref="GDB:4563254"
                complement(124038..124168)
                /note="SHGC-16876:The location is between each flanking
                site of PCR primers."
                /db_xref="GDB:732985"
                126979..127201
                /note="P38/39:The location is between each flanking site
                of PCR primers."
                /db_xref="GDB:728415"
                127118..128676
                /gene="FY"

BASE COUNT    71522 a 50229 c 47327 g 70606 t
ORIGIN
Query Match   100.0%; Score 18; DB 90; Length 239684;
Best Local Similarity 100.0%; Pred. No.31;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY            1 GCCTTCTGCTGCTCTT 18
Db 230065 GCCTTCTGCTGCTCTT 230048

RESULT 13
AC008420
LOCUS         Homo sapiens chromosome 5 clone CTC-296f5, WORKING DRAFT SEQUENCE,
DEFINITION   11 unordered pieces.
ACCESSION    AC008420
VERSION      AC008420.4 GI:7708843
KEYWORDS     HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1 (bases 1 to 126091)
AUTHORS      DOE Joint Genome Institute.
TITLE        Sequencing of Human Chromosome 5
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 126091)
AUTHORS      DOE Joint Genome Institute.
TITLE        DOE Joint Genome Institute.
JOURNAL      Direct Submission
COMMENT      Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
                Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                On May 5, 2000 this sequence version replaced gi:7454121.
                -----Genome Center
                Center: Joint Genome Institute
                Center Code: JGI
                Web site: http://www.jgi.doe.gov
                -----
                Project Information
                Center Project Name: 298968
                Center Clone name: CIT-HSPC_296F5
                -----
                Summary Statistics
                Consensus quality: 114778 bases at least Q40
                Consensus quality: 121878 bases at least Q30
                Consensus quality: 123441 bases at least Q20
                Estimated insert size: 132000; pulse field gel estimation
                Estimated insert size: 125091; sum-of-contigs estimation

```

Quality coverage: 4.98 in Q20 bases; pulse field gel estimation
Quality coverage: 5.26 in Q20 bases; sum-of-conflicts estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 2082: contig of 2082 bp in length
* 2083 2182: gap of unknown length
* 2183 4882: contig of 2700 bp in length
* 4883 4982: gap of unknown length
* 4983 8359: contig of 3377 bp in length
* 8360 8459: gap of unknown length
* 8460 17239: contig of 8780 bp in length
* 17240 17339: gap of unknown length
* 17340 25631: contig of 8292 bp in length
* 25632 25731: gap of unknown length
* 25732 35006: contig of 9275 bp in length
* 35007 35107: gap of unknown length
* 35107 50093: contig of 14987 bp in length
* 50094 50193: gap of unknown length
* 50194 65728: contig of 15535 bp in length
* 65729 65828: gap of unknown length
* 65829 83647: contig of 17819 bp in length
* 83648 83747: gap of unknown length
* 83748 103152: contig of 19405 bp in length
* 103153 103252: gap of unknown length
* 103253 126091: contig of 22839 bp in length.

FEATURES

source
1. 126091
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-296F5"
/clone_lib="Caltech human BAC library C"
BASE COUNT 38442 a 23224 c 22362 g 41029 t 1034 others
ORIGIN

Query Match 94.4%; Score 17; DB 60; Length 126091;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CCTTTCCTGCTCTCTT 18
|||||
Db 34013 CCTTTCCTGCTCTCTT 34029

RESULT 14
CNS07AAN 1010 bp DNA STS 12-JAN-2001
DEFINITION T7 end of clone BC0AA002G10 of library BC0AA from strain CBS 767 of
Debaromyces hansenii, sequence tagged site.
ACCESSION AL36341
KEYWORDS AT36341.1 GI:12219754
STS.
SOURCE Debaromyces hansenii.
ORGANISM Debaromyces hansenii.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaromyces.

REFERENCE 1 (bases 1 to 1010)
AUTHORS Leplingle,A., Casaregola,S., Neuveglise,C., Bon,E., Nguyen,H.,
Artiguenave,F., Wincker,P. and Galliardin,C.
TITLE Genomic Exploration of the Hemiascomycetous Yeasts: 14.
Debaromyces hansenii var. hansenii
JOURNAL FEBS Lett. 487 (1), 82-86 (2000)
PUBMED 11152889
REFERENCE 2 (bases 1 to 1010)
AUTHORS Soucieu,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bottlin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,

de-Montigny,J., Dujon,B., Durrens,P., Leplingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogoropoulos,O., Porter,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissbach,J.
TITLE Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of
yeast species for molecular evolution studies(1)
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
PUBMED 11152876
REFERENCE 3 (bases 1 to 1010)

AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex - FRANCE (E-mail :
secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This STS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxi,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaromyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

FEATURES

source
1. 1010
Location/Qualifiers
/organism="Debaromyces hansenii"
/strain="CBS 767"
/variety="hansenii"
/db_xref="taxon:4959"
/clone="BC0AA002G10"
/clone_lib="BC0AA"
/note="end : 77"
misc-feature
complement(<60..>515)
/note="similar to Saccharomyces cerevisiae ORF YNR033w [AB21 : para-aminobenzoate synthase]"
misc-feature
complement(<132..>551)
/note="similar to Saccharomyces cerevisiae ORF YKL211c [TRP3 : anthranilate synthase component II]"
evidence=not_experimental

BASE COUNT 291 a 213 c 158 g 346 t 2 others
ORIGIN

Query Match 91.1%; Score 16.4; DB 54; Length 1010;
Best Local Similarity 94.4%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTTTCCTGCTCTCTT 18
|||||
Db 259 GCCTTTCCTGCTCTCTT 276

RESULT 15
LOCUS I09686 1198 bp PAT 02-DEC-1994
DEFINITION Sequence 3 from Patent WO 9004640.
ACCESSION I09686
VERSION I09686.1 GI:587606
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1198)
AUTHORS Kinet,J-P. and Metzger,H.
TITLE CDNAS CODING FOR THE gamma SUBUNIT OF THE HIGH-AFFINITY RECEPTOR
FOR IMMUNOGLOBULIN E
JOURNAL Patent: WO 9004640-A 3 03-MAY-1990;
FEATUES Location/Qualifiers
1. 1198
source
/organism="unknown"

BASE COUNT 389 a 244 c 244 g 321 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 1198;
 Best Local Similarity 94.4%; Pred. No. 1,1e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTTTCCTGCTCTCTT 18
 |||||
 Db 832 GCCTTTCCTGCTCTCTT 815

Search completed: April 19, 2001, 23:59:31
 Job time: 9448 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:47 : Search time 547.68 Seconds
(without alignments)
19.187 Million cell updates/sec

Title: US-09-016-464-11

Perfect score: 18
Sequence: 1 GCCCTTCCTGCTCTCTT 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_0401:*

- 1: /SIDS2/gcgdata/geneseq/geneseq/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseq/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseq/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseq/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseq/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseq/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseq/NA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseq/NA1987.DAT:*
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- 10: /SIDS2/gcgdata/geneseq/geneseq/NA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseq/NA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseq/NA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseq/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseq/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseq/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseq/NA1995.DAT:*
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- 18: /SIDS2/gcgdata/geneseq/geneseq/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseq/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	18	Human IGE receptor
2	18	100.0	18	20	Human IGE receptor
3	18	100.0	18	21	Human IGE receptor
4	18	100.0	18	21	Human IGE receptor
5	18	100.0	39	20	Human IGE receptor
6	18	100.0	39	21	Human IGE receptor
7	18	100.0	39	21	Human IGE receptor
8	18	100.0	378	20	Human IGE receptor
9	18	100.0	378	21	Human IGE receptor
10	18	100.0	378	21	Human IGE receptor
11	18	100.0	773	19	Human IGE receptor

C 12	18	100.0	1068	21	A27470
C 13	18	100.0	1088	10	N90126
C 14	18	100.0	1150	14	O34840
C 15	18	100.0	1174	14	O51020
C 16	18	100.0	1193	11	O04644
C 17	18	100.0	1197	18	T85615
C 18	18	100.0	1198	19	V36343
C 19	18	100.0	1198	21	F20935
C 20	18	100.0	1198	21	A44813
C 21	18	100.0	1199	12	O14736
C 22	18	100.0	1199	21	F20934
C 23	18	100.0	7659	21	A34812
C 24	18	100.0	7800	21	F20842
C 25	18	100.0	7800	21	A34720
C 26	18	100.0	7803	20	X55272
C 27	18	100.0	21742	21	F20938
C 28	18	100.0	21742	21	A34816
C 29	18	100.0	114955	20	X33491
C 30	18	100.0	117609	21	F21435
C 31	18	100.0	117609	21	F21435
C 32	17	94.4	344	21	A31614
C 33	17	94.4	374	21	A31950
C 34	16.4	91.1	2270	20	Z24865
C 35	16	88.9	874	21	C33737
C 36	15.4	85.6	196	21	C05429
C 37	15.4	85.6	199	20	X51460
C 38	15.4	85.6	432	20	X97619
C 39	15.4	85.6	868	21	A02142
C 40	15.4	85.6	1095	13	O27259
C 41	15.4	85.6	1095	15	O63707
C 42	15.4	85.6	1095	19	V19644
C 43	15.4	85.6	78925	21	C89888
C 44	14.8	82.2	109	20	Z32130
C 45	14.8	82.2	293	20	V86486

ALIGNMENTS

RESULT 1	
ID T76084	standard; DNA; 18 BP.
AC T76084;	
DT 12-SEP-1997	(first entry)
XX	Human IGE receptor alpha antisense oligonucleotide H0MIGFalphaS1.
DE	Asthma; airway epithelium; adenovirus free; cystic fibrosis;
KW	chronic obstructive pulmonary disease; bronchitis; immunoglobulin; ss.
XX	
OS	Synthetic.
XX	
PN	W09640162-A1.
XX	
PD	19-DEC-1996.
XX	
PF	06-JUN-1996; 96WO-US09306.
XX	
PR	07-JUN-1995; 95US-0474497.
XX	
PA	(UYEC-) UNIV EAST CAROLINA.
XX	
PI	Metzger WJ, Nyce JW;
XX	
DR	WPI; 1997-051871/05.
XX	
PT	Treatment of airway diseases such as asthma - by topically applying
PT	adenovirus-free antisense oligo:nucleotide to airway epithelium of
XX	subject
XX	
PS	Example 5; Page 25; 71pp; English.

XX A method for treating airway disease in a subject has been produced.
CC Which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC HUM7491phasi1 specific for the human IGE receptor alpha subunit.
CC The method can be used to treat airway diseases such as cystic fibrosis,
CC asthma, chronic obstructive pulmonary disease, bronchitis and other
CC airway diseases characterised by an inflammatory response. By
CC eliminating adenosine from the antisense ON, its liberation upon
CC antisenase degradation is prevented, thereby preventing adenosine-
CC induced bronchoconstriction in patients with hyper-reactive airways.
XX Sequence 18 BP; 0 A; 6 C; 3 G; 9 T; 0 other;

Query Match 100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCCTTCTGCTGTTCTT 18
| | | | | | | | | | | | | | | | | |
Db 1 gccttcctcggtctctt 18

RESULT 2
X53889
ID X53889 standard; DNA: 18 BP.
XX X53889;
XX
XX
DT 05-JUL-1999 (first entry)
XX
XX
DE Human IGE receptor alpha subunit antisense oligonucleotide.
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW Impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
XX
OS Synthetic.
XX
XX
PN WO913886-A1.
XX
XX
PD 25-MAR-1999.
XX
XX
PF 17-SEP-1998; 98WO-US19419.
XX
XX
PR 09-JUN-1998; 98US-0093972.
PR 17-SEP-1997; 97US-0059160.
XX
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
XX
PI Nyce JW;
XX
XX
DR WPI: 1999-229400/19.
XX
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
XX
XX
PS Disclosure: Page 44; 120pp; English.
XX
XX
CC The specification describes antisense oligonucleotides (X52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding

CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences X55272-74. These multiple target
CC oligonucleotides (specifically X55180-271) can be used for the antisense
CC treatment of diseases and conditions. Typical diseases and conditions
CC are those associated with impaired respiration and inflammation,
CC including lung diseases, pulmonary vasoconstriction, inflammation,
CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC metastases, as well as all types of cancers which may metastasize or have
CC metastasized to the lungs, including breast and prostate cancer.
XX Sequence 18 BP; 0 A; 6 C; 3 G; 9 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCCTTCTGCTGTTCTT 18
| | | | | | | | | | | | | | | | | |
Db 1 gccttcctcggtctctt 18

RESULT 3
F19454
ID F19454 standard; DNA: 18 BP.
XX F19454;
XX
XX
AC F19454;
XX
XX
DT 14-MAR-2001 (first entry)
XX
XX
DE Human IGE receptor alpha polynucleotide fragment #1021.
XX
XX
DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200062736-A2.
XX
XX
PD 26-OCT-2000.
XX
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
XX
PR 06-APR-1999; 99US-0127958.
XX
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
XX
PI Nyce JW;
XX
XX
DR WPI: 2000-679539/66.
XX
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX
PS Claim 14; Page 131; 1592pp; English.
XX
XX
CC The present invention describes low adenosine (A) content antisense

CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antisthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulin and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impaired respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.

XX Sequence 18 BP: 0 A; 6 C; 3 G; 9 T; 0 other;

Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGTTCTCTT 18
|||||
Db 1 gccttcctgcttctctt 18

RESULT 4
A33332 ID A33332 standard; DNA; 18 BP.

AC A33332:
XX

DT 28-JUL-2000 (first entry)

XX Low adenosine antisense oligonucleotide SEQ ID NO:1021.

DE Human: adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antisthmatic; cytostatic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

PN WO200009525-A2.

PD 24-FEB-2000.

PF 03-AUG-1999; 99WO-US17712.

PR 03-AUG-1998; 98US-0095212.

PA (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;
PI

XX WPI; 2000-205971/18.
DR New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers

PS Claim 18; Page 393; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antisthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A33313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.

XX Sequence 18 BP: 0 A; 6 C; 3 G; 9 T; 0 other;

Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGTTCTCTT 18
|||||
Db 1 gccttcctgcttctctt 18

RESULT 5
X53883 ID X53883 standard; DNA; 39 BP.

AC X53883:
XX

DT 05-JUL-1999 (first entry)

XX Human Ige receptor alpha subunit antisense oligonucleotide.

DE Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impaired respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX chronic obstructive pulmonary disease; leukemia; lymphoma;
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX prostate cancer; ss.

OS Synthetic.

PN WO9113886-A1.

PD 25-MAR-1999.
 XX
 PF 17-SEP-1998; 98MO-US19419.
 XX
 PR 09-JUN-1998; 98US-0093972.
 XX
 PR 17-SEP-1997; 97US-0059160.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 1999-229400/19.
 XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 XX
 PS Disclosure: Page 44; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (X52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have
 CC metastasized to the lungs, including breast and prostate cancer.
 XX
 SQ Sequence 39 BP; 0 A; 7 C; 11 G; 21 T; 0 other;
 XX
 Query Match 100.0%; Score 18; DB 20; Length 39;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCCTTCTCTGTTCTCTT 18
 ||||||||||||||||
 DB 1 gccttcctcgtctcctt 18
 RESULT 6
 F19448 ID F19448 standard; DNA: 39 BP.
 XX
 AC F19448;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human IGE receptor alpha polynucleotide fragment #1015.
 XX
 KM Low adenosine antisense oligonucleotide: phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antialstatic; analgesic; hypotensive; cycostatic;
 KM respiratory obstruction; pulmonary; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 XX
 OS Homo sapiens.

XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000MO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Claim 14; Page 131; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antialstatic, hypotensive and cycostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 39 BP; 0 A; 7 C; 11 G; 21 T; 0 other;
 XX
 Query Match 100.0%; Score 18; DB 21; Length 39;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCCTTCTCTGTTCTCTT 18
 ||||||||||||||||
 DB 1 gccttcctcgtctcctt 18
 RESULT 7
 A33326 ID A33326 standard; DNA: 39 BP.
 XX
 AC A33326;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Low adenosine antisense oligonucleotide SEQ ID NO:1015.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW.
 XX
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Claim 18; Page 392; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A3313 to A35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
 CC to A33992) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 XX
 SQ Sequence 39 BP; 0 A; 7 C; 11 G; 21 T; 0 other;

Query Match 100.0%; Score 18; DB 21; Length 39;
 Best Local Similarity 100.0%; Pred. No. 8.5;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGTTCTCTT 18
 ||||||||||||||||
 Db 1 gccttcctggtctctt 18

RESULT 8
 X54568

ID X54568 standard; DNA; 378 BP.
 XX
 AC X54568;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human IGE receptor alpha subunit antisense oligonucleotide.
 KW
 KW Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9913886-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19419.
 XX
 PR 09-JUN-1998; 98US-0093972.
 PR 17-SEP-1997; 97US-0059160.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW.
 XX
 DR WPI; 1999-229400/19.
 XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 XX
 PS Disclosure; Page 44; 120pp; English.

XX The specification describes antisense oligonucleotides (X52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have
 CC metastasized to the lungs, including breast and prostate cancer.
 XX
 SQ Sequence 378 BP; 24 A; 86 C; 106 G; 114 T; 48 other;

Query Match 100.0%; Score 18; DB 20; Length 378;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGTTCTCTT 18
 ||||||||||||||||
 Db 1 gccttcctggtctctt 18

RESULT 9
 F20137 standard; DNA: 378 BP.
 AC F20137:
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human IGE receptor alpha polynucleotide fragment #1704.
 XX
 KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antialstatic; analgesic; hypotensive; cyostatic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 KM
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW:
 XX
 DR WPI: 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 PS
 PS Claim 14: Page 130; 1592pp: English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (1) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antialstatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (1) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the

CC present invention.
 XX
 SQ Sequence 378 BP; 24 A; 86 C; 106 G; 114 T; 48 other;
 XX
 Query Match 100.0%; Score 18; DB 21; Length 378;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCCCTTCTGCTGTTCTT 18
 DB 1 gccttcctggtcctt 18
 RESULT 10
 A34015
 ID A34015 standard; DNA: 378 BP.
 XX
 AC A34015;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:1704.
 XX
 KM Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KM phosphorothioate; impaired respiration; inflammation; allergy;
 KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KM antiallergic; antialstatic; cyostatic; analgesic; impaired airway;
 KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 KM
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA
 PI Nyce JW:
 XX
 DR WPI: 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 PS
 PS Disclosure: Page 476; 1343pp: English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antialstatic, cyostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A32313 to A35312 represent the

CC extracellular portion of the receptor and are not glycosylated i.e. they
 CC do not have transmembrane domains or signal peptides. The recombinant
 CC proteins may be used in immunoassays to determine the immune status of
 CC patients with chronic diseases of the immune system, e.g. AIDS, systemic
 CC lupus erythematosus (SLE), multiple myeloma (MM), or rheumatoid
 CC arthritis. In addition, pharmaceutical compositions containing
 CC recombinant proteins may be used to treat or prevent autoimmune diseases,
 CC allergies or tumours, especially AIDS, rheumatoid arthritis or MM.
 XX
 SQ Sequence 1068 BP: 330 A: 215 C: 229 G: 294 T: 0 other:

Query Match 100.0%; Score 18; DB 21; Length 1068;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGCTTCCTT 18
 |||
 DB 765 GCCTTCTGCTTCCTT 748

RESULT 13
 N90126/c
 ID N90126 standard; cDNA: 1088 BP.

AC N90126;

DT 01-NOV-1989 (first entry)

DE cDNA encoding human mast cell IGE receptor alpha subunit.

XX cDNA: immunoglobulin E receptor alpha subunit; treats
 KW allergies; design non-peptide drugs; human.

OS Homo sapiens (Human); mast cell line, KU812.

XX
 FH Key Location/Qualifiers
 FT CDS 35..805
 FT /*tag= a

XX W08905352-A.

XX 15-JUN-1989.

XX 29-NOV-1988; 88WO-US04255.

XX 01-DEC-1987; 87US-0127214.

XX (HARD) HARVARD COLLEGE.

XX Sitranganian R, Shlimizu A, Leder P, Benfey P;

XX WPI: 1989-192698/26.

DR P-PSDB; P90385.

XX cDNA encoding IGE receptor alpha-subunit - used to treat allergies.

XX Disclosure: fig 4; 18pp; English.

XX cDNA sequence encoding immunoglobulin E receptor alpha
 CC subunit of human mast cell IGE surface receptor (see corresp. P90385).
 CC used to produce antibodies which can diagnose IGE receptor levels,
 CC measure and treat allergies, and design non-peptide drugs.

XX Sequence 1088 BP: 347 A: 216 C: 229 G: 296 T: 0 other;

DB 760 GCCTTCTGCTTCCTT 743

RESULT 14

ID Q34840/c
 Q34840 standard; DNA: 1150 BP.

AC Q34840;

DT 18-APR-1996 (revised)

DT 07-MAY-1993 (first entry)

DE Human high affinity IGE receptor alpha subunit gene.

XX Allergic response; antagonist; drug screening; vaccine; allergic;
 KW reaction; diagnosis; therapy; FCERI; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 124..847

FT /*tag= a

FT misc_feature 601

FT /*tag= b
 /note= "sequence unreadable at this point"

FT misc_feature 757
 /note= "sequence unreadable at this point"

FT /*tag= c
 /note= "sequence unreadable at this point"

FT /*tag= d
 /note= "sequence unreadable at this point"

XX US7547892-A.

XX 01-DEC-1992.

XX 02-JUL-1990; 90US-0230085.

XX 24-FEB-1988; 88US-0160457.

XX 02-JUL-1990; 90US-0547892.

XX (USSH) US DEPT HEALTH & HUMAN SERVICE.

XX Kinet JP;

XX WPI: 1993-008901/01.

DR P-PSDB; R30483.

XX Novel DNA encoding alpha sub-unit of human high affinity IGE

XX receptor - useful as antagonist to prevent allergic response, as

XX reagent in drug screening and for antibody generation

XX Disclosure: Fig 1; 34pp; English.

XX The sequence is that of the gene encoding the human IGE high affinity

XX receptor alpha subunit (FCERI). It may be used to synthesise the

XX human FCERI alpha subunit or to synthesise cDNA sequences to

XX construct DNA probes useful in diagnostic assays.

XX Sequence 1150 BP: 373 A: 237 C: 227 G: 310 T: 3 other;

Query Match 100.0%; Score 18; DB 14; Length 1150;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGCTTCCTT 18
 |||
 DB 802 GCCTTCTGCTTCCTT 785

RESULT 15
 051020/c

ID Q51020 standard; DNA; 1174 BP.
 XX
 AC Q51020;
 XX
 XX 21-JUN-1994 (first entry)
 DT
 XX Human FcεRI alpha gene.
 DE
 XX IGE; Immunoglobulin E receptor; beta subunit; basophils; allergy;
 KM aggregation; signal transduction; diagnosis; antagonist; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH CDS 107..881
 FT /*tag= a
 FT
 XX
 XX W09321317-A.
 PN
 XX
 XX 28-OCT-1993.
 PD
 XX
 XX 16-APR-1993; 93WO-US03419.
 PF
 XX 16-APR-1992; 92US-0869933.
 PR
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
 PA
 XX
 XX Kinet JP;
 PI
 XX
 XX WPI; 1993-351727/44.
 DR
 XX P-PSDB; R42336.
 DR
 XX
 XX Immunoglobulin E receptor human beta sub-unit isolation - using
 PT 1st strand reverse transcripts from human basophils as templates
 PT for a polymerase chain reaction, used to treat and diagnose
 PT allergic diseases
 PT
 XX
 XX Claim 1; Fig 1; 154pp; English.
 PS
 XX
 CC The sequence is that of the human FcεRI alpha subunit, isolated by
 CC using first strand reverse transcriptase from human basophils by PCR.
 CC The gene and its prod. can be used to identify human beta subunit
 CC FcεRI inhibitors (immunoglobulin E receptor) which inhibit the
 CC binding of IGE to its receptor and inhibit the aggregation function
 CC of the receptor or the signal transducing function related to
 CC allergic response. Such inhibitors can be used for the treatment or
 CC prevention of allergic disease.
 CC See also Q51021-4.
 CC
 XX
 SQ Sequence 1174 BP; 378 A; 240 C; 241 G; 315 T; 0 other;

Query Match 100.0%; Score 18; DB 14; Length 1174;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCCTGCTCTCTT 18
 |||
 DB 832 GCCTTCCTGCTCTCTT 815

Search completed: April 20, 2001, 00:12:48
 Job time: 10010 sec

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OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:24:40 ; Search time 7150.85 seconds
(without alignments)
0.368 Million cell updates/sec

Title: US-09-016-464-11

Perfect score: 18

Sequence: 1 GCCCTTCCTGCTCTCTT 18

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
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27: gb_est35:*
28: gb_est36:*
29: gb_est37:*
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31: gb_est39:*
32: gb_est40:*
33: em_estba:*
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 232: gb_gss32:*
 233: gb_gss33:*
 234: gb_gss34:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	18	100.0	446	23	A1676097
2	18	100.0	479	150	BF593204
3	18	100.0	540	23	A1685796
4	18	100.0	669	117	AW612525
5	17	94.4	606	220	AZ364398
6	17	94.4	672	224	AZ625866
7	17	94.4	1109	151	BF687201
8	16.4	91.1	217	215	AZ057458
9	16.4	91.1	288	129	BB261457
10	16.4	91.1	385	120	AW844472
11	16.4	91.1	413	203	AQ164555
12	16.4	91.1	423	202	AQ136574
13	16.4	91.1	437	172	BG007999
14	16.4	91.1	451	155	R21504
15	16.4	91.1	477	2	AA136161
16	16.4	91.1	504	5	AA131343
17	16.4	91.1	517	224	AZ598851
18	16.4	91.1	534	211	AQ783598

```

c 19 16.4 91.1 566 218 A2256839
c 20 16.4 91.1 570 23 A1676114
c 21 16.4 91.1 579 214 A0979656
c 22 16.4 91.1 677 122 AM961166
c 23 16.4 91.1 691 225 A2653020
c 24 16.4 91.1 704 230 CNS03115
c 25 16.4 91.1 835 147 BF340453
c 26 16.4 91.1 892 231 CNS03RBN
c 27 16.4 91.1 915 229 CNS01SK7
c 28 16.4 91.1 176 20 A1424413
c 29 16.4 91.1 268 155 R48504
c 30 16.4 91.1 291 15 A1079718
c 31 16.4 91.1 300 11 AA724048
c 32 16.4 91.1 313 114 AA391826
c 33 16.4 91.1 317 13 AA886783
c 34 16.4 91.1 320 207 A0536919
c 35 16.4 91.1 354 1 AA009729
c 36 16.4 91.1 364 13 AA813601
c 37 16.4 91.1 367 9 AA603763
c 38 16.4 91.1 397 18 A1285640
c 39 16.4 91.1 400 4 AA252209
c 40 16.4 91.1 404 21 A1540265
c 41 16.4 91.1 406 18 A1268519
c 42 16.4 91.1 413 9 AA581561
c 43 16.4 91.1 428 19 A1365587
c 44 16.4 91.1 429 11 AA708100
c 45 16.4 91.1 431 107 A0160595

```

ALIGNMENTS

```

RESULT 1
LOCUS A1676097
DEFINITION wc05c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314294.3'
ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION A1676097
VERSION A1676097.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bpr/image/image.html
Insert Length: 625 Std Error: 0.00
Seq primer: -40UP from Gibco.
FEATURES
source
location/Qualifiers
1..446
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2314294"
/clone_lib="NCI_CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)

```

with a modified polylinker; plasmid DNA from the normalized library NCI_CGAP_Pr28 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo.

Query Match 100.0%; Score 18; DB 23; Length 446;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 18; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCCTGCTCTCTT 18

Db 322 GCCTTCCTGCTCTCTT 339

RESULT 2

```

LOCUS BF593204 479 bp mRNA EST 12-DEC-2000
DEFINITION 7050c04.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3577351.3'
similar to SW:FECA_HUMAN P12319 HIGH AFFINITY IMMUNOGLOBULIN
EPSILON RECEPTOR ALPHA-SUBUNIT PRECURSOR ;, mRNA sequence.
ACCESSION BF593204
VERSION BF593204.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 325.
FEATURES
source
location/Qualifiers
1..479
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3577351"
/clone_lib="NCI_CGAP_Kid1"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site: 1; Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clonoids 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

```

BASE COUNT 143 a 82 c 85 g 169 t

ORIGIN

Query Match 100.0%; Score 18; DB 150; Length 479;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGCTGTTCTCTT 18
 |||
 DB 318 GCCTTCTGCTGTTCTCTT 335

RESULT 3
 A1685796 540 bp mRNA EST 27-MAY-1999
 LOCUS tu20q08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2251646 3'
 DEFINITION similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
 ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
 ACCESSION A1685796
 VERSION A1685796.1 GI:4897090
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 540)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html

FEATURES
 source
 Trace considered overall poor quality
 Seq primer: 40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:2251646"
 /clone_11b="NCI_CGAP_Pr28"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: prostate; Vector: p77T3D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI_CGAP_Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 1101192-1101959, and 1217928-1220615).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 156 a 100 c 104 g 180 t
 ORIGIN

Query Match 100.0%; Score 18; DB 23; Length 540;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGCTGTTCTCTT 18
 |||
 DB 317 GCCTTCTGCTGTTCTCTT 334

RESULT 4
 AM612525 669 bp mRNA EST 23-MAR-2000
 LOCUS hn03f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954053 3'
 DEFINITION similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
 ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
 ACCESSION AM612525
 VERSION AM612525.1 GI:73177711
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 669)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 image.llnl.gov/image/html/resources.shtml
 Seq primer: 40UP from Gibco
 High quality sequence stop: 438.
 Location/Qualifiers
 1..669
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:2954053"
 /clone_11b="NCI_CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: p77T3D-Pac (Pharmacia) with
 a modified polylinker; Site: 1. Not 1; Site 2: Eco RI;
 Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (clones 132376-132391, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatima Bonaldo."

BASE COUNT 195 a 131 c 122 g 220 t 1 others
 ORIGIN

Query Match 100.0%; Score 18; DB 117; Length 669;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGCTGTTCTCTT 18
 |||
 DB 323 GCCTTCTGCTGTTCTCTT 340

RESULT 5
 AZ364398 606 bp DNA GSS 02-OCT-2000
 LOCUS IM011D11R Mouse 10kb plasmid UGCCIM library Mus musculus genomic
 DEFINITION clone UGCCIM011D11 R, DNA sequence.
 ACCESSION AZ364398
 VERSION AZ364398.1 GI:10478098
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 606)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: D column: 11
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 606.
FEATURES
source location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0110D11"
/clone_11b="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (9114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 209 a 122 c 163 g 111 t 1 others
ORIGIN

Query Match 94.4%; Score 17; DB 220; Length 606;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTTCCCTGCTCTCT 18
|||||
Db 494 CCTTCCCTGCTCTCT 478

RESULT 6
A2625866 672 bp DNA GSS 13-DEC-2000
LOCUS 1M0465115R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0465115 R, DNA sequence.
ACCESSION A2625866
VERSION A2625866.1 GI:11748056
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 672)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0465 row: I column: 15
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 672.
FEATURES
source location/Qualifiers
1. 672
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0465115"
/clone_11b="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (9114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 171 a 176 c 113 g 212 t
ORIGIN

Query Match 94.4%; Score 17; DB 224; Length 672;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCTTCCCTGCTCTCT 18
|||||
Db 324 CCTTCCCTGCTCTCT 340

RESULT 7
BF687201 1109 bp mRNA EST 22-DEC-2000
LOCUS 602102226F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:4220478
DEFINITION 5', mRNA sequence.
ACCESSION BF687201
VERSION BF687201.1 GI:11972609
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1109)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLM9804 row: C column: 07
High quality sequence stop: 662.

FEATURES
source
1. 1109
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="4220478"
/clone_11b="NCI-CGAP_K1414"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Kidney; Vector: pCMV-Sport6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP library. 1"

BASE COUNT 367 a 261 c 318 g 163 t

ORIGIN

Query Match 94.4%; Score 17; DB 151; Length 1109;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CCTTCTCGTCTCTT 18
|||||

Db 719 CCTTCTCGTCTCTT 703

RESULT 8
LOCUS AZ057458 217 bp DNA GSS 30-MAR-2000
DEFINITION RPI-23-426E23.TV RPI-23 Mus musculus genomic clone RPI-23-426E23
, DNA sequence.
ACCESSION AZ057458
KEYWORDS AZ057458.1 GI:7348695
SOURCE GSS.
ORGANISM house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 217)
REFERENCE Zhao, S., Niewman, W., Feldblum, T., Malek, J., Shatman, S., Akinet, B., Levins, M., McGinn, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.
AUTHORS Mouse BAC End Sequences from Library RPI-23
Unpublished (1999)
Other GSSs: RPI-23-426E23.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPI-23. For BAC library availability, please contact Pieter de Jong
(pleter@jgim.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)

or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/Bac_end_intro.html
Plate: 426 row: E column: 23
Seq primer: 17
Class: BAC ends.

FEATURES
source
1. 217
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPI-23-426E23"
/clone_11b="RPI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1; EcoRI; Site: 2; EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI MethyIase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 80 a 81 c 56 g 0 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 215; Length 217;
Best Local Similarity 94.4%; Pred. No. 8.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCCTTCTCGTCTCTT 18
|||||

Db 32 GCCTTCTCGTCTCTT 15

RESULT 9
LOCUS BB261457 288 bp mRNA EST 07-JUN-2000
DEFINITION BB261457 RIKEN full-length enriched, 7 days neonate cerebellum Mus musculus cDNA clone A730098N05 3', mRNA sequence.

ACCESSION BB261457
VERSION BB261457.1 GI:8957909
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 288)

AUTHORS Kono, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamanaoka, T., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
RIKEN Mouse ESTs (Kono, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9036
Email: genome-res@cc.riken.go.jp,
URL: <http://genome.irc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

High quality sequence stop: 413.
Location/Qualifiers

FEATURES
source

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1..413
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelOBAC11; BAC clones in
E-Coli DH10B"
BASE COUNT      110 a      82 c      87 g      132 t      2 others
ORIGIN
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Query Match
Best Local Similarity 94.4%; Pred. No. 9e+02; Length 413;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTTCTCGTTCCTT 18
|||||
DB 198 GCCTTCTCGTTCCTT 215

RESULT 12
LOCUS A0136574 423 bp DNA GSS 23-SEP-1998
DEFINITION HS_3112_A2.B11.77 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3112 Col=22 Row=C, DNA sequence.
ACCESSION A0136574
VERSION A0136574.1 GI:3523640
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 423)
Mahalax,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahalax GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3112 row: C column: 22
Class: BAC ends
High quality sequence stop: 423.

FEATURES
source

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1..423
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelOBAC11; BAC clones in
E-Coli DH10B"
BASE COUNT      115 a      104 c      69 g      135 t
ORIGIN
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Query Match
Best Local Similarity 94.4%; Pred. No. 9.1e+02; Length 423;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GCCTTCTCGTTCCTT 18
|||||

DB 379 GCCTTCTCGTTCCTT 396

RESULT 13
LOCUS BG007999 437 bp mRNA EST 24-JAN-2001
DEFINITION OVA-GN0314-281100-607-h07 GN0314 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG007999
VERSION BG007999.1 GI:12452744
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 437)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Laboratory of Cancer Genetics
Simpson A.J.G.
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV4&ct=QV4-GN0314-
281100-607-h07&ct=2000-11-28&ct=1)
Seq primer: puc 18 forward
High quality sequence start: 2
High quality sequence stop: 432.
Location/Qualifiers

FEATURES
source

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1..437
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0314"
/dev_stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
Application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT      133 a      91 c      89 g      124 t
ORIGIN
```

Query Match
Best Local Similarity 94.4%; Pred. No. 9.1e+02; Length 437;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GCCTTCTCGTTCCTT 18
|||||

DB 169 GCCTTCTCGTTCCTT 186

RESULT 14
LOCUS R21504 451 bp mRNA EST 18-APR-1995
DEFINITION yh19a01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:130152 3' similar to gb:J04765 OSTEOPONTIN PRECURSOR (HUMAN
); mRNA sequence.
ACCESSION R21504

```

VERSION      R21504.1  GI:776285
KEYWORDS
SOURCE       human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1 (bases 1 to 451)
AUTHORS      Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
              M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Merra,M., Parsons,J.,
              Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Waterston
              R., Williamson,A., Wohlmann,P. and Wilson,R.
              The WashU-Merck EST Project
TITLE        Unpublished (1995)
JOURNAL      Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@wustl.wustl.edu
              Insert Size: 1418
              High quality sequence stops: 293
              Source: IMAGE Consortium, LNL.
              This clone is available royalty-free through LNL; contact the
              IMAGE Consortium (info@image.lnl.gov) for further information.
              Insert Length: 1418   Std Error: 0.00
              Seq primer: -21m13
              High quality sequence stop: 293.
FEATURES
  source
    1..451
      /organism="Homo sapiens"
      /db_xref="GDB:546275"
      /db_xref="taxon:9606"
      /clone="IMAGE:130152"
      /clone_lib="Soares_pregnant_uterus_NbHPU"
      /sex="Female"
      /dev_stage="Placenta obtained at birth (full term)"
      /lab_host="DH10B (ampicillin resistant)"
      /note="Organ: Placenta; Vector: pT73D (Pharmacia) with a
      modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
      strand cDNA was primed with a Not I - oligo(dT) primer [5'
      AACGTGACAAATTCGCGCGCGCGAGATTTTCTTTTCTTTT 3'],
      double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not I
      and Eco RI sites of the modified pT73 vector. Library
      went through one round of normalization. Library
      constructed by Bento Soares and M.Fatima Bonaldo. "
BASE COUNT   152 a      78 c      65 g      150 t      6 others
ORIGIN
Query Match          91.1%; Score 16.4; DB 155; Length 451;
Best Local Similarity 94.4%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  GCCTTCTGCTCTCTT 18
          |||||
DB      356  GCCTTCATGCTCTCTT 373

RESULT 15
AA136161      477 bp      mRNA      EST      30-NOV-1996
LOCUS         2k90c06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
DEFINITION   IMAGE:490090 5', mRNA sequence.
ACCESSION   AA136161
VERSION     AA136161.1  GI:1697390
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1 (bases 1 to 477)
AUTHORS      Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman

```

```

TITLE        Unpublished (1995)
JOURNAL      Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@wustl.wustl.edu
              This clone is available royalty-free through LNL; contact the
              IMAGE Consortium (info@image.lnl.gov) for further information.
              Seq primer: -28m13 rev2 from Amersham
              High quality sequence stop: 390.
FEATURES
  source
    1..477
      /organism="Homo sapiens"
      /db_xref="GDB:380467"
      /db_xref="taxon:9606"
      /clone="IMAGE:490090"
      /clone_lib="Soares_pregnant_uterus_NbHPU"
      /sex="Female"
      /dev_stage="adult"
      /lab_host="DH10B"
      /note="Organ: uterus; Vector: pT73-Pac; Site.1: Not I;
      Site.2: Eco RI; 1st strand cDNA was primed with a Not I -
      oligo(dT) primer [5'
      AACGTGACAAATTCGCGCGCGCTTTTCTTTTCTTTT 3'],
      double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not I
      and Eco RI sites of the modified pT73 vector. Library
      went through one round of normalization. Library
      constructed by M. Fatima Bonaldo. "
BASE COUNT   130 a      92 c      110 g      142 t      3 others
ORIGIN
Query Match          91.1%; Score 16.4; DB 2; Length 477;
Best Local Similarity 94.4%; Pred. No. 9.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  GCCTTCTGCTCTCTT 18
          |||||
DB      345  GCCTTCTGCTCTATT 328

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Search completed: April 19, 2001, 23:24:43
 Job time: 8160 sec

100

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:29 ; Search time 280.46 Seconds
(without alignments)
11.206 Million cell updates/sec

Title: US-09-016-464-11
Perfect score: 18
Sequence: 1 GCCTTCCTGCTCTCTT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/2/1na/5A.COMB.seq:*
2: /cgn2_6/prodata/2/1na/5B.COMB.seq:*
3: /cgn2_6/prodata/2/1na/6A.COMB.seq:*
4: /cgn2_6/prodata/2/1na/6B.COMB.seq:*
5: /cgn2_6/prodata/2/1na/CTUS.COMB.seq:*
6: /cgn2_6/prodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	100.0	699	2	US-08-756-387B-7 Sequence 7, Appli
C 2	18	100.0	774	2	US-08-756-387B-4 Sequence 4, Appli
C 3	18	100.0	774	2	US-08-756-387B-5 Sequence 5, Appli
C 4	18	100.0	1174	1	US-07-869-933-10 Sequence 10, Appli
C 5	18	100.0	1174	4	US-09-103-663-10 Sequence 10, Appli
C 6	18	100.0	1198	2	US-08-756-387B-1 Sequence 1, Appli
C 7	18	100.0	1198	2	US-08-756-387B-3 Sequence 3, Appli
C 8	15.4	85.6	1095	1	US-08-097-828-4 Sequence 4, Appli
C 9	15.4	85.6	1095	1	US-08-480-756-4 Sequence 4, Appli
C 10	15.4	85.6	1095	2	US-08-462-403-4 Sequence 4, Appli
C 11	15.4	85.6	1095	5	PCT-US92-00331-4 Sequence 4, Appli
C 12	15.4	85.6	1095	5	PCT-US93-10419-4 Sequence 4, Appli
C 13	14.8	82.2	148	2	US-08-284-941-5 Sequence 5, Appli
C 14	14.8	82.2	148	5	US-08-447-642-5 Sequence 5, Appli
C 15	14.8	82.2	148	5	PCT-US93-02147A-5 Sequence 5, Appli
C 16	14.8	82.2	708	3	US-09-015-734-6 Sequence 6, Appli
C 17	14.8	82.2	708	3	US-09-015-734-6 Sequence 8, Appli
C 18	14.8	82.2	765	3	US-09-015-734-4 Sequence 4, Appli
C 19	14.8	82.2	765	3	US-09-015-734-5 Sequence 5, Appli
C 20	14.8	82.2	1015	3	US-09-015-734-1 Sequence 1, Appli
C 21	14.8	82.2	1015	3	US-09-015-734-3 Sequence 3, Appli
C 22	14.8	82.2	1560	1	US-07-669-171-1 Sequence 1, Appli
C 23	14.8	82.2	1569	1	US-07-669-171-3 Sequence 3, Appli
C 24	14.8	82.2	2207	6	5221620-3 Patent No. 5221620
C 25	14.8	82.2	2537	6	5168051-1 Patent No. 5168051
C 26	14.8	82.2	2658	2	US-08-910-927B-4 Sequence 4, Appli
C 27	14.8	82.2	2745	5	PCT-US94-03705-3 Sequence 3, Appli

28	14.8	82.2	246240	2	US-08-724-394A-20 Sequence 20, Appli
29	14.8	82.2	246240	2	US-08-724-394A-21 Sequence 21, Appli
30	14.8	82.2	246240	2	US-08-724-394A-22 Sequence 22, Appli
31	14.4	80.0	1201	4	US-09-286-805-1 Sequence 1, Appli
32	14.4	80.0	10825	3	US-08-652-265-1 Sequence 1, Appli
33	14.4	80.0	10825	3	US-08-652-265-3 Sequence 3, Appli
34	14.4	80.0	10825	3	US-08-652-265-5 Sequence 5, Appli
35	14.4	80.0	10825	3	US-08-652-265-7 Sequence 7, Appli
36	14.4	80.0	10825	4	US-08-834-497A-1 Sequence 1, Appli
37	14.4	80.0	10825	4	US-08-834-497A-3 Sequence 3, Appli
38	14.4	80.0	10825	4	US-08-834-497A-5 Sequence 5, Appli
39	14.4	80.0	10825	4	US-08-834-497A-7 Sequence 7, Appli
C 40	13.8	76.7	403	1	US-08-486-013-57 Sequence 57, Appli
C 41	13.8	76.7	403	2	US-08-482-279-57 Sequence 57, Appli
C 42	13.8	76.7	403	2	US-08-342-268-57 Sequence 57, Appli
C 43	13.8	76.7	403	3	US-09-015-968-57 Sequence 57, Appli
C 44	13.8	76.7	426	1	US-08-340-820-10 Sequence 10, Appli
C 45	13.8	76.7	426	1	US-08-593-535-10 Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-756-387B-7/c
; Sequence 7, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Masson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: NO. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
; US-08-756-387B-7

Query Match 100.0%; Score 18; DB 2; Length 699;
Best local Similarity 100.0%; Pred. No. 2.2;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTCTT 18
|||||

Db 651 GCCTTCTGCTGTTCTCTT 634

RESULT 2

US-08-756-387B-4/c
; Sequence 4, Application US/08756387B
; Patent No. 5945294

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rushlow, Keith E.
APPLICANT: Massom, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387B
FILING DATE: NO. 5945294ember 26, 1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 774 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 1..774
US-08-756-387B-4

Query Match 100.0%; Score 18; DB 2; Length 774;

Best local similarity 100.0%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTCTT 18
|||||

Db 726 GCCTTCTGCTGTTCTCTT 709

RESULT 3

US-08-756-387B-5
; Sequence 5, Application US/08756387B
; Patent No. 5945294

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rushlow, Keith E.
APPLICANT: Massom, Donald L.

TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387B
FILING DATE: NO. 5945294ember 26, 1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 774 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-756-387B-5

Query Match 100.0%; Score 18; DB 2; Length 774;

Best local similarity 100.0%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTCTT 18
|||||

Db 49 GCCTTCTGCTGTTCTCTT 66

RESULT 4

US-07-869-933-10/c
; Sequence 10, Application US/07869933
; Patent No. 5770396

GENERAL INFORMATION:

APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1174 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..880
US-07-869-933-10

Query Match 100.0%; Score 18; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTCTCTT 18
|||||

DB 832 GCCTTCTGCTCTCTT 815

RESULT 5
US-09-103-663-10/c
; Sequence 10, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (107)..(880)
US-09-103-663-10

Query Match 100.0%; Score 18; DB 4; Length 1174;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTCTCTT 18
|||||

DB 832 GCCTTCTGCTCTCTT 815

RESULT 6
US-08-756-387B-1/c
; Sequence 1, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Massom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387B
FILING DATE: No. 5945294ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1198 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..877
US-08-756-387B-1

Query Match 100.0%; Score 18; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTCTCTT 18
|||||

DB 832 GCCTTCTGCTCTCTT 815

RESULT 7
US-08-756-387B-3
; Sequence 3, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Massom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387B

FILING DATE: No. 5945294ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1198 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-756-387B-3

Query Match 100.0%; Score 18; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGCTGTTCTCTT 18
|||||
Db 367 GCCTTCTGCTGTTCTCTT 384

RESULT 8
US-08-097-828-4/C
Sequence 4, Application US/08097828
Patent No. 5464757
GENERAL INFORMATION:
APPLICANT: Potter, Ellen
APPLICANT: Behan, Dominic P.
APPLICANT: Fischer, Wolfgang H.
APPLICANT: Linton, Elizabeth A.
APPLICANT: Lowry, Philip J.
APPLICANT: Vale Jr., Wylie W.
TITLE OF INVENTION: DNA Encoding CRF Binding Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 South LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,828
FILING DATE: 19930723
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,341
FILING DATE: 15-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/967,683
FILING DATE: 26-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Schumann, James J.
REGISTRATION NUMBER: 20,856
REFERENCE/DOCKET NUMBER: 54426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)552-1311
TELEFAX: (619)552-0095
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1095 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 118..1086
NAME/KEY: mat_peptide
LOCATION: 190..1086
US-08-097-828-4

Query Match 85.6%; Score 15.4; DB 1; Length 1095;
Best Local Similarity 94.1%; Pred No. 41;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCTTCTGCTGTTCTCTT 18
|||||
Db 18 CCTTCTGCTGTTCTCTT 2

RESULT 9
US-08-480-756-4/C
Sequence 4, Application US/08480756
Patent No. 5733790
GENERAL INFORMATION:
APPLICANT: Potter, Ellen
APPLICANT: Behan, Dominic P.
APPLICANT: Linton, Elizabeth A.
APPLICANT: Lowry, Philip J.
APPLICANT: Vale Jr., Wylie W.
TITLE OF INVENTION: CRF BINDING PROTEIN ANTIBODIES AND ASSAYS USING SAME
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 South LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,756
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,341
FILING DATE: 15-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/967,683
FILING DATE: 26-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,828
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Schumann, James J.
REGISTRATION NUMBER: 20,856
REFERENCE/DOCKET NUMBER: 56508
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-552-1311
TELEFAX: 619-552-0095
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1095 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 118..1086
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 190..1086
US-08-480-756-4

Query Match 85.6%; Score 15.4; DB 1; Length 1095;
Best Local Similarity 94.1%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCTTCTCGGTCTCTT 18
|||||
Db 18 CCTTCTCGGTCTCTT 2

RESULT 10
US-08-462-403-4/C
Sequence 4, Application US/08462403
Patent No. 5844080
GENERAL INFORMATION:
APPLICANT: Potter, Ellen
APPLICANT: Behan, Dominic P.
APPLICANT: Fischer, Wolfgang H.
APPLICANT: Linton, Elizabeth A.
APPLICANT: Lowry, Philip J.
APPLICANT: Vale Jr., Wylie W.
TITLE OF INVENTION: DNA Encoding CRF Binding Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 South LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,403
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/097,828
FILING DATE: 23-JUL-1993
APPLICATION NUMBER: US 07/641,341
FILING DATE: 15-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/967,683
FILING DATE: 26-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Schumann, James J.
REGISTRATION NUMBER: 20,856
REFERENCE/DOCKET NUMBER: 54426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)552-1311
TELEFAX: (619)552-0095
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1095 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 118..1086

FEATURE:
NAME/KEY: mat_peptide
LOCATION: 190..1086
US-08-462-403-4

Query Match 85.6%; Score 15.4; DB 2; Length 1095;
Best Local Similarity 94.1%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCTTCTCGGTCTCTT 18
|||||
Db 18 CCTTCTCGGTCTCTT 2

RESULT 11
PCT-US92-00331-4/C
Sequence 4, Application PC/TUS9200331
GENERAL INFORMATION:
APPLICANT: Potter, Ellen
APPLICANT: Behan, Dominic P.
APPLICANT: Fischer, Wolfgang H.
APPLICANT: Linton, Elizabeth A.
APPLICANT: Lowry, Philip J.
APPLICANT: Vale Jr., Wylie W.
TITLE OF INVENTION: CRF Binding Protein
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 South LaSalle Street, Suite 900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00331
FILING DATE: 19920113
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,341
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Watt, Philip H.
REGISTRATION NUMBER: 25,939
REFERENCE/DOCKET NUMBER: 50843PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)372-7842
TELEFAX: (312)372-7848
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1095 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 118..1086
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 190..1086
OTHER INFORMATION:
PCT-US92-00331-4

Query Match 85.6%; Score 15.4; DB 5; Length 1095;
Best Local Similarity 94.1%; Pred. No. 41;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCTTCCGCTGCTCTT 18
|||||
DB 18 CCTTCCGCTGCTCTT 2

RESULT 12
PCT-US93-10419-4/c
Sequence 4, Application PC/TUS9310419
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: CRF Binding Protein
NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10419
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,828
FILING DATE: 23-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/967,683
FILING DATE: 26-OCT-1992

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1095 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 118..1086
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 190..1086

PCT-US93-10419-4

Query Match 85.6%; Score 15.4; DB 5; Length 1095;

Best Local Similarity 94.1%; Pred. No. 41;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCTTCCGCTGCTCTT 18
|||||
DB 18 CCTTCCGCTGCTCTT 2

RESULT 13
US-08-284-941-5/c
Sequence 5, Application US/08284941
Patent No. 5863756
GENERAL INFORMATION:

APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PAGE 4 AND
TITLE OF INVENTION: PAGE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,941
FILING DATE: 2 August 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/0105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 843-5070
TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 148 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: CDS
LOCATION: 18..131

US-08-284-941-5

Query Match 82.2%; Score 14.8; DB 2; Length 148;

Best Local Similarity 88.9%; Pred. No. 66;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCCTTCCGCTGCTCTT 18
|||||
DB 140 GCCTTCCGCTGCTCTT 123

RESULT 14
US-08-447-642-5/c
Sequence 5, Application US/08447642
Patent No. 5989890
GENERAL INFORMATION:

APPLICANT: BARR, PHILIP J
APPLICANT: KIEFER, MICHAEL C
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PAGE 4 AND
TITLE OF INVENTION: PAGE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,642
FILING DATE: 23-MAY-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,941
FILING DATE: 2 August 1994

ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L.

REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/0105

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 843-5070

TELEFAX: (415) 857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 18..131
US-08-447-642-5

Query Match 82.2%; Score 14.8; DB 2; Length 148;
Best local Similarity 88.9%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCTTCCTGCTCTCTT 18
||||| ||||| |||||
Db 140 GCCTTACCTGGTCTCTT 123

RESULT 15
PCT-US93-02147A-5/C
Sequence 5, Application PC/TUS9302147A
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PACE 4 AND
TITLE OF INVENTION: PACE 4.1 GENE AND POLYPEPTIDES IN CELLS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOLEY GOWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02147A
FILING DATE: 19930309
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,629
FILING DATE: 09-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: NEELEY PH.D., RICHARD L
REGISTRATION NUMBER: 30092
REFERENCE/DOCKET NUMBER: CHIR-009/00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-7622
TELEFAX: (415) 857-0663
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 18..131
PCT-US93-02147A-5

Query Match 82.2%; Score 14.8; DB 5; Length 148;
Best local Similarity 88.9%; Pred. No. 66;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCTTCCTGCTCTCTT 18
||||| ||||| |||||
Db 140 GCCTTACCTGGTCTCTT 123

Search completed: April 20, 2001, 00:03:30
Job time: 9667 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 03:21:14 ; Search time 1165 Seconds
(without alignments)
8.394 Million cell updates/sec

Title: US-09-016-464-11
Perfect score: 18
Sequence: 1 GCCTTCTCCTGCTCTCTT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13168883 seqs, 2603265903 residues

Total number of hits satisfying chosen parameters: 26337766

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	8 US-08-474-497-11	Sequence 11, Appl
2	18	100.0	18	14 US-09-016-464-11	Sequence 11, Appl
3	18	100.0	18	19 US-09-509-152A-1021	Sequence 1021, Ap
4	18	100.0	39	19 US-09-509-152A-1015	Sequence 1015, Ap
5	18	100.0	378	19 US-09-509-152A-1704	Sequence 1704, Ap
6	18	100.0	429	20 US-09-534-843-15195	Sequence 15195, A
7	18	100.0	444	18 US-09-431-517-17454	Sequence 17454, A
8	18	100.0	470	16 US-09-277-227-14043	Sequence 14043, A
9	18	100.0	577	20 US-09-534-843-15194	Sequence 15194, A
10	18	100.0	696	23 US-09-615-585-4	Sequence 4, Appl1
11	18	100.0	696	23 US-09-615-585-6	Sequence 6, Appl1
12	18	100.0	699	11 US-08-756-387A-7	Sequence 7, Appl1
13	18	100.0	699	16 US-09-285-873-4	Sequence 7, Appl1
14	18	100.0	773	12 US-08-897-956A-6	Sequence 6, Appl1
15	18	100.0	773	12 US-08-897-956A-6	Sequence 6, Appl1
16	18	100.0	774	1 PCT-US00-21097-2	Sequence 2, Appl1
17	18	100.0	774	11 US-08-756-387A-4	Sequence 4, Appl1
18	18	100.0	774	11 US-08-756-387A-5	Sequence 5, Appl1
19	18	100.0	774	16 US-09-285-873-4	Sequence 4, Appl1
20	18	100.0	774	16 US-09-285-873-5	Sequence 5, Appl1
21	18	100.0	1068	3 US-07-861-895-28	Sequence 28, Appl
22	18	100.0	1174	15 US-09-103-663-10	Sequence 10, Appl
23	18	100.0	1198	11 US-08-756-387A-1	Sequence 1, Appl1
24	18	100.0	1198	11 US-08-756-387A-3	Sequence 3, Appl1
25	18	100.0	1198	16 US-09-285-873-1	Sequence 1, Appl1
26	18	100.0	1198	16 US-09-285-873-3	Sequence 3, Appl1
27	18	100.0	1198	23 US-09-615-585-1	Sequence 3, Appl1
28	18	100.0	1198	23 US-09-615-585-3	Sequence 3, Appl1
29	18	100.0	7146	1 PCT-US00-21097-1	Sequence 1, Appl1
30	18	100.0	7800	19 US-09-509-152A-2409	Sequence 2409, Ap
31	17	94.4	350	15 US-09-105-307A-575	Sequence 575, Ap
32	17	94.4	350	23 US-09-605-702-13991	Sequence 13991, A
33	17	94.4	350	23 US-09-611-550-10840	Sequence 10840, A
34	17	94.4	358	29 US-09-724-866-10958	Sequence 10958, A
35	17	94.4	358	49 US-60-171-432-10958	Sequence 10958, A
36	17	94.4	374	15 US-09-105-307A-911	Sequence 911, App
37	17	94.4	404	23 US-09-611-550-7610	Sequence 7610, Ap
38	17	94.4	484	23 US-09-605-700-14320	Sequence 14320, A
39	17	94.4	484	23 US-09-611-550-13285	Sequence 13285, A
40	16.4	91.1	209	27 US-09-699-074-78	Sequence 78, Appl
41	16.4	91.1	230	17 US-09-370-505-900	Sequence 900, App
42	16.4	91.1	230	20 US-09-534-843-33603	Sequence 33603, A
43	16.4	91.1	230	41 US-60-096-463-900	Sequence 900, App
44	16.4	91.1	238	48 US-60-161-619-3450	Sequence 3450, App
45	16.4	91.1	271	50 US-60-182-316-13073	Sequence 13073, A

ALIGNMENTS

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RESULT 1
US-08-474-497-11
; Sequence 11, Application US/08474497
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,497
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-497-11

Query Match          100.0%: Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. NO. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCCGTGTTCTCTT 18
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DB 1 GCCTTCCGTGTTCTCTT 18

RESULT 2
US-09-016-464-11
; Sequence 11, Application US/09016464
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,464
FILING DATE: 30-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,497
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-016-464-11

Query Match          100.0%: Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. NO. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCCGTGTTCTCTT 18
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DB 1 GCCTTCCGTGTTCTCTT 18

RESULT 3
US-09-509-152A-1021
; Sequence 1021, Application US/09509152A
; GENERAL INFORMATION:
; APPLICANT: NYCE, JONATHAN W.
; TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
; FORMULATIONS, KITS & APPLICATIONS
; NUMBER OF SEQUENCES: 2419
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 CLARKE DRIVE
; CITY: CRANBURY
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/509,152A
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,160
; FILING DATE: 1997-09-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1021:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1021:
US-09-509-152A-1021

Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTCTT 18
|||||
DB 1 GCCTTCTGCTGTTCTCTT 18

RESULT 4

US-09-509-152A-1015

Sequence 1015, Application US/09509152A
GENERAL INFORMATION:

APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS

NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
ZIP: 08512
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-00991

TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1015:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1015:
US-09-509-152A-1015

Query Match 100.0%; Score 18; DB 19; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTCTT 18
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DB 1 GCCTTCTGCTGTTCTCTT 18

RESULT 5

US-09-509-152A-1704

Sequence 1704, Application US/09509152A
GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS

NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
ZIP: 08512
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1704:

SEQUENCE CHARACTERISTICS:
LENGTH: 378 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1704:
US-09-509-152A-1704

Query Match 100.0%; Score 18; DB 19; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTCTT 18
|||||
DB 1 GCCTTCTGCTGTTCTCTT 18

RESULT 6

US-09-534-843-15195/C

Sequence 15195, Application US/09534843

GENERAL INFORMATION:

APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mulahy, Sara J.
APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MO
FILE REFERENCE: PD-1007 CIP

CURRENT APPLICATION NUMBER: US/09/534,843
CURRENT FILING DATE: 2000-03-24
Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 49783
SOFTWARE: PERL Program
SEQ ID NO 15195

LENGTH: 429
TYPE: DNA

ORGANISM: Homo sapiens

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FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu01347286
NAME/KEY: unsure
LOCATION: 71
OTHER INFORMATION: a, t, c, g, or other
US-09-534-843-15195
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    |||
Db 190 GCCTTCTGCTGTTCTCTT 173
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RESULT 7
US-09-431-517-17454/C
Sequence 17454, Application US/09431517
GENERAL INFORMATION:
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APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-751CON1
CURRENT APPLICATION NUMBER: US/09/431,517
CURRENT FILING DATE: 1999-11-01
EARLIER APPLICATION NUMBER: US 09/170,294
EARLIER FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 31760
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17454
LENGTH: 444
TYPE: DNA
ORGANISM: Homo sapiens
US-09-431-517-17454
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```
Query Match          100.0%; Score 18; DB 18; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 GCCTTCTGCTGTTCTCTT 18
    |||
Db 311 GCCTTCTGCTGTTCTCTT 294
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```
RESULT 8
US-09-277-227-14043/C
Sequence 14043, Application US/09277227
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-766
CURRENT APPLICATION NUMBER: US/09/277,227
CURRENT FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 23680
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14043
LENGTH: 470
TYPE: DNA
ORGANISM: Homo sapiens
US-09-277-227-14043
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Query Match          100.0%; Score 18; DB 16; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 GCCTTCTGCTGTTCTCTT 18
    |||
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```
Db 349 GCCTTCTGCTGTTCTCTT 332
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```
RESULT 9
US-09-534-843-15194
Sequence 15194, Application US/09534843
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MO
FILE REFERENCE: PD-1007 CIP
CURRENT APPLICATION NUMBER: US/09/534,843
CURRENT FILING DATE: 2000-03-24
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 49783
SOFTWARE: PERL Program
SEQ ID NO 15194
LENGTH: 577
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: hu01307478
NAME/KEY: unsure
LOCATION: 527
OTHER INFORMATION: a, t, c, g, or other
US-09-534-843-15194
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Query Match          100.0%; Score 18; DB 20; Length 577;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 GCCTTCTGCTGTTCTCTT 18
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Db 175 gccttcctggttcctctt 192
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RESULT 10
US-09-615-585-4/C
Sequence 4, Application US/09615585
GENERAL INFORMATION:
APPLICANT: Weber, Eric R.
APPLICANT: Wood, Keith V.
TITLE OF INVENTION: Fc Epsilon Receptor-LUMINESCENCE INDUCING PROTEIN
TITLE OF INVENTION: CHIMERIC NUCLEIC ACID MOLECULES, FUSION PROTEINS AND
FILE REFERENCE: DI-8-C1
CURRENT APPLICATION NUMBER: US/09/615,585
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/186,412
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: 60/143,612
PRIOR FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 696
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(696)
US-09-615-585-4
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Query Match          100.0%; Score 18; DB 23; Length 696;
Best Local Similarity 100.0%; Pred. No. 2e+02;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCCTTCTGCTGTTCTCTT 18
|||||
Db 651 GCCTTCTGCTGTTCTCTT 634

RESULT 11
US-09-615-585-6
; Sequence 6, Application US/09615585
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: Wood, Keith V.
; APPLICANT: Hall, Mary P.
; TITLE OF INVENTION: FC EPSILON RECEPTOR-LUMINESCENCE INDUCING PROTEIN
; TITLE OF INVENTION: CHIMERIC NUCLEIC ACID MOLECULES, FUSION PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: DI-8-C1
; CURRENT APPLICATION NUMBER: US/09/615,585
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/186,412
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/143,612
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-615-585-6

Query Match 100.0%; Score 18; DB 23; Length 696;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGCTGTTCTCTT 18
|||||
Db 46 gccttcctgcttcctt 63

RESULT 12
US-08-756-387A-7/c
; Sequence 7, Application US/08756387A
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Massom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387A
; FILING DATE: November 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
US-08-756-387A-7

Query Match 100.0%; Score 18; DB 11; Length 699;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGCTGTTCTCTT 18
|||||
Db 651 GCCTTCTGCTGTTCTCTT 634

RESULT 13
US-09-285-873-7/c
; Sequence 7, Application US/09285873
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Massom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: November 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
US-09-285-873-7

Query Match 100.0%; Score 18; DB 16; Length 699;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTCTT 18
 |||
 DB 651 GCCTTCTGCTGTTCTCTT 634

RESULT 14

US-08-897-956-6/c
 ; Sequence 6, Application US/08897956
 ; GENERAL INFORMATION:
 ; APPLICANT: Digan, Mary Ellen
 ; APPLICANT: Lake, Philip
 ; APPLICANT: Gram, Hermann
 ; TITLE OF INVENTION: Fusion Polypeptides
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Michael Glynn, Novartis Corporation, Patent
 ; ADDRESSEE: Department
 ; STREET: 564 Morris Avenue
 ; CITY: Summit
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 07901
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/897,956
 ; FILING DATE: 21-JUL-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/022,689
 ; FILING DATE: 26-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perraro, Gregory D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 600-7244
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 522-6923
 ; TELEFAX: (908) 522-6955
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 773 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: Internal
 ; US-08-897-956-6

Query Match 100.0%; Score 18; DB 12; Length 773;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTCTT 18
 |||
 DB 726 GCCTTCTGCTGTTCTCTT 709

RESULT 15

US-08-897-956A-6/c
 ; Sequence 6, Application US/08897956A
 ; GENERAL INFORMATION:
 ; APPLICANT: Mary Ellen Digan

; APPLICANT: Philip Lake
 ; APPLICANT: Hermann Gram
 ; TITLE OF INVENTION: Fusion Polypeptides
 ; FILE REFERENCE: 600-7244/CRA
 ; CURRENT APPLICATION NUMBER: US/08/897,956A
 ; CURRENT FILING DATE: 1997-07-21
 ; PRIOR APPLICATION NUMBER: 60/022,689
 ; PRIOR FILING DATE: 1996-07-26
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 773
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion Polynucleotide
 ; US-08-897-956A-6

Query Match 100.0%; Score 18; DB 12; Length 773;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGTTCTCTT 18
 |||
 DB 726 GCCTTCTGCTGTTCTCTT 709

Search completed: April 20, 2001, 03:21:15
 Job time: 14162 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:15:00 ; Search time 101.94 Seconds
(without alignments)
24.434 Million cell updates/sec

Title: US-09-016-464-11

Perfect score: 18

Sequence: 1 GCCCTTCCTGCTCTCTT 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 segs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCF_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-09-543-679A-1021	Sequence 1021, App
2	18	100.0	39	US-09-543-679A-1015	Sequence 1015, App
3	18	100.0	378	US-09-543-679A-1704	Sequence 1704, App
4	18	100.0	1198	US-09-543-679A-2502	Sequence 2502, App
5	18	100.0	7659	US-09-543-679A-2501	Sequence 2501, App
6	18	100.0	7800	US-09-543-679A-2505	Sequence 2505, App
7	18	100.0	21742	US-09-543-679A-2505	Sequence 2505, App
8	18	100.0	117608	US-09-543-679A-3002	Sequence 3002, App
9	18	100.0	117608	US-09-543-679A-3002	Sequence 3002, App
10	15.4	85.6	176251	US-60-248-505-361	Sequence 361, App
11	15	83.3	106174	US-60-248-505-419	Sequence 419, App
12	14.8	82.2	441	US-08-276-163D-15149	Sequence 15149, A
13	14.8	82.2	496	US-08-276-163D-13828	Sequence 13828, A
14	14.8	82.2	1578	US-60-248-505-1768	Sequence 1768, App
15	14.8	82.2	9263	US-60-248-505-1561	Sequence 1561, App
16	14.8	82.2	20348	US-60-248-505-502	Sequence 502, App
17	14.8	82.2	25805	US-60-248-505-233	Sequence 233, App
18	14.8	82.2	36775	US-60-248-505-436	Sequence 436, App
19	14.8	82.2	71978	US-60-248-505-558	Sequence 558, App
20	14.8	82.2	116884	US-60-248-505-558	Sequence 558, App
21	14.8	82.2	174514	US-60-248-505-229	Sequence 229, App
22	14.8	82.2	177276	US-60-248-505-22	Sequence 22, App
23	14.8	82.2	183820	US-09-739-449-209	Sequence 209, App
24	14.4	80.0	261	US-08-276-163D-12766	Sequence 12766, A
25	14.4	80.0	410	US-09-487-566A-28	Sequence 28, App
26	14.4	80.0	926	US-09-739-449-1550	Sequence 1550, App
27	14.4	80.0	12146	US-09-277-457-27	Sequence 27, App

28	14.4	80.0	22067	US-09-820-001-3	Sequence 3, Appl
29	14.4	80.0	25439	US-60-248-505-636	Sequence 636, App
30	14.4	80.0	68686	US-60-248-505-274	Sequence 274, App
31	14.4	80.0	74334	US-60-248-505-450	Sequence 450, App
32	14.4	80.0	76127	US-60-248-505-483	Sequence 483, App
33	14.4	80.0	103631	US-60-248-505-160	Sequence 160, App
34	14.4	80.0	141589	US-09-543-679A-2480	Sequence 2480, App
35	14.4	80.0	141589	US-09-543-679A-2694	Sequence 2694, App
36	14.4	80.0	141589	US-09-543-679A-2719	Sequence 2719, App
37	14.4	80.0	146982	US-09-543-679A-3009	Sequence 3009, App
38	14.4	80.0	209274	US-09-543-679A-3004	Sequence 3004, App
39	14.4	80.0	300663	US-09-739-449-213	Sequence 213, App
40	14.4	80.0	443925	US-60-248-505-299	Sequence 299, App
41	14	77.8	2670	US-60-248-505-1356	Sequence 1356, App
42	14	77.8	4087	US-60-248-505-1871	Sequence 1871, App
43	14	77.8	8987	US-60-248-505-628	Sequence 628, App
44	14	77.8	24273	US-60-248-505-24	Sequence 24, Appl
45	14	77.8	29248	US-60-248-505-539	Sequence 539, App

ALIGNMENTS

RESULT 1
US-09-543-679A-1021
Sequence 1021, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NICE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543, 679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127, 958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1021:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1021:
US-09-543-679A-1021
Query Match 100.0%, Score 18, DB 5, Length 18;
Best Local Similarity 100.0%, Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGTTCTCTT 18
| | | | | | | | | | | | | | | |
DB 1 GCCTTCTGTTCTCTT 18

RESULT 2

US-09-543-679A-1015

Sequence 1015, Application US/09543679A

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1015:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1015:

US-09-543-679A-1015

Query Match 100.0%; Score 18; DB 5; Length 39;

Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGTTCTCTT 18
| | | | | | | | | | | | | | | |
DB 1 GCCTTCTGTTCTCTT 18

RESULT 3

US-09-543-679A-1704

Sequence 1704, Application US/09543679A

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1704:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1704:
US-09-543-679A-1704

Query Match 100.0%; Score 18; DB 5; Length 378;

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGTTCTCTT 18
| | | | | | | | | | | | | | | |
DB 1 GCCTTCTGTTCTCTT 18

RESULT 4

US-09-543-679A-2502/c

Sequence 2502, Application US/09543679A

GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2502:
SEQUENCE CHARACTERISTICS:
LENGTH: 1198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2502:
US-09-543-679A-2502

Query Match 100.0%; Score 18; DB 5; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCCGTCGTCCTT 18
|||||

DB 832 GCCTTCCGTCGTCCTT 815

RESULT 5
US-09-543-679A-2501/c
Sequence 2501, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2501:
SEQUENCE CHARACTERISTICS:
LENGTH: 7659 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2501:
US-09-543-679A-2501

Query Match 100.0%; Score 18; DB 5; Length 7659;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCCGTCGTCCTT 18
|||||

DB 6806 GCCTTCCGTCGTCCTT 6789

RESULT 6
US-09-543-679A-2409
Sequence 2409, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2409:
SEQUENCE CHARACTERISTICS:
LENGTH: 7800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2409:
US-09-543-679A-2409

Query Match 100.0%; Score 18; DB 5; Length 7800;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCCGTCGTCCTT 18
|||||

DB 1330 GCCTTCCGTCGTCCTT 1347

RESULT 7
US-09-543-679A-2505/c
Sequence 2505, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,

COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2505:
SEQUENCE CHARACTERISTICS:
LENGTH: 21742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2505:
US-09-543-679A-2505

Query Match 100.0%; Score 18; DB 5; Length 21742;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTCGTTCCTCTT 18
|||||
DB 9184 GCCTTCTCGTTCCTT 9167

RESULT 8
US-09-543-679A-3002
Sequence 3002, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3002:
SEQUENCE CHARACTERISTICS:
LENGTH: 117608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3002:
US-09-543-679A-3002

APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3002:
SEQUENCE CHARACTERISTICS:
LENGTH: 117608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3002:
US-09-543-679A-3002

Query Match 100.0%; Score 18; DB 5; Length 117608;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTTCTCGTTCCTCTT 18
|||||
DB 1330 GCCTTCTCGTTCCTT 1347

RESULT 9
US-09-543-679A-3002/C
Sequence 3002, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3002:
SEQUENCE CHARACTERISTICS:
LENGTH: 117608 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3002;
US-09-543-679A-3002

Query Match 100.0%; Score 18; DB 5; Length 117608;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTTCTGCTCTCT 18
|||||
Db 101586 GCCTTCTGCTCTCT 101569

RESULT 10
US-60-248-505-361
; Sequence 361, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361
; LENGTH: 176251
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(176251)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-505-361

Query Match 85.6%; Score 15.4; DB 6; Length 176251;
Best Local Similarity 94.1%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCCTTCTGCTCTCT 18
|||||
Db 43226 cttctcgtctctct 43242

RESULT 11
US-60-248-505-419
; Sequence 419, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 419
; LENGTH: 106174
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(106174)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-505-419

Query Match 83.3%; Score 15; DB 6; Length 106174;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TTTCCTGCTCTCTCT 18
|||||
Db 64947 tttctcgtctctct 64961

RESULT 12
US-08-276-163D-15149/C
; Sequence 15149, Application US/08276163D
; GENERAL INFORMATION:
; APPLICANT: Adams, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
; FILE REFERENCE: PO14
; CURRENT APPLICATION NUMBER: US/08/276,163D
; CURRENT FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 15314
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15149
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (29)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (36)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (149)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (201)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (209)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (231)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (240)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (287)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (289)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (293)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (319)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (321)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (330)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (333)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (334)
; OTHER INFORMATION: n equals a,t,g, or c

```
NAME/KEY: misc feature
LOCATION: (339)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (340)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (342)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (349)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (352)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (361)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (367)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (368)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (372)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (385)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (390)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (394)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (395)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (397)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (401)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (407)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (420)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (438)
OTHER INFORMATION: n equals a,t,g, or c
US-08-276-163D-15149

Query Match      82.2%; Score 14.8; DB 4; Length 441;
Best Local Similarity 88.9%; Pred. No. 72;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 1 GCCTTCCTGCTTCCTT 18
Db 117 GCCTTACTGTTACTT 100
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```
RESULT 13
US-08-276-163D-13828
Sequence 13828, Application US/08276163D
GENERAL INFORMATION:
APPLICANT: Adams, et. al.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
FILE REFERENCE: PO14
```

```
CURRENT APPLICATION NUMBER: US/08/276,163D
CURRENT FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 15314
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13828
LENGTH: 496
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (10)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (185)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (276)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (279)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (281)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (296)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (319)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (339)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (379)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (380)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (393)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (405)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (410)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (420)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (434)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (435)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (438)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (447)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (464)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (467)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (480)
OTHER INFORMATION: n equals a,t,g, or c
US-08-276-163D-13828
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Query Match 82.2%; Score 14.8; DB 4; Length 496;
Best Local Similarity 88.9%; Pred. No. 73;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGCTCTT 18
|||||
Db 205 gccttcctgacctctt 222

RESULT 14

US-60-248-505-1768/c
; Sequence 1768, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1768
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Human
US-60-248-505-1768

Query Match 82.2%; Score 14.8; DB 6; Length 1678;
Best Local Similarity 88.9%; Pred. No. 83;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGCTCTT 18
|||||
Db 1523 GCCTCTCTGATCTCTT 1506

RESULT 15

US-60-248-505-1561/c
; Sequence 1561, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1561
; LENGTH: 9263
; TYPE: DNA
; ORGANISM: Human
US-60-248-505-1561

Query Match 82.2%; Score 14.8; DB 6; Length 9263;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCTTCTGCTGCTCTT 18
|||||
Db 1410 GCCTCTCTGATCTCTT 1393

Search completed: April 20, 2001, 00:15:10
Job time: 9447 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:59:31 ; Search time 2028.86 Seconds
(without alignments)
54.633 Million cell updates/sec

Title: US-09-016-464-12

Perfect score: 18
Sequence: 1 GCGTGTGTGTCTCCTCT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
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31: em_htg_inv2:*
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95: gb_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	18	100.0	1127	9	AR075859	AR075859 Sequence
2	18	100.0	1127	92	HSFCERGS	X06049 Human Lymph
3	18	100.0	1460	9	A07098	A07098 Artificial
4	18	100.0	1503	9	AX026812	AX026812 Sequence
5	18	100.0	1504	93	HUMFCERA	M14766 Human FC-ep
6	18	100.0	1504	9	A05303	A05303 Artificial
7	18	100.0	1504	9	A06297	A06297 Artificial
8	18	100.0	1504	9	A10540	A10540 Artificial
9	18	100.0	1504	9	A10542	A10542 H.sapiens 1
10	18	100.0	1504	9	A10995	A10995 Artificial
11	18	100.0	1504	9	A10996	A10996 Artificial

FEATURES
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Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
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/transl_table=11
/protein_id="CAA00609.1"
/db_xref="GI:412978"
/translation="MEGGYSEIEELPRRCRGRTQIVLGLVTAAIMAGLLTLL
HMDPTQSLKOLEERAARVSOVKNSHEDQAQKSTQISQLEELAEQRL
KSQDELWNLNGLDLSSFKSQELNERNEASDLERREVTLRMELQVSSFCV
NTCPERKWNFORKCYFGKGTQWVHARYACDMGQLVSHSPEDQFLTKHASHTG
SWIGLRNLDLKEEFTWVGSHVDYSNMAFGPTSRSGEDCYMMSGRWMDAFCDRK
IGAWCDRLATCTPPASEGSAESMGPDSPDPDGRLLPTPSAPLHS"

BASE COUNT 340 a 439 c 424 g 257 t
ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 1460;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
|||||

Db 45 GCCTGTCTGTCTCTCT 28

RESULT 4
AX026812/c 1503 bp DNA PAT 16-SEP-2000
LOCUS
DEFINITION Sequence 18 from Patent EP1006183.
ACCESSION AX026812
VERSION AX026812.1 GI:10187945
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1503)
REFERENCE
AUTHORS Recombinant soluble fc receptors
TITLE Patent: EP 1006183-A 18 07-JUN-2000;
JOURNAL MAX PLANCK GESELLSCHAFT (DE)
FEATURES
source Location/Qualifiers
1..1503
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 345 a 456 c 431 g 271 t
ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 1503;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
|||||

Db 81 GCCTGTCTGTCTCTCT 64

RESULT 5
HUMECERA/c 1503 bp mRNA PRI 08-NOV-1994
LOCUS
DEFINITION Human fc-epsilon receptor CD23 antigen (Ige receptor) mRNA complete
cDS.
ACCESSION M14766
VERSION M14766.1 GI:182449
KEYWORDS fc-epsilon receptor; Ige receptor; cell surface receptor;
glycoprotein.
SOURCE Human EBV transformed B-cell line RPMI-8866, cDNA to mRNA, clone
pfc-eps10n-R-1.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1503)
REFERENCE
AUTHORS Kikutani, H., Inui, S., Sato, R., Barsunian, E. L., Owaki, H.,
Yamasaki, K., Kaisho, T., Uchibayashi, N., Hardy, R. R., Hirano, T.,
Tsunasawa, S., Sakiyama, F., Suenura, M. and Kishimoto, T.
Molecular structure of human lymphocyte receptor for immunoglobulin
E
JOURNAL Cell 47 (5), 657-665 (1986)
MEDLINE 87051737
COMMENT Draft entry and clean copy of sequence [1] kindly provided by
H. Kikutani, 05-MAR-1987.
LOCATION/Qualifiers
1..1503
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="1q21-q23"
/contig="1503"
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186..1148
/gene="FCBP1"
/note="Fc-epsilon receptor old gene name 'FCB1A'"
/codon_start=1
/db_xref="GDB:600-119-072"
/protein_id="AAA52435.1"
/db_xref="GI:182450"
/translation="MEGGYSEIEELPRRCRGRTQIVLGLVTAAIMAGLLTLL
HMDPTQSLKOLEERAARVSOVKNSHEDQAQKSTQISQLEELAEQRL
KSQDELWNLNGLDLSSFKSQELNERNEASDLERREVTLRMELQVSSFCV
NTCPERKWNFORKCYFGKGTQWVHARYACDMGQLVSHSPEDQFLTKHASHTG
SWIGLRNLDLKEEFTWVGSHVDYSNMAFGPTSRSGEDCYMMSGRWMDAFCDRK
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633..1148
/gene="FCBP1"
/note="Fc-epsilon receptor soluble form"

BASE COUNT 345 a 456 c 431 g 271 t
ORIGIN 47 bp upstream of SalI site.

Query Match 100.0%; Score 18; DB 93; Length 1503;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
|||||

Db 81 GCCTGTCTGTCTCTCT 64

RESULT 6
A05303/c 1504 bp mRNA PAT 24-NOV-1993
LOCUS
DEFINITION Artificial sequence for human Fc epsilon-receptor.
ACCESSION A05303
VERSION A05303.1 GI:490378
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE
AUTHORS Kishimoto, T., Suenura, M., Kikutani, H. and Barsunian, E. L.
TITLE Human low affinity Fc epsilon-receptor, the isolation, the
JOURNAL recombinant preparation and purification thereof
Patent: EP 0259615-A 7 16-MAR-1988;
Kishimoto, Tadami, Prof
LOCATION/Qualifiers
1..1504
/organism="synthetic construct"

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CDS
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    186..1151
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    /product="human Fc epsilon-receptor"
    /protein_id="CAA00444.1"
    /db.xref="GI:490379"
    /translation="MEGQYSEIEELPRRCRCRGTOIVLGLVTAALMAGLLTLLL
    WHMDTOSIKOLEERAAARVSOVSNLSEHGDDMAOKSOSTOISOELEELRABQORL
    KSQDELISNMLNGLOADLSSPKSOELNRENESDLLEPRREVTLRMLELYSSGFVC
    NTCPEKWNIFORKCYIFGKGRQWVHARACDMEGQLYSHSPEDQFLTRHASHTG
    SWIGLRNLDLKEGFIWVDSHYVSNMAGPEPTSSQGEDCVMMRSGRMWDAFCDRK
    LGAWCDRLATCTPPASGSAESMGPDSPDPDGRLPPTSPAPLHS"

BASE COUNT      346 a      456 c      431 g      271 t

ORIGIN
Query Match      100.0%; Score 18; DB 9; Length 1504;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCTGTCTGTCTGCTCCT 18
        |||||||
Db       81 GCCTGTCTGTCTGCTCCT 64

RESULT 7
LOCUS      A06297      1504 bp      mRNA      PAT      24-NOV-1993
DEFINITION Artificial sequence for human Fc epsilon-receptor, reverse
ACCESSION  A06297
VERSION     A06297.1 GI:489002
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial construct.
REFERENCE   1 (bases 1 to 1504)
AUTHORS     Kishimoto, T., Suemura, M., Kikutani, H. and Barsumian, E. L.
TITLE       Human low affinity Fc epsilon-receptor, the isolation, the
JOURNAL     recombinant preparation and purification thereof
            Patent: EP 0259615-A 9 16-MAR-1988;
            Kishimoto, Tadamltsu, Prof
FEATURES
    source          1..1504
                    /organism="synthetic construct"
                    /db.xref="taxon:32630"
BASE COUNT      271 a      431 c      456 g      346 t

ORIGIN
Query Match      100.0%; Score 18; DB 9; Length 1504;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCTGTCTGTCTGCTCCT 18
        |||||||
Db       1424 GCCTGTCTGTCTGCTCCT 1441

RESULT 8
LOCUS      A10540      1504 bp      mRNA      PAT      14-SEP-1993
DEFINITION Artificial mRNA for human low affinity Fc-epsilon-receptor.
ACCESSION  A10540
VERSION     A10540.1 GI:490733
KEYWORDS    Fc-epsilon receptor; low-affinity receptor.
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
REFERENCE   1 (bases 1 to 1504)
AUTHORS     Kishimoto, T., Suemura, M., Kikutani, H. and Barsumian, E. L.
TITLE       Human low affinity Fc epsilon-receptor, the isolation and
            Human low affinity Fc epsilon-receptor, the isolation and

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JOURNAL      purification thereof
            Patent: EP 0257114-A 5 02-MAR-1988;
            Kishimoto, Tadamltsu, Prof
FEATURES
    source          Location/Qualifiers
                    1..1504
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                    /db.xref="taxon:32630"
CDS
    186..1151
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    KSQDELISNMLNGLOADLSSPKSOELNRENESDLLEPRREVTLRMLELYSSGFVC
    NTCPEKWNIFORKCYIFGKGRQWVHARACDMEGQLYSHSPEDQFLTRHASHTG
    SWIGLRNLDLKEGFIWVDSHYVSNMAGPEPTSSQGEDCVMMRSGRMWDAFCDRK
    LGAWCDRLATCTPPASGSAESMGPDSPDPDGRLPPTSPAPLHS"

BASE COUNT      346 a      456 c      431 g      271 t

ORIGIN
Query Match      100.0%; Score 18; DB 9; Length 1504;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCTGTCTGTCTGCTCCT 18
        |||||||
Db       81 GCCTGTCTGTCTGCTCCT 64

RESULT 9
LOCUS      A10542      1504 bp      mRNA      PAT      14-SEP-1993
DEFINITION H.sapiens low affinity Fc-epsilon-receptor.
ACCESSION  A10542
VERSION     A10542.1 GI:489152
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominoidea; Homo.
REFERENCE   1 (bases 1 to 1504)
AUTHORS     Kishimoto, T., Suemura, M., Kikutani, H. and Barsumian, E. L.
TITLE       Human low affinity Fc epsilon-receptor, the isolation and
JOURNAL     purification thereof
            Patent: EP 0257114-A 7 02-MAR-1988;
            Kishimoto, Tadamltsu, Prof
FEATURES
    source          1..1504
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                    /db.xref="taxon:9606"
BASE COUNT      271 a      431 c      456 g      346 t

ORIGIN
Query Match      100.0%; Score 18; DB 9; Length 1504;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCCTGTCTGTCTGCTCCT 18
        |||||||
Db       1424 GCCTGTCTGTCTGCTCCT 1441

RESULT 10
LOCUS      A10995      1504 bp      mRNA      PAT      15-NOV-1993
DEFINITION Artificial sequence for human low affinity Fc epsilon receptor.
ACCESSION  A10995
VERSION     A10995.1 GI:490901
KEYWORDS

```

SOURCE	synthetic construct.
ORGANISM	artificial sequence.
REFERENCE	1 (bases 1 to 1504)
AUTHORS	Kishimoto,T., Suemura,M., Kikutani,H. and Barsumian,E.L.
TITLE	Human low affinity Fc epsilon-receptor, the isolation, the recombinant preparation and purification thereof
JOURNAL	Patent: EP 0258492-A 12 09-MAR-1988;
FEATURES	Kishimoto, Tadamltsu, Prof
source	Location/Qualifiers
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	/db_xref="taxon:32630"
CDS	186..1151
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	/product="human low affinity Fc epsilon receptor"
	/protein_id="CA00932.1"
	/db_xref="GI:490902"
	/translation="MEEGYSEIEELPRRCRCRGTOVLGLVTAIMAGLITLLIL WHWPTQSLKQLEERAAENVQVSKNLESHHGDDMAOKSOSTQISOLEELRARDQR KSOLELWNLNGLOADLSFRKSOELNDRNASDLLELRREYVKLRMELGVSSGFVQ NTCEKXINFEQRKCYFGKGTQWHAAYACDDMEGQVSIHSEEDFLTKHASHTG SWIGRLNDLGEFRIWDGSHVDYSNNAFGPPTSQSGEDCVMMRGSRMWDADCDRR LGAIVCRLATCTPPASBSAESMGPSRPPDRLRTPPSAPLHS"
BASE COUNT	346 a 457 c 430 g 271 t
ORIGIN	
Query Match	100.0%; Score 18; DB 9; Length 1504;
Best Local Similarity	100.0%; Pred. No. 8.1;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 GCCTGTGCTGTGCTCCT 18 Db 81 GCCTGTGCTGTGCTCCT 64
RESULT 11	
A10996	A10996 1504 bp mRNA PAT 15-NOV-1993
LOCUS	Artificial sequence for human low affinity Fc epsilon receptor.
DEFINITION	A10996
ACCESSION	A10996
VERSION	A10996.1 GI:489235
KEYWORDS	
SOURCE	synthetic construct.
ORGANISM	artificial sequence.
REFERENCE	1 (bases 1 to 1504)
AUTHORS	Kishimoto,T., Suemura,M., Kikutani,H. and Barsumian,E.L.
TITLE	Human low affinity Fc epsilon-receptor, the isolation, the recombinant preparation and purification thereof
JOURNAL	Patent: EP 0258492-A 13 09-MAR-1988;
FEATURES	Kishimoto, Tadamltsu, Prof
source	Location/Qualifiers
	1..1504
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	/db_xref="taxon:32630"
BASE COUNT	271 a 430 c 457 g 346 t
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Query Match	100.0%; Score 18; DB 9; Length 1504;
Best Local Similarity	100.0%; Pred. No. 8.1;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 GCCTGTGCTGTGCTCCT 18 Db 1424 GCCTGTGCTGTGCTCCT 1441
RESULT 12	
A11841/c	

LOCUS	AI1841	1515 bp	DNA	PAT	24-NOV-1993
DEFINITION	Nucleotide sequence 33 from patent number EP0259615.				
ACCESSION	AI1841				
VERSION	AI1841.1	GI:492536			
KEYWORDS	.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 1515)				
AUTHORS	Kishimoto,T., Suemura,M., Kikutani,H. and Barsamian,E.L.				
TITLE	Human low affinity Fc epsilon-receptor, the isolation, the recombinant preparation and purification thereof				
JOURNAL	Patent: EP 0259615-A 33 16-MAR-1988;				
	Kishimoto, Tadamitsu, Prof				
FEATURES	Location/Qualifiers				
source	1..1515				
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	/db_xref="taxon:32644"				
BASE COUNT	352 a	458 c	432 g	273 t	
ORIGIN					
Query Match	100.0%; Score 18; DB 9; Length 1515;				
Best Local Similarity	100.0%; Pred. No. 8.1;				
Matches	18; Conservative	0;	Mismatches	0; Indels	0; Gaps
OY	1 GCCTGTGTCGTCTCCTCT 18				
Db	88 GCCTGTGTCGTCTCCTCT 71				
RESULT 13					
AI1365/c	AI1365	1515 bp	DNA	PAT	19-JAN-1994
LOCUS	pFC-epsilonR-1 DNA from patent EP0324879.				
DEFINITION	AI1365				
ACCESSION	AI1365.1	GI:491638			
VERSION					
KEYWORDS	.				
SOURCE	synthetic construct.				
ORGANISM	synthetic construct				
REFERENCE	artificial sequence.				
AUTHORS	1 (bases 1 to 1515)				
TITLE	Kishimoto,T., Suemura,M., Kikutani,H., Barsamian,E.L.,				
	Schneider,F.J., Schwendenwein,R., Sommergruber,W. and Sletty,P.				
	Soluble recombinant Fc-epsilon-receptor, the preparation and the				
	use thereof				
JOURNAL	Patent: EP 0324879-A 1 26-JUL-1989;				
	Kishimoto, Tadamitsu, Prof				
FEATURES	Location/Qualifiers				
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CDS	193..1158				
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	/protein_id="CAA01096.1"				
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	KSDQLEISWNLGQADLSERKSOEFLMRNASDLRLREYVKLRLELOVSSGPGVC				
	NTCEKMINQKQKCYFGKGTQKQVHVARFACDDWEGQVLSIHSPEEDFLTKHASHTG				
	SMGIRLNDLGEPIVWDGSHVDYVNAPAGPPTSRSGEDCVMMRGSGRMWDACDRRR				
	LGAVVCRLATCTPPASEGSAESMGSPRPDPDRPLTPSPAPLHS"				
BASE COUNT	352 a	458 c	432 g	273 t	
ORIGIN					
Query Match	100.0%; Score 18; DB 9; Length 1515;				
Best Local Similarity	100.0%; Pred. No. 8.1;				
Matches	18; Conservative	0;	Mismatches	0; Indels	0; Gaps
OY	1 GCCTGTGTCGTCTCCTCT 18				

Db 88 GCCTGTCTGTCTCTCT 71

RESULT 14

A13484/c

LOCUS A13484 1515 bp DNA PAT 11-JUL-1995

DEFINITION pFc-epsilon R-1 DNA from patent EP0321842.

ACCESSION A13484

VERSION A13484.1 GI:1246949

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Patent: EP 0321842-A 8 28-JUN-1989;

Kishimoto, Tadamltsu, Prof

Location/Qualifiers

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193. .1158

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/db_xref="GI:1246950"

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NTCEPKWINFORKCYFEGKGTQWVHAYACDDMEGQLVSIHSPEDDFLTRKASHTG

SMIGLRNLDLGEFLWVDSHVDYSNMAYGPTSRSGEDCVMMRGSGRWMDAFCDRK

LGAWYCDRLATCTPPASEGSAESMGPDSPDRPDDRLPTPSAPLHS"

BASE COUNT 352 a 458 c 432 g 273 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 18; DB 9; Length 1515;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTCTGTCTCTCT 18
|||||

Db 88 GCCTGTCTGTCTCTCT 71

RESULT 15

A14649/c

LOCUS A14649 1515 bp DNA PAT 28-MAR-1994

DEFINITION pFc epsilon R-1.

ACCESSION A14649

VERSION A14649.1 GI:512665

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Patent: EP 0321601-A 1 28-JUN-1989;

Kishimoto, Tadamltsu, Prof

Location/Qualifiers

1. .1515

/organism="synthetic construct"

/db_xref="taxon:32630"

193. .1158

/codon_start=1

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SMIGLRNLDLGEFLWVDSHVDYSNMAYGPTSRSGEDCVMMRGSGRWMDAFCDRK
LGAWYCDRLATCTPPASEGSAESMGPDSPDRPDDRLPTPSAPLHS"
BASE COUNT 352 a 458 c 432 g 273 t
ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 1515;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTCTGTCTCTCT 18
|||||

Db 88 GCCTGTCTGTCTCTCT 71

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Job time: 9450 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:48 ; Search time 547.68 Seconds
(without alignments)
19,187 Million cell updates/sec

Title: US-09-016-464-12

Perfect score: 18
Sequence: 1 GCCTGTCTGTCTCTCT 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	18	100.0	18	18	T76087	Human Ige receptor
2	18	100.0	18	18	T76073	Human FC-epsilon r
3	18	100.0	18	20	X53892	Human Ige receptor
4	18	100.0	18	20	X53872	Human FC-epsilon C
5	18	100.0	18	21	F19437	Human Ige receptor
6	18	100.0	18	21	F19457	Human Ige receptor
7	18	100.0	18	21	A33315	Low adenosine anti
8	18	100.0	18	21	A33335	Low adenosine anti
9	18	100.0	279	20	X54573	Human Ige receptor
10	18	100.0	279	21	F20142	Human Ige receptor
11	18	100.0	279	21	A34020	Human adenosine re

12	18	100.0	291	21	F20143	Human low adenosin
13	18	100.0	291	21	A34021	Human adenosine re
14	18	100.0	299	20	X54562	Human FC-epsilon C
15	18	100.0	299	21	F20131	Human Ige receptor
16	18	100.0	299	21	A34009	Human adenosine re
17	18	100.0	1127	20	Z09902	Human FC-epsilon R
18	18	100.0	1465	9	N81437	pCL-2 cDNA Insert
19	18	100.0	1494	9	N90344	Plasmid pFC-epsilo
20	18	100.0	1503	21	F21303	Human low adenosin
21	18	100.0	1503	21	A35181	Human adenosine re
22	18	100.0	1504	9	N81485	ECORI insert from
23	18	100.0	1504	9	N81367	ECORI insert from
24	18	100.0	1504	9	N81512	Sequence of a gene
25	18	100.0	1515	10	N90134	FC epsilon recepto
26	18	100.0	1529	9	N81612	DNA encoding Fc ga
27	18	100.0	1530	21	F21304	Human low adenosin
28	18	100.0	1530	21	A35182	Human adenosine re
29	18	100.0	1531	8	N70107	DNA encoding Ige b
30	18	100.0	1549	9	N82252	Human low affinity
31	18	100.0	3108	21	F21302	Human low adenosin
32	18	100.0	3108	21	A35180	Human adenosine re
33	18	100.0	6532	21	F21305	Human low adenosin
34	18	100.0	6532	21	A35183	Human adenosine re
35	18	100.0	7800	21	F20842	Human multiple tar
36	18	100.0	7800	21	A34720	Human adenosine re
37	18	100.0	7803	20	X55272	Human adenosine re
38	18	100.0	114955	20	X53491	Human adenosine Al
39	18	100.0	117609	21	F21435	Human receptor-rel
40	16.4	91.1	343	21	C17882	Human secreted pro
41	16	88.9	2084	19	V34286	Human secreted pro
42	16	88.9	9520	10	N91779	Sequence encoding
43	15.4	85.6	1239	21	C77156	Human ORFX ORF2711
44	15.4	85.6	3659	7	N60204	Interferon-pseudo-
45	15.4	85.6	4332	19	V31717	Kaposi's sarcoma a

ALIGNMENTS

RESULT 1	
ID T76087	standard; DNA; 18 BP.
AC T76087;	
DT 12-SEP-1997	(first entry)
DE Human Ige receptor Fc epsilon R antisense oligonucleotide HSJGBFRAS1.	
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;	
KW chronic obstructive pulmonary disease; bronchitis; immunoglobulin; ss.	
OS Synthetic.	
XX WO96440162-A1.	
PN 19-DEC-1996.	
PD 06-JUN-1996;	96WO-US09306.
PF 07-JUN-1995;	95US-0474497.
PR (UYEC-) UNIV EAST CAROLINA.	
PA Metzger WJ, Nyce JW;	
PI WPI; 1997-051871/05.	
DR Treatment of airway diseases such as asthma - by topically applying	
XX PT adenosine-free antisense oligo:nucleotide to airway epithelium of	
PT subject	
PS Example 5; Page 25; 71pp; English.	

XX A method for treating airway disease in a subject has been produced;
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC H5GEBRASI specific for the human IGE receptor FC epsilon R. The
CC method can be used to treat airway diseases such as cystic fibrosis,
CC asthma, chronic obstructive pulmonary disease, bronchitis and other
CC airway diseases characterised by an inflammatory response. By
CC eliminating adenosine from the antisense ON, its liberation upon
CC antisense degradation is prevented, thereby preventing adenosine-
CC induced bronchoconstriction in patients with hyper-reactive airways.
XX Sequence 18 BP: 0 A: 7 C: 4 G: 7 T: 0 other:
SQ

Query Match 100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTGTCGTCCT 18
1 | | | | | | | | | | | | | | | | | | | |
Db 1 gccctgtctgtccct 18

RESULT 2
T76073
ID T76073 standard; DNA: 18 BP.
XX
AC T76073:
XX
DT 11-SEP-1997 (first entry)
XX
DE Human FC-epsilon receptor antisense oligonucleotide HUMIGERC23AS1.
XX
XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
KM chronic obstructive pulmonary disease; bronchitis; immunoglobulin; ss.
KM
OS Synthetic.
XX
PM WO9640162-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-0509306.
XX
PR 07-JUN-1995; 95US-0474497.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Metzger WJ, Nyce JW;
XX
DR WPI: 1997-051871/05.
XX
XX Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
XX
PS Claim 5; Page 25; 71pp; English.
XX
XX A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC HUMIGERC23ASI specific for the human FC-epsilon receptor CD23
CC antigen (IGE receptor). The method can be used to treat airway diseases
CC such as cystic fibrosis, asthma, chronic obstructive pulmonary disease,
CC bronchitis and other airway diseases characterised by an inflammatory
CC response. By eliminating adenosine from the antisense ON, its liberation
CC upon antisense degradation is prevented, thereby preventing adenosine-
CC induced bronchoconstriction in patients with hyper-reactive airways.
XX
SQ Sequence 18 BP: 0 A: 7 C: 4 G: 7 T: 0 other:

Query Match 100.0%; Score 18; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTGTCGTCCT 18
1 | | | | | | | | | | | | | | | | | | | |
Db 1 gccctgtctgtccct 18

RESULT 3
X53892
ID X53892 standard; DNA: 18 BP.
XX
AC X53892:
XX
DT 05-JUL-1999 (first entry)
XX
DE Human IGE receptor antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
KM impaired respiration; inflammation; lung disease;
KM pulmonary vasoconstriction; inflammation; allergic rhinitis;
KM acute asthma; allergy; asthma; impeded respiration;
KM respiratory distress syndrome; pain; cystic fibrosis;
KM pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KM prostate cancer; ss.
XX
XX Synthetic.
XX
PM WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-0519419.
XX
PR 09-JUN-1998; 98US-0093972.
XX
PR 17-SEP-1997; 97US-0059160.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI: 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
PT
XX
PS Disclosure: Page 44; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (X52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences X55272-74. These multiple target
CC oligonucleotides (specifically X55180-271) can be used for the antisense
CC treatment of diseases and conditions. Typical diseases and conditions
CC are those associated with impaired respiration and inflammation,
CC including lung diseases, pulmonary vasoconstriction, inflammation,
CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC metastases, as well as all types of cancers which may metastasize or have

CC metastasized to the lungs, including breast and prostate cancer.
 XX Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
 |||
 Db 1 gccctgtctgtctctct 18

RESULT 4
 X53872
 ID X53872 standard; DNA; 18 BP.
 AC X53872;
 XX
 DT 05-JUL-1999 (first entry)
 XX

DE Human Fc-epsilon CD23 antigen antisense oligonucleotide fragment.
 XX Antisense oligonucleotide: multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.

XX Synthetic.
 OS
 XX WO913886-A1.
 PN
 XX 25-MAR-1999.
 PD
 XX 17-SEP-1998; 98WO-US19419.
 PF
 XX 09-JUN-1998; 98US-0093972.
 PR 17-SEP-1997; 97US-0059160.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 1999-229400/19.
 XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 XX vasoconstriction
 XX
 PS Disclosure: Page 43; 120pp; English.
 XX

CC The specification describes antisense oligonucleotides (X52866-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,

CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have
 CC metastasized to the lungs, including breast and prostate cancer.

SQ Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
 |||
 Db 1 gccctgtctgtctctct 18

RESULT 5
 F19437
 ID F19437 standard; DNA; 18 BP.
 XX
 AC F19437;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human IGE receptor polynucleotide fragment #1004.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX Homo sapiens.
 OS
 XX WO200062736-A2.
 PN
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000MO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 XX
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 XX trigger adenosine receptors during metabolism, useful e.g. for treating
 XX cancers and respiratory obstructions -
 XX
 PS Claim 14; Page 130; 1592pp; English.
 XX

CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and

	Query Match	100.08;	Score 18;	DB 21;	length 18;
	Best Local Similarity	100.08;	Pred. No. 9;		
	Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 GCCTGTGTCGTCTCCTCT 18				
bb	1 gcctgtgtctgtctctctct 18				

DT 14-MAR-2001 (first entry)

DE Human IgE receptor polynucleotide fragment #1024.

KM low adeosine antisenase oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; ROS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.

OS	Homo sapiens.
XX	
PN	MO200062736-A2.
XX	
PD	26-OCT-2000.
XX	
PE	24-MAR-2000; 2000MO-US08020.
XX	
PR	06-APR-1999; 9905-0127958
XX	
PA	(UYEC-) UNIV EAST CAROLINA.
PA	(NYCE-) NYCE J W.

DR WPT; 2000-679539/66.

PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX
Claim 14: Page 131; 1592pp; English.

xx The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiallergic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. F18434 to F21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 other;

Query Match	100.0%	Score 18;	DB 21;	Length 18;
Best Local Similarity	100.0%	Pred. NO. 9;		
Matches 18; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	GCCTGTGTCGTCTCCT	18
	1		18
Db	1	gcctgtgtctgtctctct	18

A33315
ID A33315 standard; DNA; 18 BP.

DT 28-JUL-2000 (first entry)

DE	Low adenosine antisense oligonucleotide SEQ ID NO:1004
DE	Low adenosine antisense oligonucleotide SEQ ID NO:1004

KM Human adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphorothioate; impaired respiration; inflammation; allergy;
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KM antiallergic; antiasthmatic; cytoskeletal; analgesic; impaired airway;
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

PN W0200009525-A2.

PD 24-FEB-2000

PF 03-AUG-1999; 99WO-US17712.

PR 03-AUG-1998; 98US-0095212.

PA (UYEC-) UNIV EAST CAROLINA

PI	Nyce JW;	XX
XX		XX
XX	WP1: 2000-205971/18.	XX
XX		XX
P7	New antisense oligonucleotides useful for treating e.g. pulmonary	XX
P7	vasoconstriction, inflammation, allergies, asthma, hypertension,	XX
P7	bronchitis, emphysema, respiratory distress syndrome, ischemia or	XX
P7	cancers -	XX
PS	Claim 18; Page 391; 1343pp; English.	XX
XX		XX
CC	The present invention describes a new composition comprising an antisense	CC
CC	oligonucleotide (ON) with low adenosine (up to 15%), which targets	CC
CC	nucleic acids involved in bronchoconstriction, allergies, and/or	CC
CC	inflammation. The ON can have antiinflammatory, antiallergic,	CC
CC	antiasthmatic, cytostatic and analgesic activities. The compositions are	CC
CC	useful for the treatment of diseases associated with inflammation,	CC
CC	impaired airways, including lung disease and diseases whose secondary	CC
CC	effects afflict the lungs of a subject. They can be used for treating	CC
CC	e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,	CC
CC	impaired respiration, respiratory distress syndrome, pain, cystic	CC
CC	fibrosis, pulmonary hypertension, emphysema, chronic obstructive	CC
CC	pulmonary disease (COPD), and cancers such as leukemias, lymphomas,	CC
CC	carcinomas, and cancers which may metastasize to the lungs, including	CC
CC	breast and prostate cancer. The reduction of the adenosine content of the	CC
CC	ONS reduces side effects. The A-containing ONS break down with the-	CC
CC	release of deoxyadenosine which activates adenosine receptors causing	CC
CC	bronchoconstriction and inflammation. A32313 to A35312 represent the	CC
CC	nucleotide sequences given in the sequence listing from the present	CC
CC	invention, which correspond to SEQ ID NO:1 to 2815, and then the last	CC
CC	185 sequences are also called SEQ ID NO:1 to 185, but the sequences	CC
CC	differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323	CC
CC	to A33992) are specifically claimed ONS from the present invention.	CC
CC	N.B. Sequences given in the disclosure of the present invention do not	CC
CC	match up with their corresponding SEQ ID NO: sequences given in the	CC
CC	sequence listing.	CC
XX		XX
XX	Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 other;	XX
XX		XX
QY	Query Match 100.0%; Score 18; DB 21; Length 18;	QY
Db	Best Local Similarity 100.0%; Pred. NO. 9;	Db
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	1 GCCTGTGTCGTGCTCTCT 18	
	1 gctctgtctgtcctctct 18	
RESULT 8		
ID A33335	A33335 standard; DNA; 18 BP.	
XX A33335;		
XX		
DE 28-JUL-2000 (first entry)		
XX		
XX	Low adenosine antisense oligonucleotide SEQ ID NO:1024.	
XX		
XX	Human: adenosine receptor; low adenosine antisense oligonucleotide;	
KW phosphorothioate; impaired respiration; inflammation; allergy;		
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;		
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;		
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;		
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;		
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;		
XX cancer; leukemia; lymphoma; carcinoma; metastasis; ss.		
OS Homo sapiens.		
XX		
PN WO200009525-A2.		
XX		

PD 24-FEB-2000.

PF 03-AUG-1999; 99WO-US17712.

PR 03-AUG-1998; 98US-0095212.

PX (UYEC-) UNIV EAST CAROLINA.

PA

PL Nyce JW;

PT WPI; 2000-205971/18.

PP New antisense oligonucleotides useful for treating e.g. pulmonary
bronchitis, emphysema, respiratory distress syndrome, ischemia or
cancers -

PS Claim 18; Page 393; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
oligonucleotide (ON) with low adenosine (up to 15%), which targets
nucleic acids involved in bronchoconstriction, allergies, and/or
inflammation. The ON can have anti-inflammatory, antiallergic,
antiasmatic, cytostatic and analgesic activities. The compositions are
useful for the treatment of diseases associated with inflammation,
impaired airways, including lung disease and diseases whose secondary
effects afflict the lungs of a subject. They can be used for treating
e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
impeded respiration, respiratory distress syndrome, pain, cystic
fibrosis, pulmonary hypertension, emphysema, chronic obstructive
pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
carcinomas, and cancers which may metastasize to the lungs, including
breast and prostate cancer. The reduction of the adenosine content of the
ON reduces side effects. The A-containing ONs break down with the
release of deoxyadenosine which activates adenosine receptors causing
bronchoconstriction and inflammation. A32313 to A35312 represent the
nucleotide sequences given in the sequence listing from the present
invention, which correspond to SEQ ID NO:1 to 2815, and then the last
185 sequences are also called SEQ ID NO:1 to 185, but the sequences
differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
to A33992) are specifically claimed ONs from the present invention.
N.B. Sequences given in the disclosure of the present invention do not
match up with their corresponding SEQ ID NO: sequences given in the
sequence listing.

CC

CS Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 other;

SQ

Query Match 100.0%; Score 18; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 GCCTGAGTGTGCCTCCT 18
| | | | | | | | | | | | |
Db 1 gccctgttcctccctcct 18

RESULT 9
X54573 X54573 standard; DNA; 279 BP.

XX X54573:

DT 05-JUL-1999 (first entry)

DE Human IGF receptor antisense oligonucleotide fragment.

KW Antisense oligonucleotide; multiple target; antisense treatment;
impaired respiration; inflammation; lung disease;
pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
respiratory distress syndrome; pain; cystic fibrosis;
pulmonary hypertension; pulmonary vasoconstriction; emphysema;

KM immunosuppressive; antisthmatic; analgesic; hypotensive; cyrostatic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 XX
 OS Homo sapiens.
 PN WO20062736-AZ.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX (NYCE/) NYCE J W.
 PI
 XX Nlyce JW;
 XX
 DR WPI: 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 PS
 XX Claim 14; Page 131; 1592pp; English.
 XX
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antisthmatic, hypotensive and cyostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. P18444 to P21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 CC
 XX
 XX Sequence 279 BP; 7 A; 92 C; 87 G; 78 T; 15 other;
 SQ

Query Match 100.0%; Score 18; DB 21; Length 279;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GCCTGTGCTGTCNCCT 18
 1 ||||||||||||||||
 1 gccctgctgcgcctcct 18

RESULT 11
ID A34020 standard; DNA: 279 BP.
XX
AC A34020;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:1709.
XX
KW Human: adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN MO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99MO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 477; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cyostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33922) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 279 BP: 7 A; 92 C; 87 G; 78 T; 15 other;

Query Match 100.0%; Score 18; DB 21; Length 279;
Best Local Similarity 100.0%; Pred. No. 10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTGTCGTGCTCCCT 18
|||
Db 1 gcctgctcgtcctcct 18
RESULT 12
ID F20143 standard; DNA: 291 BP.
XX
AC F20143;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide #1710.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
KW respiratory obstruction; pulmonary obstruction; impaired respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN MO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000MO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 543; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,

CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 291 BP; 7 A; 97 C; 89 G; 83 T; 15 other;

Query Match 100.0%; Score 18; DB 21; Length 291;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTGTCCTCCT 18
Db 1 gctctgtctctgtctctct 18
|||||

RESULT 13
A34021 A34021 standard; DNA; 291 BP.
XX
AC A34021;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:1710.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.
XX
XX WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
XX 03-AUG-1998; 98US-0095212.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX NYce JW;
XX
XX WPI: 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
XX Disclosure: Page 477; 1343pp; English.
XX
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive

CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONS reduces side effects. The A-containing ONS break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONS from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
SQ Sequence 291 BP; 7 A; 97 C; 89 G; 83 T; 15 other;

Query Match 100.0%; Score 18; DB 21; Length 291;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTGTCCTCCT 18
Db 1 gctctgtctctgtctctct 18
|||||

RESULT 14
X54562 X54562 standard; DNA; 299 BP.
XX
AC X54562;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human Fc-epsilon CD23 antigen antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
XX Synthetic.
XX
XX WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US19419.
XX
XX 09-JUN-1998; 98US-0093972.
XX
XX 17-SEP-1997; 97US-0059160.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX NYce JW;
XX
XX WPI: 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
XX
XX Disclosure: Page 43; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (X52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene

CC Initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have
 CC metastasized to the lungs, including breast and prostate cancer.

SQ Sequence 299 BP; 7 A; 98 C; 93 G; 94 T; 7 other:

Query Match

Best Local Similarity 100.0%; Score 18; DB 20; Length 299;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTCTGTCTCTCT 18
 |||||
 DB 1 gcctgtctgtctctct 18

RESULT 15

F20131
 ID F20131 standard; DNA; 299 BP.

AC F20131;

DT 14-MAR-2001 (first entry)

XX Human Ige receptor polynucleotide fragment #1698.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000: 2000WO-US08020.

XX 06-APR-1999: 990S-0127958.

XX (UYEC-) UNIT EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX NYCE JW;

XX MPI: 2000-679539/66.

PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -

PS Claim 14; Page 130; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.

SQ Sequence 299 BP; 7 A; 98 C; 93 G; 94 T; 7 other:

Query Match

Best Local Similarity 100.0%; Score 18; DB 21; Length 299;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTCTGTCTCTCT 18
 |||||
 DB 1 gcctgtctgtctctct 18

Search completed: April 20, 2001, 00:12:48
 Job time: 10010 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:24:43 ; Search time 7150.85 Seconds
(without alignments)
0.368 Million cell updates/sec

Title: US-09-016-464-12
Perfect score: 18
Sequence: 1 GCCGTGCTGTCCTCCT 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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 234: gb_gss34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	17	94.4	338	170	BF896460	BF896460 RC2-WT014
c 2	17	94.4	596	170	BF899308	BF899308 PM1-WT019
c 3	16.4	91.1	114	138	BE702687	BE702687 RC5-NN106
c 4	16.4	91.1	185	130	BB303490	BB303490 BB303490
c 5	16.4	91.1	261	216	A2092343	A2092343 RPCI-23-4
c 6	16.4	91.1	268	156	T33792	T33792 EST59214 Hu
c 7	16.4	91.1	282	111	AW165136	AW165136 f602c10. x
c 8	16.4	91.1	291	139	BE766439	BE766439 IL3-WT010
c 9	16.4	91.1	300	156	T06523	T06523 EST04412 Fe
c 10	16.4	91.1	310	156	R88642	R88642 ym95g04.r1
c 11	16.4	91.1	313	115	AW428309	AW428309 65635 MAR
c 12	16.4	91.1	320	155	R23066	R23066 yh31c03.r1
c 13	16.4	91.1	321	115	AW465982	AW465982 BP230021A
c 14	16.4	91.1	334	8	AA491657	AA491657 ne78g04.s
c 15	16.4	91.1	361	153	H87070	H87070 ysf74d06.r1
c 16	16.4	91.1	369	170	BF874319	BF874319 IL3-ET011
c 17	16.4	91.1	389	137	BE654378	BE654378 UI-M-AK1-
c 18	16.4	91.1	393	115	AW462556	AW462556 BP230009B

19	16.4	91.1	398	156	R87340	R87340 ym8a01.r1
20	16.4	91.1	401	170	BF920202	BF920202 QV2-Nr014
21	16.4	91.1	415	156	R62702	R62702 y110b02.r1
22	16.4	91.1	422	5	AA310047	AA310047 EST180891
23	16.4	91.1	423	153	H63483	H63483 yf53h01.r1
24	16.4	91.1	425	156	R70055	R70055 y14b01.r1
25	16.4	91.1	428	167	BE46114	BE46114 WHE1141.B
26	16.4	91.1	431	140	BE876730	BE876730 601488295
27	16.4	91.1	431	202	AQ11131	AQ11131 C1F-HSP-2
28	16.4	91.1	438	156	R89677	R89677 ym97h03.r1
29	16.4	91.1	443	153	H45396	H45396 ypn9g09.r1
30	16.4	91.1	445	167	BE44550	BE44550 WHE1125.H
31	16.4	91.1	447	168	BF740720	BF740720 QV1-HB003
32	16.4	91.1	451	143	BF043658	BF043658 BP250015B
33	16.4	91.1	451	139	BE750845	BE750845 202500.MA
34	16.4	91.1	456	3	AA160870	AA160870 z062f07.s
35	16.4	91.1	477	21	A1545700	A1545700 fb75c02.y
36	16.4	91.1	482	153	H40946	H40946 y005c02.r1
37	16.4	91.1	484	8	AA493249	AA493249 nh54h05.s
38	16.4	91.1	484	213	AQ884967	AQ884967 HS-5517.B
39	16.4	91.1	497	12	AA827876	AA827876 od56g07.s
40	16.4	91.1	500	148	BF441484	BF441484 257692.MA
41	16.4	91.1	507	166	BE383351	BE383351 601298266
42	16.4	91.1	511	166	BE382823	BE382823 601297866
43	16.4	91.1	520	212	AQ822796	AQ822796 HS-2205.B
44	16.4	91.1	527	156	R74264	R74264 y157b05.r1
45	16.4	91.1	528	173	BC081346	BC081346 H3064A12-

ALIGNMENTS

RESULT 1
BF896460/c 338 bp mRNA EST 18-JAN-2001

LOCUS BF896460 RC2-MT0148-241100-017-b09 MT0148 Homo sapiens cDNA, mRNA sequence.

DEFINITION BF896460

VERSION BF896460.1 GI:12287919

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 338)

Authors Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT 20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC2&ct2=RC2-MT0148-

241100-017-b09&ct3=2000-11-24&ct4=1)

Seg primer: puc 18 forward

High quality sequence start: 18

High quality sequence stop: 338.

Location/Qualifiers

1..338

/organism="Homo sapiens"

/db_xref="taxon:9606"

FEATURES

Source

/clone_11b="MT0148"

/dev_stage="Adult"

/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 68 a 91 c 122 g 57 t

Query Match 94.4%; Score 17; DB 170; Length 338;

Best local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTGCC 17

Db 168 GCCTGTCTGTCTGCC 152

RESULT 2
BF899308/c 596 bp mRNA EST 18-JAN-2001

LOCUS BF899308 PM1-MT0198-011200-002-e08 MT0198 Homo sapiens cDNA, mRNA sequence.

DEFINITION BF899308

VERSION BF899308.1 GI:12290767

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 596)

Authors Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT 20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&ct2=PM1-MT0198-

011200-002-e08&ct3=2000-12-01&ct4=1)

Seg primer: puc 18 forward

High quality sequence start: 17

High quality sequence stop: 507.

Location/Qualifiers

1..596

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_11b="MT0198"

/dev_stage="Adult"

/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 142 a 152 c 187 g 115 t

ORIGIN

Query Match 94.4%; Score 17; DB 170; Length 596;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTCTGTCTCTCT 17
 ||||||||||||||||
 DB 484 GCCTGTCTGTCTCTCC 468

RESULT 3

BE702687 114 bp mRNA EST 12-SEP-2000
 LOCUS BE702687
 DEFINITION RCS-NN1066-280700-023-H05 NN1066 Homo sapiens CDNA, mRNA sequence.
 ACCESSION BE702687
 VERSION BE702687.1 GI:10090429
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 114)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNALS Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 COMMENT 20202663

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-3704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=cl2-RCS-NN1066-280
 700-023-H05&cl=2000-07-28&cl=1)
 Seq primer: puc 18 forward
 High quality sequence start: 39
 High quality sequence stop: 114.

FEATURES
 source
 1..114
 Location/Qualifiers

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1lb="NN1066"
 /dev_stage="Adult"
 /note="Organ: nervous normal; Vector: puc18; Site:1: SmaI;
 Site:2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 16 a 55 c 19 g 24 t
 ORIGIN

Query Match 91.1%; Score 16.4; DB 138; Length 114;
 Best Local Similarity 94.4%; Pred. No. 7.8e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 GCCTGTCTGTCTCTCT 18
 ||||||||||||||||
 DB 27 GCCTGTCTGTCTCTCT 44

RESULT 4

BB303490/c 185 bp mRNA EST 10-JUL-2000
 LOCUS BB303490
 DEFINITION BB303490 RIKEN full-length enriched, adult male corpora
 quadrigemina Mus musculus CDNA clone B230104M05 3', mRNA sequence.
 ACCESSION BB303490
 VERSION BB303490
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 185)
 Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci,
 P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
 Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
 Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
 Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata,
 Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
 Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya,
 T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
 Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
 M., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Konno, H., et al.)
 Unpublished (2000)
 Contact: Yoshihide Hayashizaki
 Genome Exploration Research Group, Life Science Tsukuba Center,
 Genome Science Laboratory
 The Institute of Physical and Chemical Research (RIKEN), Genomic
 Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: +81-298-36-9013
 Fax: +81-298-36-9098
 Email: genome-res@cc.riken.go.jp/
 URL: http://genome.etc.riken.go.jp/
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagata, S., Sasaki,
 N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermostabilization and thermostabilization of the thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
 Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.etc.riken.go.jp) for
 further details.

FEATURES
 source

1..185
 Location/Qualifiers
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_1lb="B230104M05"
 /clone_1lb="RIKEN full-length enriched, adult male corpora
 quadrigemina"
 /sex="male"
 /tissue_type="corpora quadrigemina"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Site:1: SalI; Site:2: BamHI; CDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGGAGAGAGATCCACAGACCTTTTCTTTTCTTTT 3'], cDNA was

Db 162 GCCTGTCTGTCTCTCT 145

|||||

RESULT 7

AM165136 282 bp mRNA

LOCUS fe02c10.x1 zebrafish Mashu MPIMG EST Danio rerio cDNA 3', mRNA

DEFINITION

sequence.

ACCESSION

AM165136

VERSION

AM165136.1 GI:6342312

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Washu zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@wustl.edu
CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone Distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Resourcenet/centrum/primaridenbank, Berlin, Germany (web address:
www.rzpd.de)
Seq primer: 17' ET from Amersham
High quality sequence stop: 253.
Location/Qualifiers

FEATURES

source

1. 282
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish Mashu MPIMG EST"
/sex="mixed"
/tissue_type="26 somite embryos, adult livers, shield
stage embryos"
/lab_host="XLI-blue MRF"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
strand cDNA was primed with a Not I - oligo(dT)15 primer
[5'pCAGTGTCTGTAGATCGCGCGCCGCTTTTCTTTTCTTTT3'];
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Wenach lab; ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebrafish late somitogenesis (26 ss), adult liver or
embryonic shield stage (5.6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single cDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
control."

BASE COUNT

90 a 51 c 49 g 92 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 111; Length 282;
Best Local Similarity 94.4%; Pred. No. 8.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18

Db 225 GCCTGTCTGTCTCTCT 208

RESULT 8

BE766439

LOCUS

IL3-NT0104-020800-232-F02 NT0104 Homo sapiens CDNA, mRNA sequence.

ACCESSION

BE766439

VERSION

BE766439.1 GI:1096363

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the RAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=6t2-IL3-NT0104-020
800-232-F02&t3=2000-08-02&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 291.
Location/Qualifiers

FEATURES

source

1. 291
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0104"
/dev_stage="Adult"
/note="Organ: nervous.tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT

52 a 100 c 63 g 76 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 139; Length 291;
Best Local Similarity 94.4%; Pred. No. 8.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18

Db 77 GCCTGTCTGTCTCTCT 94

RESULT 9

T06523/c

LOCUS T06523 300 bp mRNA EST 30-JUN-1993
 DEFINITION EST04412 Fetal brain, Stratagene (cat#936206) Homo sapiens CDNA
 clone HFBD061, mRNA sequence.
 ACCESSION T06523
 VERSION T06523.1 GI:317672
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 300)
 Adams,M.D., Kerilavage,A.R., Fields,C. and Venter,J.C.
 3,400 expressed sequence tags identify diversity of transcripts
 from human brain
 Nature Genet. 4, 256-267 (1993)
 JOURNAL MEDLINE
 MEDLINE 9336420
 COMMENT Contact: Adams, MD
 The Institute for Genomic Research
 932 Clopper Road, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: mdadams@tigr.org
 Seq primer: M13-21.
 FEATURES
 source
 Location/Qualifiers
 1..300
 /organism="Homo sapiens"
 /db_xref="ATCC (Inhost):83182"
 /db_xref="taxon:9606"
 /clone="HFBD061"
 /clone_11b="Fetal brain, Stratagene (cat#936206)"
 /note="Vector: LambdaZAP-II; 17-18 wk gestation, female;
 oligo-dr + random primed cDNA synthesis; lambdaZAP-II
 vector, 1.0kb average inser size."
 BASE COUNT 81 a 70 c 97 g 46 t 6 others
 ORIGIN

Query Match 91.1%; Score 16.4; DB 156; Length 300;
 Best Local Similarity 94.4%; Pred. No. 8.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GCCTGCTCTGTCCTCT 18
 ||||||||| |||||
 Db 241 GCCTGCTCTGTCCTCT 224

RESULT 10
 LOCUS R88642 310 bp mRNA EST 24-AUG-1995
 DEFINITION ym95g04.r1 Soares adult brain N2b4HB55Y Homo sapiens CDNA clone
 IMAGE:166710 5', similar to gb:U05086 Human smg p25a GDP
 dissociation inhibitor homologue mRNA, partial (HUMAN);, mRNA
 sequence.
 R88642
 R88642.1 GI:953469
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 310)
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
 Rittlin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Watson,
 R., Williamson,A., Wohldmann,P. and Wilson,R.
 The WashU-Merck EST Project
 Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu

Insert Size: 1864
 High quality sequence stops: 163 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1864 Std Error: 0.00
 Seq primer: M13RPI
 High quality sequence stop: 163.
 FEATURES
 source
 Location/Qualifiers
 1..310
 /organism="Homo sapiens"
 /db_xref="GDB:587405"
 /db_xref="taxon:9606"
 /clone="IMAGE:166710"
 /clone_11b="Soares adult brain N2b4HB55Y"
 /sex="Male"
 /dev_stage="55-year old"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: brain; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTCCATCTGGAAGTGGAGCGCGCGCTTTTCTTTTCTTTTCTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 53. Library constructed by Bento
 Soares and M.Falima Bonaldi. The adult brain RNA was
 provided by Dr. Donald H. Gilden. Tissue was acquired
 17-18 hours after death which occurred in consequence of a
 ruptured aortic aneurysm. RNA was prepared from a pool of
 tissues representing the following areas of the brain:
 frontal, parietal, temporal and occipital cortex from the
 left and right hemispheres, subcortical white matter,
 basal ganglia, thalamus, cerebellum, midbrain, pons and
 medulla."
 BASE COUNT 69 a 94 c 68 g 75 t 4 others
 ORIGIN

Query Match 91.1%; Score 16.4; DB 156; Length 310;
 Best Local Similarity 94.4%; Pred. No. 8.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GCCTGCTCTGTCCTCT 18
 ||||||||| |||||
 Db 151 GCCTGCTCTGTCCTCT 168

RESULT 11
 LOCUS AM428309 313 bp mRNA EST 07-JUL-2000
 DEFINITION 65635 MARC 4BOV Bos taurus CDNA 5', mRNA sequence.
 ACCESSION AM428309
 VERSION AM428309.1 GI:6956256
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 313)
 Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
 Bennett,G.A., Fahrrekrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
 ,W.M. and Keele,J.W.
 Design and use of four pooled tissue normalized cDNA libraries for
 EST discovery in cattle
 Unpublished (2000)
 COMMENT Contact: Smith RPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -nmatch 12 options.

PCR PRIMERS
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGACG
Plate: 43 row: G column: 16
Seq primer: ATTAGTGACACTATAG.

FEATURES

SOURCE

Location/Qualifiers

1..313

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 4BOY"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from day 20 and day 40

embryos."

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BASE COUNT

45 a 119 c 90 g 59 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 115; Length 313;
Best Local Similarity 94.4%; Pred. No. 8.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCCGTGTCGTCTCCT 18

|||||

Db 230 GCCGTGTCGTCTCCT 247

RESULT 12

LOCUS

R23066 320 bp mRNA EST 20-APR-1995

DEFINITION

YH1C03.r1 Soares Placenta NB2HP Homo sapiens CDNA clone

IMAGE:131332 5' similar to gb:L05086 Human smg p25A GDP

disassociation inhibitor homologue mRNA, partial (HUMAN);, mRNA

sequence.

R23066

R23066.1 GI:777954

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 320)

Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M., Holman

, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,

Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston

, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Mashu-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 997

High quality sequence stops: 241

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 997 Std Error: 0.00

Seq primer: M13RPI

High quality sequence stop: 241.

Location/Qualifiers

1..320

/organism="Homo sapiens"

/db_xref="GDB:536812"

BASE COUNT

57 a 96 c 81 g 86 t

ORIGIN

Query Match 91.1%; Score 16.4; DB 155; Length 320;
Best Local Similarity 94.4%; Pred. No. 8.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCCGTGTCGTCTCCT 18

|||||

Db 112 GCCGTGTCGTCTCCT 129

RESULT 13

LOCUS

AM465982 321 bp mRNA EST 24-FEB-2000

DEFINITION

BP230021A20H5 Soares normalized bovine placenta Bos taurus CDNA

clone BP230021A20H5 5', mRNA sequence.

AM465982

AM465982.1 GI:7036150

EST.

cow.

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 321)

Lewin, H.A., Soares, M.B., Rebetz, M., Pardinas, J., Liu, L. and Larson

, J.H.

Bovine ESTs

Unpublished (2000)

Contact: Lewin, H. A.

W. M. Keck Center for Comparative and Functional Genomics

University of Illinois at Urbana-Champaign

340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL

61801, USA

Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National

Research Initiative, Animal Genome Resource Grant Ag 99-3205-6534

to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED

from Washington University Genome Center. Vector Trimmi g:

Cross-match from Washington University Genome Center PHRAP suite.

Sequences submitted are vector free and at least 200 bp in length.

PCR Primers

FORWARD: TAATGACACTCTATAGG

BACKWARD: ATTAACCTCTACTAAG

Insert Length: 321 Std Error: 0.00

Plate: BP230021A20 row: H column: 5

Seq primer: AGCGATATCAATTTCCACACGGA

High quality sequence stop: 321.

FEATURES

SOURCE

Location/Qualifiers

1..321

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone="BP230021A20H5"

/clone_lib="Soares normalized bovine placenta"

/sex="female"

/lab_host="DH10B"

/note="Organ: placenta; Vector: pT73Pac; Site_1: EcoRI;


```

QY      1 GCCTGTCTGTCTCCT 18
          |||
Db     284 GCCTGTCTGTCTCCT 301

```

Search completed: April 19, 2001, 23:24:46
Job time: 8163 sec

Fri Apr 20 10:22:52 2001

us-09-016-464-12.rst

Page 10

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:30 ; Search time 280.46 seconds
(without alignments)
11.206 Million cell updates/sec

Title: US-09-016-464-12

Perfect score: 18

Sequence: 1 GCCTGTCTGTCTCTCT 18

Scoring table: IDENTITY_NUC

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	100.0	1127	2	US-08-453-024-1
C 2	18	100.0	1127	4	US-08-070-162-1
C 3	15.4	85.6	4332	3	US-08-728-603-14
C 4	15.4	85.6	32207	4	US-08-770-379-20
C 5	15.4	85.6	32207	4	US-08-757-669A-20
C 6	14.8	82.2	692	1	US-08-592-126-123
C 7	14.8	82.2	2955	1	US-08-687-379-5
C 8	14.8	82.2	2955	1	US-08-687-379-7
C 9	14.8	82.2	17410	1	US-07-841-646-3
C 10	14.8	82.2	17410	1	US-08-147-023-3
C 11	14.8	82.2	17410	1	US-08-447-570-3
C 12	14.8	82.2	17410	2	US-08-448-700-3
C 13	14.8	82.2	17410	2	US-08-448-699A-3
C 14	14.8	82.2	17415	3	US-08-486-343A-1
C 15	14.8	82.2	17415	5	PCT-US95-07349-1
C 16	14.4	80.0	1633	4	US-09-119-788-1
C 17	14.4	80.0	3268	1	US-08-369-796-1
C 18	14.4	80.0	3268	2	US-08-852-091-1
C 19	14.4	80.0	3268	2	US-08-820-754-1
C 20	14.4	80.0	3268	3	US-08-956-652-1
C 21	14.4	80.0	3268	4	US-08-956-869-1
C 22	14.4	80.0	3268	4	US-08-948-547-1
C 23	14.4	80.0	3268	5	PCT-US95-17025-1
C 24	14.4	80.0	3796	1	US-08-343-760A-1
C 25	14.4	80.0	17949	4	US-09-087-465-3
C 26	14	77.8	240	1	US-08-054-985-1
C 27	14	77.8	1131	2	US-08-432-871C-1

C 28	14	77.8	1131	4	US-08-515-495-3	Sequence 3, Appl
C 29	14	77.8	1131	4	US-09-125-099-3	Sequence 3, Appl
C 30	14	77.8	1131	4	US-09-125-099-7	Sequence 7, Appl
C 31	14	77.8	1131	4	US-09-125-099-9	Sequence 9, Appl
C 32	14	77.8	1131	4	US-09-125-099-11	Sequence 11, Appl
C 33	14	77.8	2076	5	PCT-US91-08442-1	Sequence 1, Appl
C 34	14	77.8	2481	1	US-08-467-568-1	Sequence 1, Appl
C 35	14	77.8	2481	2	US-09-030-582-1	Sequence 1, Appl
C 36	14	77.8	2481	5	PCT-US94-09051-1	Sequence 1, Appl
C 37	14	77.8	4749	1	US-08-452-259-1	Sequence 1, Appl
C 38	14	77.8	4749	5	PCT-US96-07336-1	Sequence 1, Appl
C 39	13.8	76.7	153	2	US-08-611-757-12	Sequence 12, Appl
C 40	13.8	76.7	153	4	PCT-US95-05980-12	Sequence 12, Appl
C 41	13.8	76.7	356	4	US-09-142-078-53	Sequence 63, Appl
C 42	13.8	76.7	379	4	US-09-142-078-57	Sequence 57, Appl
C 43	13.8	76.7	390	4	US-09-142-078-65	Sequence 65, Appl
C 44	13.8	76.7	394	4	US-09-142-078-53	Sequence 53, Appl
C 45	13.8	76.7	627	4	US-08-793-624-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-08-453-024-1/c
; Sequence 1, Application US/08453024
; Patent No. 5958707
; GENERAL INFORMATION:
; APPLICANT: de Vries, Jan
; APPLICANT: Jenh, Chung-Her
; APPLICANT: Narula, Satwant
; APPLICANT: Zavadny, Paul
; TITLE OF INVENTION: Human Interleukin-4 Antagonist/Agonist Screens
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Schering-Plough Corporation
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,162
; FILING DATE: 28-MAY-1993
; APPLICATION NUMBER: US07/869914
; FILING DATE: 16-APR-1992
; APPLICATION NUMBER: US07/770081
; FILING DATE: 03-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Dulak, No. 5958707man C.
; REGISTRATION NUMBER: 31,608
; REFERENCE/DOCKET NUMBER: JB0214K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 822 7375
; TELEFAX: 201 822 7039
; TELEX: 219165
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1127 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-453-024-1

Query Match 100.0%; Score 18; DB 2; Length 1127;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCCTGTCTGTCTCTCT 18
|||||
Db 663 GCCTGTCTGTCTCTCT 646

RESULT 2
US-08-070-162-1/c
; Sequence 1, Application US/08070162
; Patent No. 620805

GENERAL INFORMATION:

APPLICANT: de Vries, Jan
APPLICANT: Jenh, Chung-Her
APPLICANT: Narula, Salwant
APPLICANT: Zavadny, Paul
TITLE OF INVENTION: Human Interleukin-4 Antagonist/Agonist Screens
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070.162
FILING DATE: 19930528
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US07/866914
FILING DATE: 16-APR-1992
APPLICATION NUMBER: US07/770081
FILING DATE: 03-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Dulak, No. 6200805man C.
REGISTRATION NUMBER: 31,608
REFERENCE/DOCKET NUMBER: JB0214K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 822 7375
TELEFAX: 201 822 7039
TELEX: 219165

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1127 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

US-08-070-162-1

Query Match 100.0%; Score 18; DB 4; Length 1127;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCCTGTCTGTCTCTCT 18
|||||
Db 663 GCCTGTCTGTCTCTCT 646

RESULT 3
US-08-728-603-14/c
; Sequence 14, Application US/08728603
; Patent No. 6093806
; GENERAL INFORMATION:

APPLICANT: Cesarman, Ethel
APPLICANT: Knowles, Daniel M.
TITLE OF INVENTION: PROTEINS OF KAPOSI'S SARCOMA ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728.603
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 4332 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-728-603-14

Query Match 85.6%; Score 15.4; DB 3; Length 4332;
Best Local Similarity 94.1%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CCTGTCTGTCTCTCTCT 18
|||||
Db 902 CCTGTCTGTCTCTCTCT 886

RESULT 4
US-08-770-379-20
; Sequence 20, Application US/08770379
; Patent No. 5849564

GENERAL INFORMATION:

APPLICANT: Chang, Yuan

APPLICANT: Bohenzky, Roy A.

APPLICANT: Russo, James J.

APPLICANT: Edelman, Isidore S.

APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED

TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20

Query Match 85.6%; Score 15.4; DB 2; Length 32207;
Best Local Similarity 94.1%; Pred. No. 49;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGTGTCTGTCTCTCT 18
|||||
Db 28321 CCGTGTCTGTCTCTCT 28337

RESULT 5
US-08-757-669A-20
Sequence 20, Application US/08757669A
Patent No. 6183751
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-669A-20

Query Match 85.6%; Score 15.4; DB 4; Length 32207;
Best Local Similarity 94.1%; Pred. No. 49;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGTGTCTGTCTCTCT 18
|||||
Db 28321 CCGTGTCTGTCTCTCT 28337

RESULT 6
US-08-592-126-123
Sequence 123, Application US/08592126
Patent No. 5821091
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Delinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,126
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 692 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G61con.seq
US-08-592-126-123

Query Match 82.2%; Score 14.8; DB 1; Length 692;
Best Local Similarity 88.9%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCGTGTCTGTCTCTCT 18
|||||
Db 24 GCCTGTCTGTCTCTCT 41

RESULT 7
US-08-687-379-5
Sequence 5, Application US/08687379
Patent No. 5756697
GENERAL INFORMATION:
APPLICANT: Hoeger, Thomas
APPLICANT: Ultsch, Andreas

```

: APPLICANT: Bach, Alfred
: APPLICANT: Steierer, Sylvia
: APPLICANT: Lemaire, Hans-Georg
: TITLE OF INVENTION: Subunits of Glutamate Receptors, Their
: TITLE OF INVENTION: Preparation and Their Use
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kell & Weinkauff
: STREET: 1101 Connecticut Avenue
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette-3.5 Inch, 720 KB storage
: COMPUTER: IBM AT-compatible, 80286 processor
: OPERATING SYSTEM: MS-DOS version 5.1
: SOFTWARE: Wordperfect version 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/687,379
: FILING DATE: 05-AUG-1996
: CLASSIFICATION: 435
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2955 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: DEVELOPMENTAL STAGE: Adult
: TISSUE TYPE: Brain
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 28..2676
: US-08-687-379-5

Query Match      82.2%; Score 14.8; DB 1; Length 2955;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GCCTGTCCTGTCCTCCT 18
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Db 42 GCATGTTCTGTCCTCCT 59

RESULT 8
US-08-687-379-7
: Sequence 7, Application US/08687379
: Patent No. 5756697
: GENERAL INFORMATION:
: APPLICANT: Hoeger, Thomas
: APPLICANT: Ullsch, Andreas
: APPLICANT: Bach, Alfred
: APPLICANT: Steierer, Sylvia
: APPLICANT: Lemaire, Hans-Georg
: TITLE OF INVENTION: Subunits of Glutamate Receptors, Their
: TITLE OF INVENTION: Preparation and Their Use
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kell & Weinkauff
: STREET: 1101 Connecticut Avenue
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette-3.5 Inch, 720 KB storage
: COMPUTER: IBM AT-compatible, 80286 processor
: OPERATING SYSTEM: MS-DOS version 6.0
: SOFTWARE: Wordperfect version 5.1
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/687,379
: FILING DATE: 05-AUG-1996
: CLASSIFICATION: 435
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2955 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA to mRNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: DEVELOPMENTAL STAGE: Adult
: TISSUE TYPE: Brain
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 28..2676
: US-08-687-379-7

Query Match      82.2%; Score 14.8; DB 1; Length 2955;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GCCTGTCCTGTCCTCCT 18
   ||| ||| ||| ||| |||
Db 42 GCATGTTCTGTCCTCCT 59

RESULT 9
US-07-841-646-3
: Sequence 3, Application US/07841646
: Patent No. 5266683
: GENERAL INFORMATION:
: APPLICANT: OPPERMANN, HERMANN
: APPLICANT: OZKAYNAK, ENGİN
: APPLICANT: KUBERASAMPATH, THANGAVEL
: APPLICANT: RUEGER, DAVID C.
: APPLICANT: PANG, ROY H. L.
: TITLE OF INVENTION: OSTEOGENIC DEVICES
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TESTA, HURWITZ & THIBEAULT
: STREET: 53 STATE STREET
: CITY: BOSTON
: STATE: MASSACHUSETTS
: COUNTRY: U.S.A.
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/841,646
: FILING DATE: 19920221
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 810,560
: FILING DATE: 20-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 827,052
: FILING DATE: 28-JAN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 660,162
: FILING DATE: 22-FEB-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 621,988
: FILING DATE: 04-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 621,849
: FILING DATE: 04-DEC-1990
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 3192..3730
OTHER INFORMATION: /label= EXON-1
OTHER INFORMATION: /note= "START CODON BEGINS AT POSITION 3313"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10413..10414
OTHER INFORMATION: /label= GAP-1
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 10413 AND 10414 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 10696..10891
OTHER INFORMATION: /label= EXON-2
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10960..10961
OTHER INFORMATION: /label= GAP-2
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITION 10960 AND 10961 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11059..11211
OTHER INFORMATION: /label= EXON-3

FEATURE:
NAME/KEY: misc_feature
LOCATION: 11351..11352
OTHER INFORMATION: /label= GAP-3
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 11351 AND 11352 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 11420..11617
OTHER INFORMATION: /label= EXON-4
FEATURE:
NAME/KEY: misc_feature
LOCATION: 11721..11722
OTHER INFORMATION: /label= GAP-4
OTHER INFORMATION: /note= "APPROXIMATELY _____ BASES ARE ESTIMATED TO
OTHER INFORMATION: BE MISSING BETWEEN POSITIONS 11721 AND 11722 IN
OTHER INFORMATION: THIS SEQUENCE."
FEATURE:
NAME/KEY: exon
LOCATION: 13354..13436
OTHER INFORMATION: /label= EXON-5
FEATURE:
NAME/KEY: exon
LOCATION: 15044..15160
OTHER INFORMATION: /label= EXON-6
FEATURE:
NAME/KEY: exon
LOCATION: 17245..17410
OTHER INFORMATION: /label= EXON-7
US-07-841-646-3

Query Match 82.2%; Score 14,8; DB 1; Length 17410;
Best Local Similarity 88.9%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCGTGTCCTCCTCCTCT 18
Db 11036 GCCGTGTCCTCCTCCT 11053

RESULT 10
US-08-147-023-3
Sequence 3, Application US/08147023
Patent No. 5468845
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,023
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
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FEATURE:
NAME/KEY: exon
LOCATION: 10696..10891

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NAME/KEY: exon
LOCATION: 17245..17410
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US-08-147-023-3
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Best Local Similarity 88.9%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCTGTCTCTCTCCCT 18
DB 11036 GCCCGTCTCTCTCCCT 11053
RESULT 11
US-08-447-570-3
; Sequence 3, Application US/08447570
; Patent No. 5714589
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109


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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,570
FILING DATE: 21-FEB-1992
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIORITY APPLICATION DATA:
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FILING DATE: 18-OCT-1990
PRIORITY APPLICATION DATA:
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FILING DATE: 07-SEP-1990
PRIORITY APPLICATION DATA:
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FILING DATE: 20-AUG-1990
PRIORITY APPLICATION DATA:
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FILING DATE: 22-FEB-1990
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FILING DATE: 17-OCT-1989
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FILING DATE: 23-FEB-1989
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APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 3192..3730

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NAME/KEY: exon
LOCATION: 11059..11211
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NAME/KEY: exon
LOCATION: 11420..11617
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FEATURE:
NAME/KEY: misc.feature
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NAME/KEY: exon
LOCATION: 13354..13436
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FEATURE:
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LOCATION: 15044..15160
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US-08-447-570-3

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 11036 GCCGTCCTCTCTCTCTCT 11053
QY 1 GCCTGCTCTGTCCTCTCT 18

RESULT 12
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; Sequence 3, Application US/08449700
; Patent No. 5863758
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGİN
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APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,700
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
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FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
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APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
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FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: 3192..3730
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FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: exon
LOCATION: 13354..13436
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NAME/KEY: exon
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US-08-449-700-3

Query Match 82.2%; Score 14.8; DB 2; Length 17410;
Best Local Similarity 88.9%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db     11036  GCCCGTGTCTCTCCTCT  11053

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RESULT 13
US-08-449-699A-3
Sequence 3, Application US/08449699A
Patent No. 5958441
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO5
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,699A
FILING DATE: 24-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-001CP6CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
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NAME/KEY: misc_feature
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NAME/KEY: exon
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NAME/KEY: exon
LOCATION: 15044..15160
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NAME/KEY: exon
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US-08-449-699A-3

Query Match 82.2%; Score 14.8; DB 2; Length 17410;
Best Local Similarity 88.9%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

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Db 11036 GCCGCTGCTCTCCTCT 11053

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: Patent No. 6071695
: GENERAL INFORMATION:
: APPLICANT: OKAYNAK, ENGIN
: APPLICANT: OPPERMANN, HERMANN
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
: TITLE OF INVENTION: MORPHOGENIC PROTEIN EXPRESSION
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
: ADDRESSEE: INC.
: STREET: 45 SOUTH STREET
: CITY: HOPKINTON
: STATE: MA
: COUNTRY: USA
: ZIP: 07148
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/486,343A

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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, Edmund R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-091CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)-248-7000
TELEFAX: (617)-248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17415 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: homo sapiens
US-08-486-343A-1

Query Match 82.2% Score 14.8; DB 3; Length 17415;
Best Local Similarity 88.9%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 11041 GCCCGTCTCTCTCTCT 11058

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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: MORPHOGEN EXPRESSION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
ADDRESSEE: INC.
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 07148
COMPUTER READABLE FORM:
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APPLICATION NUMBER: PCT/US95/07349
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,021
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-091PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)-435-9001
TELEFAX: (508)-435-0992
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17415 base pairs
TYPE: nucleic acid
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PCT-US95-07349-1

Query Match 82.2% Score 14.8; DB 5; Length 17415;
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DB 11041 GCCCGTCTCTCTCTCT 11058

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Title: US-09-016-464-12

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36: /cgn2_6/ptodata/2/pna/US098f_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US098g_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US098h_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US098i_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US098j_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US098k_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US098l_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US098m_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	8	US-08-474-497-12	Sequence 12, Appl
2	18	100.0	18	14	US-09-016-464-12	Sequence 12, Appl
3	18	100.0	18	19	US-09-509-152A-1004	Sequence 1004, Ap
4	18	100.0	18	19	US-09-509-152A-1024	Sequence 1024, Ap
5	18	100.0	279	19	US-09-509-152A-1709	Sequence 1709, Ap
6	18	100.0	291	19	US-09-509-152A-1710	Sequence 1710, Ap
7	18	100.0	299	19	US-09-509-152A-1698	Sequence 1698, Ap
8	18	100.0	415	19	US-09-528-409-76286	Sequence 76286, A
9	18	100.0	1127	3	US-07-770-081-1	Sequence 1, Appl
10	18	100.0	1127	3	US-07-869-914-2	Sequence 2, Appl
11	18	100.0	1460	5	US-08-114-992-2	Sequence 2, Appl
12	18	100.0	1460	5	US-08-114-992A-2	Sequence 2, Appl
13	18	100.0	1460	8	US-08-462-329A-2	Sequence 2, Appl
14	18	100.0	1530	14	US-09-023-655-1075	Sequence 1075, Ap
15	18	100.0	1532	49	US-60-172-373-15826	Sequence 15826, A
16	18	100.0	7800	19	US-09-509-152A-2409	Sequence 2409, Ap
17	18	100.0	32768	52	US-60-207-316-55	Sequence 55, Appl
18	100.0	32768	54	US-60-229-525-239	Sequence 239, Appl	
19	18	100.0	147087	53	US-60-212-664-2	Sequence 2, Appl
20	17	94.4	348	24	US-09-637-886-2467	Sequence 2467, Ap
21	17	94.4	5623	17	US-09-359-922-8923	Sequence 8923, Ap
22	17	94.4	5623	17	US-09-359-922-8923	Sequence 8923, Ap
23	17	94.4	32768	55	US-60-230-435-591	Sequence 591, Appl
24	16.4	91.1	18	8	US-08-474-497-10	Sequence 10, Appl
25	16.4	91.1	18	14	US-09-016-464-10	Sequence 10, Appl
26	16.4	91.1	188	20	US-09-534-843-28532	Sequence 28532, A
27	16.4	91.1	222	22	US-09-594-596-3517	Sequence 3517, Ap
28	16.4	91.1	222	25	US-09-654-617-449121	Sequence 449121, A
29	16.4	91.1	222	27	US-09-684-016-449121	Sequence 449121, A
30	16.4	91.1	222	46	US-60-141-131-111	Sequence 111, Appl
31	16.4	91.1	225	20	US-09-534-843-28467	Sequence 28467, A
32	16.4	91.1	228	20	US-09-534-843-28506	Sequence 28506, A
33	16.4	91.1	236	20	US-09-534-843-28503	Sequence 28503, A
34	16.4	91.1	250	20	US-09-534-843-28518	Sequence 28518, A
35	16.4	91.1	251	20	US-09-534-843-28470	Sequence 28470, A
36	16.4	91.1	254	20	US-09-534-843-28517	Sequence 28517, A
37	16.4	91.1	268	20	US-09-534-843-28481	Sequence 28481, A
38	16.4	91.1	282	20	US-09-534-843-28480	Sequence 28480, A
39	16.4	91.1	285	20	US-09-534-843-28511	Sequence 28511, A
40	16.4	91.1	289	20	US-09-534-843-28526	Sequence 28526, A
41	16.4	91.1	293	20	US-09-534-843-28516	Sequence 28516, A
42	16.4	91.1	297	20	US-09-534-843-28537	Sequence 28537, A
43	16.4	91.1	300	3	US-07-952-911-1631	Sequence 1631, Ap
44	16.4	91.1	300	20	US-09-534-843-28515	Sequence 28515, A
45	16.4	91.1	303	20	US-09-534-843-28493	Sequence 28493, A

ALIGNMENTS

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RESULT 1
US-08-474-497-12
; Sequence 12, Application US/08474497
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,497
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-497-12

Query Match      100.0%; Score 18; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTGTCGTCTCCT 18
    |||
Db 1 GCCTGTGTCGTCTCCT 18

RESULT 2
US-09-016-464-12
; Sequence 12, Application US/09016464
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,464
FILING DATE: 30-Jan-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,497
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-016-464-12

Query Match      100.0%; Score 18; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTGTCGTCTCCT 18
    |||
Db 1 GCCTGTGTCGTCTCCT 18

RESULT 3
US-09-509-152A-1004
; Sequence 1004, Application US/09509152A
; GENERAL INFORMATION:
; APPLICANT: NYCE, JONATHAN W.
; TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
; FORMULATIONS, KITS & APPLICATIONS
; NUMBER OF SEQUENCES: 2419
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: EPIDERMIS PHARMACEUTICALS, INC.
; STREET: 7 CLARKE DRIVE
; CITY: CRANBURY
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/509,152A
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,160
; FILING DATE: 1997-09-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 1004:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1004:
US-09-509-152A-1004

Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTGTCGTCTCCT 18
|||||
DB 1 GCCTGTGTCGTCTCCT 18

RESULT 4

US-09-509-152A-1024
Sequence 1024, Application US/09509152A
GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1024:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1024:
US-09-509-152A-1024

Query Match 100.0%; Score 18; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTGTCGTCTCCT 18
|||||
DB 1 GCCTGTGTCGTCTCCT 18

RESULT 5
US-09-509-152A-1709

Sequence 1709, Application US/09509152A
GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1709:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1709:
US-09-509-152A-1709

Query Match 100.0%; Score 18; DB 19; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTGTCGTCTCCT 18
|||||
DB 1 GCCTGTGTCGTCTCCT 18

RESULT 6
US-09-509-152A-1710
Sequence 1710, Application US/09509152A
GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 1710:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1710:
US-09-509-152A-1710

Query Match 100.0%; Score 18; DB 19; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 1 GCCTGTCTGTCTCTCT 18

RESULT 7
US-09-509-152A-1698
Sequence 1698, Application US/09509152A
GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPICGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 1698:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1698:
US-09-509-152A-1698

Query Match 100.0%; Score 18; DB 19; Length 299;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 1 GCCTGTCTGTCTCTCT 18

RESULT 8
US-09-528-409-76286/c
Sequence 76286, Application US/09528409
GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
FILE REFERENCE: 774
CURRENT APPLICATION NUMBER: US/09/528,409
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,453
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 76286
LENGTH: 415
TYPE: DNA
ORGANISM: Homo sapiens
US-09-528-409-76286

Query Match 100.0%; Score 18; DB 19; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 67 GCCTGTCTGTCTCTCT 50

RESULT 9
US-07-770-081-1/c
Sequence 1, Application US/07770081
GENERAL INFORMATION:
APPLICANT: Jenh, Chung-Her
APPLICANT: Narula, Satwant
APPLICANT: Zavadny, Paul
TITLE OF INVENTION: Human Interleukin-4 Antagonist/Agonist Screen
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 4.00B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/770,081
FILING DATE: 19911003

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Dulak, Norman C.
REGISTRATION NUMBER: 31,608
REFERENCE/DOCKET NUMBER: JB0214
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 822 7375
TELEFAX: 201 822 7039
TELEX: 219165
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1127 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
US-07-770-081-1

Query Match 100.0%; Score 18; DB 3; Length 1127;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 663 GCCTGTCTGTCTCTCT 646

RESULT 10
US-07-869-914-2/c
Sequence 2, Application US/07869914
GENERAL INFORMATION:
APPLICANT: de Vries, Jan
APPLICANT: Jenh, Chung-Her
APPLICANT: Zavadny, Paul
TITLE OF INVENTION: Human Interleukin-4 Antagonist/Agonist Screen
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 4.00B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,914
FILING DATE: 19920416
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Dulak, Norman C.
REGISTRATION NUMBER: 31,608
REFERENCE/DOCKET NUMBER: JB0262
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 822 7375
TELEFAX: 201 822 7039
TELEX: 219165
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1127 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
US-07-869-914-2

Query Match 100.0%; Score 18; DB 3; Length 1127;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 663 GCCTGTCTGTCTCTCT 646

RESULT 11
US-08-114-992-2/c
Sequence 2, Application US/08114992
GENERAL INFORMATION:
APPLICANT: Hofstetter, Hans
APPLICANT: Kilchherr, Erich
APPLICANT: Schmitz, Albert
TITLE OF INVENTION: Preparation of Binding Factor Related
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: U.S.A.
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,992
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/744,151
FILING DATE: 13-AUG-1991
APPLICATION NUMBER: US 07/617,487
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/073,788
FILING DATE: 15-JUL-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8617862
FILING DATE: 22-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8626622
FILING DATE: 07-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Villamizar, JoAnn
REGISTRATION NUMBER: 30,598
REFERENCE/DOCKET NUMBER: 4-16003/1+2/+/CONT/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 785-7121
TELEFAX: (914) 347-5769
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1460 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 146..1108
US-08-114-992-2

Query Match 100.0%; Score 18; DB 5; Length 1460;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCTGTCTGTCTCTCT 18
|||||

Db 45 GCCTGTCTCTCTCTCT 28

RESULT 12

US-08-114-992A-2/C

Sequence 2, Application US/08114992A

GENERAL INFORMATION:

APPLICANT: Hofstetter, Hans

APPLICANT: Kilchert, Erich

APPLICANT: Schmitz, Albert

TITLE OF INVENTION: Preparation of Binding Factor Related

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: U.S.A.

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/114,992A

FILING DATE: 1-SEP-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/744,151

FILING DATE: 13-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/617,487

FILING DATE: 21-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/073,788

FILING DATE: 15-JUL-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8617862

FILING DATE: 22-JUL-1986

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8626622

FILING DATE: 07-NOV-1986

ATTORNEY/AGENT INFORMATION:

NAME: Villamizar, Johann

REGISTRATION NUMBER: 30,598

REFERENCE/DOCKET NUMBER: 4-16003/1+2+/CONT/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (914) 785-7121

TELEFAX: (914) 347-5769

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1460 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 146..1108

US-08-114-992A-2

Query Match 100.0%; Score 18; DB 5; Length 1460;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
|||||

Db 45 GCCTGTCTCTCTCTCT 28

RESULT 13

US-08-462-329A-2/C

Sequence 2, Application US/08462329A

GENERAL INFORMATION:

APPLICANT: Hofstetter, Hans

APPLICANT: Kilchert, Erich

APPLICANT: Schmitz, Albert

TITLE OF INVENTION: Preparation of Binding Factor Related

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: U.S.A.

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,329A

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/114,992

FILING DATE: 1-SEP-1993

APPLICATION NUMBER: US 07/744,151

FILING DATE: 13-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/617,487

FILING DATE: 21-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/073,788

FILING DATE: 15-JUL-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8617862

FILING DATE: 22-JUL-1986

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8626622

FILING DATE: 07-NOV-1986

ATTORNEY/AGENT INFORMATION:

NAME: Villamizar, Johann

REGISTRATION NUMBER: 30,598

REFERENCE/DOCKET NUMBER: 4-16003/1+2+/CONT/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (914) 785-7121

TELEFAX: (914) 347-5769

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1460 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 146..1108

US-08-462-329A-2

Query Match 100.0%; Score 18; DB 8; Length 1460;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCTCT 18
|||||

Db 45 GCCTGTCTCTCTCTCT 28

RESULT 14

```

US-09-023-655-1075/c
; Sequence 1075, Application US/09023655
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1075:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9182447
; US-09-023-655-1075

Query Match          100.0%; Score 18; DB 14; Length 1530;
Best local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTGTCTGTCTCTCT 18
    |||
Db 113 GCCTGTGTCTGTCTCTCT 96

RESULT 15
US-60-172-373-15826/c
; Sequence 15826, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Deep, Diah
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 15826
; LENGTH: 1532

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 405265.2
; US-60-172-373-15826

Query Match          100.0%; Score 18; DB 49; Length 1532;
Best local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTGTCTGTCTCTCT 18
    |||
Db 113 GCCTGTGTCTGTCTCTCT 96

Search completed: April 20, 2001, 03:21:16
Job time: 14163 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:15:10 ; Search time 101.94 Seconds
(without alignments)
24.434 Million cell updates/sec

Title: US-09-016-464-12
Perfect score: 18
Sequence: 1 GCCTGCTCTGCTCTCT 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 seqs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	US-09-543-679A-1004	Sequence 1004, Ap
2	18	100.0	18	US-09-543-679A-1024	Sequence 1024, Ap
3	18	100.0	279	US-09-543-679A-1709	Sequence 1709, Ap
4	18	100.0	291	US-09-543-679A-1710	Sequence 1710, Ap
5	18	100.0	299	US-09-543-679A-1698	Sequence 1698, Ap
6	18	100.0	1503	US-09-543-679A-2870	Sequence 2870, Ap
7	18	100.0	1530	US-09-543-679A-2871	Sequence 2871, Ap
8	18	100.0	3108	US-09-543-679A-2869	Sequence 2869, Ap
9	18	100.0	6532	US-09-543-679A-2872	Sequence 2872, Ap
10	18	100.0	7800	US-09-543-679A-2409	Sequence 2409, Ap
11	18	100.0	117608	US-09-543-679A-3002	Sequence 3002, Ap
12	16.4	91.1	122715	US-60-248-505-46	Sequence 46, Appl
13	16.4	91.1	122716	US-60-248-505-507	Sequence 507, Appl
14	15	83.3	79470	US-60-248-505-175	Sequence 175, Appl
15	15	83.3	92585	US-60-248-505-383	Sequence 383, Appl
16	14.8	82.2	143068	US-09-543-679A-2672	Sequence 2672, Ap
17	14.8	82.2	143068	US-09-543-679A-2839	Sequence 2839, Ap
18	14.8	82.2	143063	US-60-248-505-394	Sequence 394, Appl
19	14.8	82.2	152740	US-09-543-679A-2840	Sequence 2840, Ap
20	14.8	82.2	479874	US-60-248-505-72	Sequence 72, Appl
21	14.4	80.0	18648	US-09-543-679A-2626	Sequence 2626, Ap
22	14.4	80.0	22749	US-60-248-505-437	Sequence 437, Appl
23	14.4	80.0	46050	US-09-820-003-3	Sequence 3, Appl
24	14.4	80.0	98573	US-60-248-505-542	Sequence 542, Appl
25	14.4	80.0	357304	US-60-248-505-243	Sequence 243, Appl
26	14	77.8	14	US-09-543-679A-1700	Sequence 1700, Ap
27	14	77.8	1131	US-09-173-463-1	Sequence 1, Appl

C	28	14	77.8	1446	5	US-09-809-391-139	Sequence 139, App
	29	13.8	76.7	355	5	US-09-442-385-1079	Sequence 1079, Ap
	30	13.8	76.7	380	4	US-08-276-163D-13713	Sequence 13713, A
C	31	13.8	76.7	487	4	US-08-276-163D-1775	Sequence 1775, Ap
	32	13.8	76.7	490	4	US-08-276-163D-12534	Sequence 12534, A
C	33	13.8	76.7	504	6	US-60-248-505-1627	Sequence 1627, Ap
C	34	13.8	76.7	506	4	US-08-276-163D-7906	Sequence 7906, Ap
C	35	13.8	76.7	687	5	US-09-739-449-5623	Sequence 5623, Ap
C	36	13.8	76.7	1920	5	US-09-739-449-3889	Sequence 3889, Ap
C	37	13.8	76.7	2245	6	US-60-248-505-1806	Sequence 1806, Ap
C	38	13.8	76.7	6022	6	US-60-248-505-1380	Sequence 1380, Ap
C	39	13.8	76.7	6401	6	US-60-248-505-295	Sequence 295, Appl
C	40	13.8	76.7	19387	6	US-60-248-505-223	Sequence 223, Appl
C	41	13.8	76.7	22081	6	US-60-248-505-38	Sequence 38, Appl
C	42	13.8	76.7	29171	6	US-60-248-505-258	Sequence 258, Appl
C	43	13.8	76.7	29172	6	US-60-248-505-462	Sequence 462, Appl
C	44	13.8	76.7	37996	6	US-60-248-505-447	Sequence 447, Appl
C	45	13.8	76.7	46465	6	US-60-248-505-318	Sequence 318, Appl

ALIGNMENTS

RESULT 1
US-09-543-679A-1004
; Sequence 1004, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT & METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED WITH BRONCHOCONSTRICITION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1004:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1004:
US-09-543-679A-1004
Query Match 100.0%; Score 18; DB 5; Length 18;
Best local Similarity 100.0%; Pred. No. 2.1;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;

APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1710:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1710:
US-09-543-679A-1710

Query Match 100.0%; Score 18; DB 5; Length 291;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 1 GCCTGTCTGTCTCTCT 18

RESULT 5
US-09-543-679A-1698
Sequence 1698, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1698:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1698:

US-09-543-679A-1698

Query Match 100.0%; Score 18; DB 5; Length 299;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 1 GCCTGTCTGTCTCTCT 18

RESULT 6
US-09-543-679A-2870/C
Sequence 2870, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2870:
SEQUENCE CHARACTERISTICS:
LENGTH: 1503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2870:
US-09-543-679A-2870

Query Match 100.0%; Score 18; DB 5; Length 1503;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 81 GCCTGTCTGTCTCTCT 64

RESULT 7
US-09-543-679A-2871/C
Sequence 2871, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2871:
SEQUENCE CHARACTERISTICS:
LENGTH: 1530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2871:
US-09-543-679A-2871

Query Match 100.0%; Score 18; DB 5; Length 1530;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCCT 18
|||||

Db 113 GCCTGTCTCTCTCCT 96

RESULT 8
US-09-543-679A-2869/c
Sequence 2869, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2869:
SEQUENCE CHARACTERISTICS:
LENGTH: 3108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2869:
US-09-543-679A-2869

Query Match 100.0%; Score 18; DB 5; Length 3108;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTCTCTCCT 18
|||||

Db 1401 GCCTGTCTCTCTCCT 1384

RESULT 9
US-09-543-679A-2872/c
Sequence 2872, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2872:
SEQUENCE CHARACTERISTICS:

LENGTH: 6532 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2872:
US-09-543-679A-2872

Query Match 100.0%; Score 18; DB 5; Length 6532;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 5115 GCCTGTCTGTCTCTCT 5098

RESULT 10
US-09-543-679A-2409
Sequence 2409, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2409:
SEQUENCE CHARACTERISTICS:
LENGTH: 7800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2409:
US-09-543-679A-2409

Query Match 100.0%; Score 18; DB 5; Length 7800;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 1031 GCCTGTCTGTCTCTCT 1048

RESULT 11
US-09-543-679A-3002
Sequence 3002, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 3002:
SEQUENCE CHARACTERISTICS:
LENGTH: 117608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3002:
US-09-543-679A-3002

Query Match 100.0%; Score 18; DB 5; Length 117608;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGTCTGTCTCTCT 18
|||||
DB 1031 GCCTGTCTGTCTCTCT 1048

RESULT 12
US-60-248-505-46/C
Sequence 46, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
FILE REFERENCE: C1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46
LENGTH: 122715
TYPE: DNA
ORGANISM: human

US-60-248-505-46

Query Match 91.1%; Score 16.4; DB 6; Length 122715;

Best Local Similarity 94.4%; Pred. No. 22; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTGTCTCTCT 18
||||| |||||||
Db 72895 GCCTGGTCTGTCTCTCT 72878RESULT 13
US-60-248-505-507/c

; Sequence 507, Application US/60248505

; GENERAL INFORMATION:

; APPLICANT: Beasley, Ellen

; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

; FILE REFERENCE: c1000918

; CURRENT APPLICATION NUMBER: US/60/248,505

; CURRENT FILING DATE: 2000-11-15

; NUMBER OF SEQ ID NOS: 1998

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 507

; LENGTH: 122716

; TYPE: DNA

; ORGANISM: human

US-60-248-505-507

Query Match 91.1%; Score 16.4; DB 6; Length 122716;

Best Local Similarity 94.4%; Pred. No. 22; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCCTGTCTGTCTCTCT 18
||||| |||||||
Db 72896 GCCTGGTCTGTCTCTCT 72879RESULT 14
US-60-248-505-175

; Sequence 175, Application US/60248505

; GENERAL INFORMATION:

; APPLICANT: Beasley, Ellen

; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

; FILE REFERENCE: c1000918

; CURRENT APPLICATION NUMBER: US/60/248,505

; CURRENT FILING DATE: 2000-11-15

; NUMBER OF SEQ ID NOS: 1998

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 175

; LENGTH: 79470

; TYPE: DNA

; ORGANISM: human

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (1)...(79470)

; OTHER INFORMATION: n = A,T,C or G

US-60-248-505-175

Query Match 83.3%; Score 15; DB 6; Length 79470;

Best Local Similarity 100.0%; Pred. No. 96; Mismatches 0; Indels 0; Gaps 0;

OY 3 CTGTGTCTGTCTCTCC 17
||||| |||||||
Db 69576 ctgtgtctgtctctcc 69590

RESULT 15

US-60-248-505-383

; Sequence 383, Application US/60248505

; GENERAL INFORMATION:

; APPLICANT: Beasley, Ellen

; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

; FILE REFERENCE: c1000918

; CURRENT APPLICATION NUMBER: US/60/248,505

; CURRENT FILING DATE: 2000-11-15

; NUMBER OF SEQ ID NOS: 1998

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 383

; LENGTH: 92585

; TYPE: DNA

; ORGANISM: human

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (1)...(92585)

; OTHER INFORMATION: n = A,T,C or G

US-60-248-505-383

Query Match 83.3%; Score 15; DB 6; Length 92585;

Best Local Similarity 100.0%; Pred. No. 96; Mismatches 0; Indels 0; Gaps 0;

OY 3 CTGTGTCTGTCTCTCC 17
||||| |||||||
Db 82691 ctgtgtctgtctctcc 82705Search completed: April 20, 2001, 00:15:19
Job time: 9456 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:59:33 ; Search time 2028.86 Seconds
(without alignments)
78.914 Million cell updates/sec

Title: US-09-016-464-13

Perfect score: 26
Sequence: 1 TCTCCCTGGGCTCTGCTCTCTCTC 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 segs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pi1:*
13: gb_pi2:*
14: gb_pi3:*
15: gb_pi4:*
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17: em_ba2:*
18: em_fun:*
19: em_hcgo_hum:*
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91: em_pi44:*
92: em_pi45:*
93: em_pi46:*
94: em_pi47:*
95: em_pi48:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	26	100.0	2355	93	H0MHDG	M60445 Human hist1
2	26	100.0	2396	92	HSHTSDG	X54297 Human mRNA
3	26	100.0	32351	93	H0MHDG	D16583 Human gene
4	26	100.0	62333	78	AC087584	AC087584 Homo sapi
5	26	100.0	117330	67	AC022087	AC022087 Homo sapi
6	26	100.0	194156	61	AC009851	AC009851 Homo sapi
7	20.8	80.0	82032	85	AC002458	AC002458 Human BAC
8	20.2	77.7	14364	1	AE000675	AE000675 Aquifex a
9	20.2	77.7	94581	85	AC003662	AC003662 Homo sapi
10	20.2	77.7	146500	85	AC004453	AC004453 Homo sapi
11	20.2	77.7	166370	72	AC036218	AC036218 Homo sapi

c	12	20.2	77.7	176689	89	AL162414	Human DNA
c	13	20.2	77.7	180547	89	AL139331	Human DNA
c	14	20.2	77.7	238521	76	AC078932	Mus muscu
c	15	20.2	77.7	258978	75	AC073819	Mus muscu
c	16	20.2	77.7	293043	75	AC073707	Mus muscu
c	17	20	76.9	2192	94	AF281018	Rattus no
c	18	19.8	76.2	168872	78	AC073325	Human sapi
c	19	19.8	76.2	193954	73	AC063926	Human sapi
c	20	19.6	75.4	2667	88	AF127135	Human sapi
c	21	19.6	75.4	9909	88	AF166330	Human sapi
c	22	19.6	75.4	27588	74	AC068464	Human sapi
c	23	19.6	75.4	37349	87	AC010524	Human sapi
c	24	19.6	75.4	42095	85	DMC103E12	AL132651 Drosophi
c	25	19.6	75.4	42245	85	AC004476	Human sapi
c	26	19.6	75.4	48975	61	AC008998	Human sapi
c	27	19.6	75.4	50821	12	AC020579	Arbidiops
c	28	19.6	75.4	92911	66	AC020218	Drosophi
c	29	19.6	75.4	105357	62	AC011483	Human sapi
c	30	19.6	75.4	118610	60	AC002344	Human sapi
c	31	19.6	75.4	127282	85	AC005155	Human sapi
c	32	19.6	75.4	140936	60	AC008630	Human sapi
c	33	19.6	75.4	153464	71	AC027421	Human sapi
c	34	19.6	75.4	157986	70	AC025860	Human sapi
c	35	19.6	75.4	159146	75	AC073621	Human sapi
c	36	19.6	75.4	163280	79	AL163538	Human sapi
c	37	19.6	75.4	163937	69	AC025385	Human sapi
c	38	19.6	75.4	165608	65	AC018473	Human sapi
c	39	19.6	75.4	167467	74	AC068071	Human sapi
c	40	19.6	75.4	169447	79	AL353789	Human sapi
c	41	19.6	75.4	176118	74	AC068670	Human sapi
c	42	19.6	75.4	178523	74	AC068531	Human sapi
c	43	19.6	75.4	180257	60	AC007044	Human sapi
c	44	19.6	75.4	187540	75	AC073970	Human sapi
c	45	19.6	75.4	191918	70	AC026484	Human sapi

ALIGNMENTS

RESULT	1						
HUMHDC/c							
LOCUS	HUMHDC	2355 bp	mRNA	PRI	08-NOV-1994		
DEFINITION	Human histidine decarboxylase (HDC) mRNA, complete cds.						
ACCESSION	M60445						
VERSION	M60445.1	GI:183924					
KEYWORDS	histidine decarboxylase.						
SOURCE	Human peripheral blood erythrocyte leukemia cell line HEL 92.1.7, CDNA to mRNA, clone HEL 31B1.						
ORGANISM	Homo sapiens						
REFERENCE	1 (bases 1 to 2355)						
AUTHORS	Zahnov,C.A., Yl.H.F., McBride,O.W. and Joseph,D.R.						
TITLE	Cloning of the cDNA encoding human histidine decarboxylase from an erythrocyte leukemia cell line and mapping of the gene locus to chromosome 15						
JOURNAL	DNA Seq. 1 (6), 395-400 (1991)						
MEDLINE	92119328						
FEATURES							
SOURCE	Location/Qualifiers						
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	/cell_line="HEL 92.1.7"						
	/cell_type="erythrocyte leukemia"						
	/tissue_type="peripheral blood"						
	/map="Unassigned"						
	52..2040						
	/gene="HDC"						
	52..2040						
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	/EC_number="4.1.1.22"						
	/codon_start=1						
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gene							
CDS							

/product="histidine decarboxylase"							
/protein_id="AAC41698.1"							
/db_xref="GI:183925"							
/translation="MMEPEYREGRGVNHYICVLSVBERVTPVPOGYLRAQLP							
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LRGNKILKMTSEPDADSCINARLVAVASDQASVSEKGLISLVKMKFLPYDNTS							
LRGALOKAIEEDKORGLVYVCATGTCVCAFDCLSELGPICAREGLPDIADAY							
AGTAPLCPDFRGLKGIETVADSPFNPSKMMVHEDCTGFVWKYKYLQOTFSVNPY							
LRHANSVATDFHMQIPLSRFSVSLMVPYRSFGVKNLOAHVHGTETMAKVFESYV							
RNDSEIIPAKRHGLVYFRKGNCLLENVAKITAGRIFLIPATIDKLIIRFV							
TSQPTTRDILRDNLIRDAVTLISQCHTSPSPRGNLSIQIGARAAVACGTSLS							
VSGAGDDPVQARKIYKQPVQAGAPMRRENGLHETLIDPYDDCFSEADATKHKLS							
SFLPSYLVQTKTKRVSLSQNSVPAVSAQKRLPTEASVKNKNGSSRVIRFSRFDMM							
LKSAFPKRLIKFYSPSPBESSGCGILPCCPIQANV"							
BASE COUNT	556 a	622 c	619 g	558 t			
ORIGIN	Chromosome 15.						
Query Match	100.0%	Score 26;	DB 93;	Length 2355;			
Best Local Similarity	100.0%	Pred. No. 0.22;					
Matches	26;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Query	1	TCTCCCTGGGCTCTGCTCCTTC	26				
Db	52	TCTCCCTGGGCTCTGCTCCTTC	27				
RESULT	2						
HSNISDEC/c							
LOCUS	HSNISDEC	2396 bp	mRNA	PRI	12-SEP-1993		
DEFINITION	Human mRNA for histidine decarboxylase (EC 4.1.1.22).						
ACCESSION	X54297						
VERSION	X54297.1	GI:32108					
KEYWORDS	cardoxylase; histidine carboxylase.						
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	1 (bases 1 to 2396)						
AUTHORS	Yamauchi,K.						
TITLE	Direct Submission						
JOURNAL	Submitted (06-AUG-1990) Yamauchi K., Tohoku University, School of Medicine, The First Dept. of Internal Medicine, 1-1 Seiryomachi Aobaku Sendai, Miyagi 980, Japan						
REFERENCE	2 (bases 1 to 2396)						
AUTHORS	Yamauchi,K., Sato,K., Tanno,Y., Ohkawara,Y., Maeyama,K., Watanabe,T., Satoh,K., Yoshizawa,M., Shibahara,S. and Takishima,T.						
TITLE	Nucleotide sequence of the cDNA encoding H-histidine decarboxylase derived from human basophilic leukemia cell line, KU-812-F						
JOURNAL	Nucleic Acids Res. 18 (19), 5891 (1990)						
MEDLINE	91016941						
COMMENT	Data kindly reviewed (05-NOV-1990) by Yamauchi K.						
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	/note="H-histidine decarboxylase"						
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	/db_xref="GI:32109"						
	/db_xref="SWISS-PROT:P19113"						
	/translation="MMEPEYREGRGVNHYICVLSVBERVTPVPOGYLRAQLP						
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	LRGNKILKMTSEPDADSCINARLVAVASDQASVSEKGLISLVKMKFLPYDNTS						
	LRGALOKAIEEDKORGLVYVCATGTCVCAFDCLSELGPICAREGLPDIADAY						
	AGTAPLCPDFRGLKGIETVADSPFNPSKMMVHEDCTGFVWKYKYLQOTFSVNPY						
	LRHANSVATDFHMQIPLSRFSVSLMVPYRSFGVKNLOAHVHGTETMAKVFESYV						
	RNDSEIIPAKRHGLVYFRKGNCLLENVAKITAGRIFLIPATIDKLIIRFV						
	TSQPTTRDILRDNLIRDAVTLISQCHTSPSPRGNLSIQIGARAAVACGTSLS						
	VSGAGDDPVQARKIYKQPVQAGAPMRRENGLHETLIDPYDDCFSEADATKHKLS						
	SFLPSYLVQTKTKRVSLSQNSVPAVSAQKRLPTEASVKNKNGSSRVIRFSRFDMM						
	LKSAFPKRLIKFYSPSPBESSGCGILPCCPIQANV"						

RNDSPFEIPAKRHLCVFRKGPNCLENTENKELAKAGRLFLIPATITQDKLIIFETV
 TSGFTTRDDILIRDAATLILSOHCTSPSPRVGNLISQIGARAMAGCTSIOS
 VSGAGDDPVQARKITIKOPRVGAGMKRENGIHEHTLDPYDDCSEEPADATKRLS
 SFLPSYLSVOTKKTKTVRSLSGNSVPSVSAQKPLPTASVKNNGSSSVRIFSRPEDMM
 LKKSAPFKRLIKFYSVSPFECCSSQCGLOLPCCPIDAMV

polyA-site

BASE COUNT 558 a 637 c 636 g 565 t

ORIGIN

Query Match 100.0%; Score 26; DB 92; Length 2396;
 Best Local Similarity 100.0%; Pred. No. 0.22;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCTTGCGCTCTGCTCCTTC 26

Db 103 TCTCCTTGCGCTCTGCTCCTTC 78

RESULT 3

LOCUS HUMLHDC 32351 bp DNA PRI 14-APR-2000

DEFINITION Human gene for L-histidine decarboxylase, complete cds.

ACCESSION D16583

VERSION D16583.1 GI:516770

KEYWORDS L-histidine decarboxylase.

SOURCE Homo sapiens DNA, clones lambda HDC[1, 2, 3 and 4].

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (sites)

Yatsunami, K., Ohsu, H., Tsuchikawa, M., Higuchi, T., Ishibashi, K.,

Shida, A., Shima, K., Nakagawa, S., Yamauchi, K., Yamamoto, M.,

Hayashi, N., Watanabe, T. and Ichikawa, A.

Structure of the L-histidine decarboxylase gene

J. Biol. Chem. 269 (2), 1554-1559 (1994)

94117478

2 (bases 1 to 32351)

Yatsunami, K.

Unpublished (1993)

3 (bases 1 to 32351)

Yatsunami, K.

Direct Submission

Submitted (02-JUL-1993) to the DDBJ/EMBL/GenBank databases. Kimio

Yatsunami, Japan Tobacco INC., Pharmaceutical Basic Research Lab.;

1-13-2 Fukuura Kanazawa-ku, Yokohama, Kanagawa 236, Japan

(Tel:045-786-7690(ex.3390), Fax:045-786-7692)

Submitted (02-JUL-1993) to DDBJ by:

Kimio Yatsunami

Dept. of Pharmaceutical

Basic Research Lab

Japan Tobacco INC.

1-13-2 Fukuura, Kanazawa-ku

Yokohama, Kanagawa 236

Japan

Phone: 045-786-7690 X3390

Fax: 045-786-7692.

Location/Qualifiers

FEATURES

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/db_xref="taxon:9606"

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protein_bind

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misc_signal

misc_signal

misc_signal

misc_signal

misc_signal

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6788..6793

/bound_molecule="GATA binding protein"

protein_bind

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/bound_molecule="GATA binding protein"

protein_bind

6895..6900

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7183..7188

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GC_signal

7221..7226

TATA_signal

7252..7259

/note="TATA-like sequence"

protein_bind

7268..7272

/bound_molecule="LBP-1"

exon

7278..7414

protein_bind

7292..7296

/bound_molecule="LBP-1"

CDS

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18247..18381,18638..18781,19245..19311,20137..20299,

20391..20481,24567..24665,29671..29772,29907..30653)

/RC_number="4.1.1.22"

/codon_start=1

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/protein_id="BAA04015.1"

/db_xref="GI:516771"

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VSGAGDDPVQARKITIKOPRVGAGMKRENGIHEHTLDPYDDCSEEPADATKRLS

SFLPSYLSVOTKKTKTVRSLSGNSVPSVSAQKPLPTASVKNNGSSSVRIFSRPEDMM

LKKSAPFKRLIKFYSVSPFECCSSQCGLOLPCCPIDAMV"

7415..9599

/number=1

exon

9600..9772

/number=2

Intron

9773..14490

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exon

14491..14604

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14605..15460

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15461..15583

/number=4

Intron

15584..18246

/number=4

exon

18247..18381

/number=5

Intron

18382..18637

/number=5

exon

18638..18781

/number=6

Intron

18782..19244

/number=6

exon

19245..19311

/number=7

Intron

19312..20136

/number=7

exon

20137..20299

/number=8

Intron

20300..20390

/number=8

exon

20391..20390

/number=8

Intron

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exon                20391..20481
                    /number=9
Intron              20482..24566
                    /number=9
exon                24567..24665
                    /number=10
Intron              24666..29670
                    /number=10
exon                29671..29772
                    /number=11
Intron              29773..29906
                    /number=11
exon                29907..30962
                    /number=12
BASE COUNT          8594 a 7026 c 7405 g 9326 t
ORIGIN
Query Match        100.0%; Score 26; DB 93; Length 32351;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTCCCTGGGCTGCGCTTCCTTC 26
Db 7384 TCTCCCTGGGCTGCGCTTCCTTC 7359

RESULT 4
LOCUS AC087584 62333 bp DNA HTG 10-JAN-2001
DEFINITION Homo sapiens chromosome 15 clone RP11-294011 map 15, LOW-PASS
ACCESSION AC087584
VERSION AC087584.1 GI:12061459
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 62333)
Birten,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-294011
Unpublished
2 (bases 1 to 62333)
Birten,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barne,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,T., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearrellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Faro,S., Ferreira,P., Fitzhugh,M., Gage,D., Galagan,J.,
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Huime,W., Iliev,I., Johnson,R.,
Jones,C., Karates,A., Larocque,K., Lamazares,R., Landers,T.,
Lenoczky,J., Levine,R., Liu,G., Maclean,C., MacDonald,P.,
Marquis,N., Mathews,C., McCarthy,M., McEwan,P., McKernan,K.,
McSheeters,R., Meldrim,J., Menus,L., Mihova,T., Mleena,C.H.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Plerre,N., Pollara,V., Raymond,C., Retter,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Roselli,M.,
Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P.,
Sougnac,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Travers,M., Travis,N., Trigglio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zalnoun,J.,
Zemek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-JAN-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

```

```

Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L12440
Center clone name: 294_O_11
* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
702 801: gap of 100 bp
802 1487: contig of 686 bp in length
1488 1587: gap of 100 bp
1588 2313: contig of 726 bp in length
2314 2413: gap of 100 bp
2414 3121: contig of 708 bp in length
3122 3221: gap of 100 bp
3222 3913: contig of 692 bp in length
3914 4013: gap of 100 bp
4014 4706: contig of 693 bp in length
4707 4806: gap of 100 bp
4807 5486: contig of 680 bp in length
5487 5586: gap of 100 bp
5587 6287: contig of 701 bp in length
6288 6387: gap of 100 bp
6388 7062: contig of 675 bp in length
7063 7162: gap of 100 bp
7163 7840: contig of 678 bp in length
7841 7940: gap of 100 bp
7941 8661: contig of 721 bp in length
8662 8761: gap of 100 bp
8762 9481: contig of 720 bp in length
9482 9581: gap of 100 bp
9582 10305: contig of 724 bp in length
10306 10405: gap of 100 bp
10406 11131: contig of 726 bp in length
11132 11231: gap of 100 bp
11232 11945: contig of 714 bp in length
11946 12045: gap of 100 bp
12046 12743: contig of 698 bp in length
12744 12843: gap of 100 bp
12844 13529: contig of 686 bp in length
13530 13629: gap of 100 bp
13630 14519: contig of 690 bp in length
14520 15122: contig of 703 bp in length
15123 15222: gap of 100 bp
15223 15906: contig of 684 bp in length
15907 16006: gap of 100 bp
16007 16704: contig of 698 bp in length
16705 16804: gap of 100 bp
16806 17532: contig of 728 bp in length
17533 17632: gap of 100 bp
17633 18317: contig of 685 bp in length
18318 18417: gap of 100 bp
18418 19134: contig of 717 bp in length
19135 19234: gap of 100 bp
19235 19904: contig of 670 bp in length
19905 20004: gap of 100 bp
20005 20711: contig of 707 bp in length
20712 20811: gap of 100 bp
20812 21584: contig of 773 bp in length
21585 21684: gap of 100 bp
21685 22390: contig of 706 bp in length

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* 22391 22490: gap of 100 bp
* 22491 23184: contig of 694 bp in length
* 23185 23284: gap of 100 bp
* 23285 23959: contig of 675 bp in length
* 23960 24059: gap of 100 bp
* 24060 24759: contig of 700 bp in length
* 24760 24859: gap of 100 bp
* 24860 25562: contig of 703 bp in length
* 25563 25662: gap of 100 bp
* 25663 26363: contig of 701 bp in length
* 26364 26463: gap of 100 bp
* 26464 27164: contig of 701 bp in length
* 27165 27264: gap of 100 bp
* 27265 27975: contig of 711 bp in length
* 27976 28075: gap of 100 bp
* 28076 28772: contig of 697 bp in length
* 28773 28872: gap of 100 bp
* 28873 29551: contig of 679 bp in length
* 29552 29651: gap of 100 bp
* 29652 30336: contig of 685 bp in length
* 30337 30436: gap of 100 bp
* 30437 31125: contig of 689 bp in length
* 31126 31225: gap of 100 bp
* 31226 31919: contig of 694 bp in length
* 31920 32019: gap of 100 bp
* 32020 32718: contig of 699 bp in length
* 32719 32818: gap of 100 bp
* 32819 33522: contig of 704 bp in length
* 33523 33622: gap of 100 bp
* 33623 34309: contig of 687 bp in length
* 34310 34409: gap of 100 bp
* 34410 35103: contig of 694 bp in length
* 35104 35203: gap of 100 bp
* 35204 35902: contig of 699 bp in length
* 35903 36002: gap of 100 bp
* 36003 36707: contig of 705 bp in length
* 36708 36807: gap of 100 bp
* 36808 37508: contig of 701 bp in length
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* 37609 38302: contig of 694 bp in length
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* 38403 39111: contig of 709 bp in length
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* 39212 39904: contig of 693 bp in length
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* 40005 40711: contig of 707 bp in length
* 40712 40811: gap of 100 bp
* 40812 41513: contig of 702 bp in length
* 41514 41613: gap of 100 bp
* 41614 42333: contig of 720 bp in length
* 42334 42433: gap of 100 bp
* 42434 43133: contig of 700 bp in length
* 43134 43233: gap of 100 bp
* 43234 43920: contig of 687 bp in length
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* 44021 44711: contig of 691 bp in length
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* 44812 45504: contig of 693 bp in length
* 45505 45604: gap of 100 bp
* 45605 46296: contig of 692 bp in length
* 46297 46396: gap of 100 bp
* 46397 47099: contig of 703 bp in length
* 47100 47199: gap of 100 bp
* 47200 47901: contig of 702 bp in length
* 47902 48001: gap of 100 bp
* 48002 48714: contig of 713 bp in length
* 48715 48814: gap of 100 bp
* 48815 49536: contig of 722 bp in length
* 49537 49636: gap of 100 bp
* 49637 50358: contig of 722 bp in length
* 50359 50458: gap of 100 bp
* 50459 51163: contig of 705 bp in length
* 51164 51263: gap of 100 bp

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* 51264 51968: contig of 705 bp in length
* 51969 52068: gap of 100 bp
* 52069 52784: contig of 716 bp in length
* 52785 52884: gap of 100 bp
* 52885 53580: contig of 696 bp in length
* 53581 53680: gap of 100 bp
* 53681 54365: contig of 685 bp in length
* 54366 54465: gap of 100 bp
* 54466 55132: contig of 667 bp in length
* 55133 55232: gap of 100 bp

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Query Match      100.0%; Score 26; DB 78; Length 62333;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCTCCCTTGCGCTCGCTCTCTC 26
Db 27455 TCTCCCTTGCGCTCGCTCTCTC 27480

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RESULT 5
LOCUS AC022087
DEFINITION Homo sapiens chromosome 15 clone CTD-3110H11, WORKING DRAFT
ACCESSION AC022087
VERSION AC022087.7 GI:11120752
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
1 (bases 1 to 117330)
Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradaran,L., Birditt,B., Bloom,S.,
Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A.,
Nesbitt,R., Traicoff,R. and Hood,L.
Sequencing of human chromosome 15 D15S146-D15S117 region
Unpublished
2 (bases 1 to 117330)
Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradaran,L., Birditt,B.,
Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
and Hood,L.
Direct Submision
Submitted (26-JAN-2000) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
On Nov 8, 2000 this sequence version replaced gi:9972272.
----- Genome Center
Center: Multimegabase Sequencing Center
Web site: http://chroma.mbl.washington.edu/msg_mwv
Contact: leeroewen@systemsbiology.org
----- Summary Statistics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
Insert size: 115000; agarose-fp
Quality coverage: 9.0x in Q20 bases; sum-of-contigs
-----
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces

```


Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics -----
Center project name: H_RG098M04

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/CTB/CHR7> or send <mailto:egreen@nhgri.nih.gov>

SOURCE INFORMATION:

This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.resgen.com>).

VECTOR: pBeltoBAC11

Selection: Chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is CTB-67M9, 200 bp overlap. Actual start of this clone is at base position 1 of CTB-98M4; actual end is at 46482 of CTB-67M9. This clone is part of an unanchored island, orientation is unknown.

This clone contains STS's SMS51856 (NID:g1254740), SMS53938 (NID:g1408133), and SMS52942 (NID:g1185336).

FEATURES

source

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/db_xref="taxon:9606"

/chromosome="7"

/clone="CTB-98M4"

/map="7q21-q22"

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/complement(430..705)

/rpt_family="L1"

/complement(756..2025)

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/complement(2096..2392)

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/complement(8295..8591)

/rpt_family="ALU"

/complement(8853..9197)

/rpt_family="MER"

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/note="similar to human EST AA042999 (NID:g1522524)"

2K56C03.r1"

10916..11100

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yd40g12.r1"

/complement(12059..12259)

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13976..14058

/rpt_family="L1"

16498..16759

/rpt_family="MER"

16774..16811

/rpt_family="MER"

16821..16923

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16933..17131

/rpt_family="MER"

/complement(20833..20906)

/rpt_family="L1"

/complement(21363..21630)

/rpt_family="ALU"

/complement(21854..21971)

/rpt_family="ALU"

/complement(23102..23193)

/rpt_family="TBE"

/complement(23581..23774)

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/complement(24019..24066)

/rpt_family="L1"

/complement(28856..35000)

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y152e07.r1"

39566..39633

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y152e07.r1"

41505..41550

/rpt_family="L1"

41708..41992

/rpt_family="ALU"

/complement(42254..42546)

/rpt_family="ALU"

/complement(42692..42739)

/note="similar to human EST AA202795 (NID:g1798518)"

/complement(42692..42739)

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/complement(42720..42763)

/note="similar to human EST W51024 (NID:g1339504)

ma10d12.r1"

42770..42912

/rpt_family="MER"

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/rpt_family="ALU"

43628..43820

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misc_feature

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misc_feature

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Query Match      80.0%; Score 20.8; DB 85; Length 82032;
Best Local Similarity 91.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CTCCTTGGGCTCTGCTCTTCT 25
Db 68718 CTCCTTGGGCTCTGCTCTTCT 68741

RESULT 8
LOCUS      AE000675      14364 bp      DNA      BCT      25-MAR-1998
DEFINITION Aquifex aeolicus section 7 of 109 of the complete genome.
ACCESSION  AE000675 AE000657
VERSION     AE000675.1 GI:2982863
KEYWORDS
SOURCE      Aquifex aeolicus.
            Aquifex aeolicus
            Bacteria; Aquificales; Aquificaceae; Aquifex.
REFERENCE   1 (bases 1 to 14364)
AUTHORS     Decker,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
            Graham,D.E., Overbeek,R., Sneed,M.A., Keller,M., Anjay,M.,
            Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
            The complete genome of the hyperthermophilic bacterium Aquifex
            aeolicus
            Nature 392 (6674), 353-358 (1998)
            98196666
TITLE       2 (bases 1 to 14364)
JOURNAL     Decker,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
MEDLINE     Graham,D.E., Overbeek,R., Sneed,M.A., Keller,M., Anjay,M.,
REFERENCE   Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
AUTHORS     Direct Submission
            Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,
            CA 92121
COMMENT     Putative indicates no similarity to known proteins
            Hypothetical indicates similarity to a protein of unknown function.
FEATURES
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CDS
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LDVQSTKEEMFKMLGCVNAVAIEKEMTONEMRYMLFEESSEVLKPEFMEG
DYIEDKHELSTLGIKSKILKRLDLKKEKGKILKRLIRLIRI"
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/db_xref="GI:2982879"
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VNLIGIISMLLFGITRPNPKILFPLAGSVAGICYSAKLMEIDREYKALIGCF
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LNTYKTLISFEFATNVERRILFYLLYGTEWSEYLIPALVGLPGLVFAIYLSRF
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SSISPSAAATGFSLSLWFLYSLSMAYSSTNLILOFVGAKRDPSPILNLNGFLSF
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GDTKPKMVAIIMNLTHIGTATLNGFGLPKGVGAGGIAISLELAFIYTFLL
IFPKKPPHLRLBPKILFKWVRIGTPTALERRATITTSFNVEGLAKFGDKVAAAO
IGLRISISPMIGCGVMASTTLGANGVAGNVCNVAHVFSAHFAIYALNSLGLIL
ILFPHYLVTPSRDEVTIEMASYIQLQIVGISQPMATASISGALKGKGKTHIFVN
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3567..4031
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EYAKKIDTAVRHHIEIDSTIEKHLKWSIDRLGVENALRGVAELIFLKSKEPGR
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VACHNGPVGNNMFAKQMTIEYKRVTPYLVGKPAIKVDGREGVTKKEEDMVFVK
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/db_xref="GI:2982867"
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DGKATLPLTGSKKMTSKSRKRVAVHILREATAVAVGVNTVKKDHPHIVRPENKOP
VRILIDPELEVPPLSAKVLNTEAPPIVTTKKENEKAELKAKGVOLILKFNKLNIL
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Best Local Similarity 88.0%; Pred. No. 69;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTCGGCTCTCT 25
Db 2186 TCTCCCTGGGCTCTCTCTCT 2210

RESULT 9
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LOCUS AC003662
DEFINITION Homo sapiens chromosome 17, clone HCIT104N19, complete sequence.
ACCESSION AC003662
VERSION AC003662.2 GI:11128430
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 94581)
Birren,B., Faerman,K., McKernan,K., Nusbaum,C., Richardson,P. and
Lander,E.
Homo sapiens chromosome 17, clone HCIT104N19
Unpublished
2 (bases 1 to 94581)
Birren,B., Faerman,K., McKernan,K., Munro,C., Nusbaum,C.,
Richardson,P., Lander,E., Baldwin,J., Barne,N., Cantu,C., Chang,A.,
Cooke,P., Daly,M.J., Depayre,E., Devon,K., Dewar,K., DuRette,B.,
Forrest,C., Gage,D., Gensheimer,S., Gerigery,K., Gilmartin,T.,
Hagos,B., Halphen,I., Harris,K., Howland,J.C., Huang,J., Hul,L.,
Jacotot,L., Linton,L., Mackenzie,J., Marquis,N., McDermott,J.,
McGurk,A., Molla,M., Morris,W., Morrow,J., Nachman,A., Naylor,J.,
O'Connor,T., Olotu,A., Peterson,K., Roberts,D., Rollins,G.,
Sarnak,A., Shiu,P., Shyam,R., Stillwell,J., Stone,C.,
Strickland,C., Sydneey,K., Tang,L., Zemseva,I., Zhao,J. and Zody,M.
Direct Submission
Submitted (08-DEC-1997) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 94581)
REFERENCE
AUTHORS
TITLE
JOURNAL
Unpublished
2 (bases 1 to 94581)
Birren,B., Faerman,K., McKernan,K., Munro,C., Nusbaum,C.,
Richardson,P., Lander,E., Baldwin,J., Barne,N., Cantu,C., Chang,A.,
Cooke,P., Daly,M.J., Depayre,E., Devon,K., Dewar,K., DuRette,B.,
Forrest,C., Gage,D., Gensheimer,S., Gerigery,K., Gilmartin,T.,
Hagos,B., Halphen,I., Harris,K., Howland,J.C., Huang,J., Hul,L.,
Jacotot,L., Linton,L., Mackenzie,J., Marquis,N., McDermott,J.,
McGurk,A., Molla,M., Morris,W., Morrow,J., Nachman,A., Naylor,J.,
O'Connor,T., Olotu,A., Peterson,K., Roberts,D., Rollins,G.,
Sarnak,A., Shiu,P., Shyam,R., Stillwell,J., Stone,C.,
Strickland,C., Sydneey,K., Tang,L., Zemseva,I., Zhao,J. and Zody,M.
Direct Submission
Submitted (08-DEC-1997) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 94581)
REFERENCE
AUTHORS
TITLE
JOURNAL
Unpublished
2 (bases 1 to 94581)
Birren,B., Faerman,K., McKernan,K., Munro,C., Nusbaum,C.,
Richardson,P., Lander,E., Baldwin,J., Barne,N., Cantu,C., Chang,A.,
Cooke,P., Daly,M.J., Depayre,E., Devon,K., Dewar,K., DuRette,B.,
Forrest,C., Gage,D., Gensheimer,S., Gerigery,K., Gilmartin,T.,
Hagos,B., Halphen,I., Harris,K., Howland,J.C., Huang,J., Hul,L.,
Jacotot,L., Linton,L., Mackenzie,J., Marquis,N., McDermott,J.,
McGurk,A., Molla,M., Morris,W., Morrow,J., Nachman,A., Naylor,J.,
O'Connor,T., Olotu,A., Peterson,K., Roberts,D., Rollins,G.,
Sarnak,A., Shiu,P., Shyam,R., Stillwell,J., Stone,C.,
Strickland,C., Sydneey,K., Tang,L., Zemseva,I., Zhao,J. and Zody,M.
Direct Submission
Submitted (03-FEB-1998) Whitehead Institute/MIT Center for Genome

REFERENCE 4 (bases 1 to 94581)
 AUTHORS Research, 320 Charles Street, Cambridge, MA 02141, USA
 Bliren,B., Fasman,K., McKernan,K., Nusbaum,C., Richardson,P.,
 Lander,E., Allen,N., Baker,J., Baldwin,J., Barina,N., Beckerly,R.,
 Boutwell,C., Byrne,S., Cantu,C., Castle,A., Cooke,P., Daly,M.J.,
 DePaeye,E., Devon,K., Dewar,K., Durette,B., Etemadli,S.,
 Ferreira,P., Forrest,C., Gage,D., Gardyna,S., Gensheimer,S.,
 Geraldery,K., Gilmarlin,T., Gray,D., Hagoz,B., Harris,K.,
 Horton,L., Howland,J.C., Hul.L., Jacotot,L., Linton,L.,
 Mackenzie,J., Marguis,N., McEwan,P., McCurt,A., Meldrum,J.,
 Molla,M., Morris,W., Morrow,J., Nachman,A., Naylor,J., O'Connor,T.,
 Pavlin,B., Peterson,K., Ranganath,S., Riley,R., Roberts,D.,
 Rollins,G., Rossello,R., Roy,A., Shyam,R., Soohoo,S., Stillwell,J.,
 Stone,C., Strickland,C., Sydney,K., Tang,L., Vassiliev,H., Vo,A.,
 Wagner,A., Wheeler,J., Wu,Y., Ye,W.J., Zemseva,I., Zhao,J. and
 Zody,M.

TITLE Direct Submission
 JOURNAL Submitted (09-NOV-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT On Nov 9, 2000 this sequence version replaced gi:2828777.
 The Staden databases, finishing information, and all
 chromatographic files used in the assembly of this clone are
 available from our anonymous ftp site.

FEATURES
 All repeats were identified using RepeatMasker: Smit, A.F.A. &
 Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html.
 Location/Qualifiers
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 /chromosome="17"
 /map="17"
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 /clone_id="Research Genetics/Cal Tech CITB978Sk-B (plates
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 239..380
 /rpt_family="LINE2"
 complement(409..702)
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 1386..1684
 repeat_region /rpt_family="AluSx"
 1768
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 3647..3934
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 3947..3987
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 /note="Probably A, possibly G or T."
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 repeat_region /note="Probably CC."
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 17963..18345
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Query Match      77.7%; Score 20.2; DB 85; Length 94581;
Best Local Similarity 88.0%; Pred. No. 56;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      2 CTCCTTGAGGCTGCTGCTCTCTC 26
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Db      51059 CTCCTTGAGGCTGCTGCTCTCTC 51035

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RESULT 10
LOCUS      AC004453 146500 bp DNA PRI 21-DEC-1999
DEFINITION Homo sapiens PAC clone RP5-844F9 from 7p12-p13, complete sequence.
ACCESSION AC004453
VERSION AC004453.1 GI:29796600
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE 1 (bases 1 to 146500)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
REFERENCE 2 (bases 1 to 146500)
AUTHORS Cordes,M. and Lacy,M.
TITLE The sequence of Homo sapiens PAC clone RP5-844F9
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 146500)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (20-MAR-1998) Department of Genetics, Washington
        University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 4 (bases 1 to 146500)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1999) Department of Genetics, Washington
        University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 5 (bases 1 to 146500)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1999) Department of Genetics, Washington
        University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
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        Center: Washington University Genome Sequencing Center
        Center code: WUGSC
        Web site: http://genome.wustl.edu/gsc
        Contact: saplens@wustl.wustl.edu
        -----
        Summary Statistics
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        Center project name: H_DJ0844F09

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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see
<http://www.nhgri.nih.gov/DIR/STB/CHR7>, send
<mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
This clone was derived from human PAC library RPI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong.

VECTOR: pCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP5-971G3. Actual start of this clone is at base position of 1 of RP5-844F9; actual end is at 146500 of RP5-844F9.

FEATURES

Source

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repeat_region 1933..2232
/rpt_family="Alu"
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repeat_region 19298..19633 /rpl_family="MIR"
repeat_region 19766..20120 /rpl_family="MIR"
repeat_region 20121..20392 /rpl_family="Retroviral"
repeat_region 20414..20715 /rpl_family="MER2_type"
repeat_region 21893..21973 /rpl_family="Alu"
repeat_region 22031..22132 /rpl_family="Alu"
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repeat_region 23242..23548 /rpl_family="Alu"
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Best Local Similarity 88.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTCCTGGGCTGCTGCTCTCTC 26
DB 126350 CTCCTGGGCTGCTGCTCTCTC 126326

RESULT 11
AC036218/c LOCUS
DEFINITION Homo sapiens chromosome 17 clone RP11-413p22 map 17, WORKING DRAFT
SEQUENCE, 30 unordered pieces.
ACCESSION AC036218.3 GI:8083313
VERSION AC036218
KEYWORDS HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 166370)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beta,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burnett,G.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burnett,G.,
Campiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collins,A., Cooke,P., DeRellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domini,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Laroque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,
Meldrum,J., Menus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rotman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rotman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced gi:8018208.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information
Center project name: L9412
Center clone name: 413_P_22
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 149856 bases at least Q40
Consensus quality: 158112 bases at least Q30
Consensus quality: 161470 bases at least Q20
Insert size: 161000; agarose-fp

```

Insert size: 163470; sum-of-contrigs
Quality coverage: 3.8 in 020 bases; agarose-fp
Quality coverage: 3.8 in 020 bases; sum-of-contrigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1
1246 1345: contig of 1245 bp in length
1346 2548: contig of 1203 bp in length
2549 2648: gap of 100 bp
2649 4304: contig of 1656 bp in length
4305 4404: gap of 100 bp
4405 6222: contig of 1818 bp in length
6223 6322: gap of 100 bp
6323 7950: contig of 1628 bp in length
7951 8050: gap of 100 bp
8051 9368: contig of 1318 bp in length
9369 9468: gap of 100 bp
9469 11022: contig of 1554 bp in length
11023 11122: gap of 100 bp
11123 13610: contig of 2488 bp in length
13611 13710: gap of 100 bp
13711 16013: contig of 2303 bp in length
16014 16113: gap of 100 bp
16114 18296: contig of 2183 bp in length
18297 18396: gap of 100 bp
18397 20894: contig of 2498 bp in length
20895 20994: gap of 100 bp
20995 24028: contig of 3034 bp in length
24029 24128: gap of 100 bp
24129 26979: contig of 2851 bp in length
26980 27079: gap of 100 bp
27080 29438: contig of 2359 bp in length
29439 29538: gap of 100 bp
29539 33176: contig of 3638 bp in length
33177 33276: gap of 100 bp
33277 36507: contig of 3231 bp in length
36508 36607: gap of 100 bp
36608 39484: contig of 2877 bp in length
39485 39584: gap of 100 bp
39585 43309: contig of 3725 bp in length
43310 43409: gap of 100 bp
43410 47549: contig of 4140 bp in length
47550 47649: gap of 100 bp
47650 51294: contig of 3645 bp in length
51295 51394: gap of 100 bp
51395 56965: contig of 5571 bp in length
56966 57065: gap of 100 bp
57066 61446: contig of 4381 bp in length
61447 61546: gap of 100 bp
61547 68174: contig of 6628 bp in length
68175 68274: gap of 100 bp
68275 75522: contig of 7248 bp in length
75523 75622: gap of 100 bp
75623 85356: contig of 9734 bp in length
85357 85456: gap of 100 bp
85457 93521: contig of 8065 bp in length
93522 93621: gap of 100 bp
93622 104074: contig of 10453 bp in length
104075 104174: gap of 100 bp
104175 119897: contig of 15723 bp in length
119898 119997: gap of 100 bp
119998 138358: contig of 18361 bp in length
138359 138458: gap of 100 bp
138459 166370: contig of 27912 bp in length.
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FEATURES
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2649. 4304  
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4405. 6222  
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6323. 7950  
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8051. 9368  
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9469. 11022  
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11123. 13610  
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13711. 16013  
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16114. 18296  
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18397. 20894  
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20995. 24028  
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24129. 26979  
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27080. 29438  
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29539. 33176  
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33277. 36507  
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vector_side:left"  
36608. 39484  
/note="assembly_fragment"  
39585. 43309  
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43410. 47549  
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47650. 51294  
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51395. 56965  
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57066. 61446  
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clone_end:sp6  
vector_side:left"  
61547. 68174  
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68275. 75522  
/note="assembly_fragment"  
75623. 85356  
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85457. 93521  
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93622. 104074  
/note="assembly_fragment"  
104175. 119897  
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Query Match 77.7%; Score 20.2; DB 72; Length 166370;
Best Local Similarity 88.0%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CTCCTGCGCTGCTGCTCTTC 26
||||| ||||| ||||| |||||
Db 147553 CTCCTGCGCTGCTGCTCTTC 147529

RESULT 12
AL162414/C
LOCUS
DEFINITION
AL162414 176689 bp DNA PRI 15-NOV-2000
Human DNA sequence from clone RP11-202G18 on chromosome 9, complete
sequence.
ACCESSION
AL162414
VERSION
AL162414.11 GI:11337694
KEYWORDS
HTG.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 176689)
AUTHORS
Laird, G.
TITLE
Direct Submission
JOURNAL
Submitted (15-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Nov 10, 2000 this sequence version replaced gi:11124640.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations.
Together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrg
RP11-202G18 is from the library RPCT-11.1 constructed at the
Roswell Park Cancer Institute by the group of Pletier de Jong. For
further details see http://bacpac.med.buffalo.edu/
VECTOR: pBAC63.6
This sequence is the entire insert of clone RP11-202G18 The true
left end of clone RP11-386D8 is at 152426 in this sequence. The
true right end of clone RP11-278D5 is at 151208 in this sequence.

FEATURES
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34..653
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1083..1332
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1515..1821
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1822..1959
/note="WIR repeat: matches 62..209 of consensus"
2409..2516
/note="WIR repeat: matches 5..124 of consensus"

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/note="AluY repeat: matches 1..305 of consensus"
repeat_region 3252..3341
/note="MER2 repeat: matches 137..210 of consensus"
repeat_region 3342..3654
/note="AluX repeat: matches 1..309 of consensus"
repeat_region 3655..3763
/note="MER2 repeat: matches 23..137 of consensus"
repeat_region 4226..4615
/note="MER2 repeat: matches 1..394 of consensus"
repeat_region 5770..5789
/note="AluY/FRAM repeat: matches 271..291 of consensus"
repeat_region 5790..6151
/note="THE1B repeat: matches 3..364 of consensus"
repeat_region 6154..7702
/note="THE1B-INTERNAL repeat: matches 3..1580 of
consensus"
repeat_region 7704..8071
/note="THE1B repeat: matches 1..364 of consensus"
repeat_region 8072..8240
/note="AluY/FRAM repeat: matches 156..271 of consensus"
repeat_region 8607..8718
/note="56 copies 2 mer aa 59% conserved"
repeat_region 8845..9058
/note="L1M4 repeat: matches 2272..2499 of consensus"
repeat_region 9428..9543
/note="MERVL repeat: matches 4431..4558 of consensus"
repeat_region 9608..9942
/note="HERVL repeat: matches 3928..4285 of consensus"
repeat_region 9990..10226
/note="HERVL repeat: matches 2595..2831 of consensus"
repeat_region 10227..10497
/note="AluX repeat: matches 39..310 of consensus"
repeat_region 10498..10646
/note="HERVL repeat: matches 2447..2595 of consensus"
repeat_region 11136..11267
/note="L1M3 repeat: matches 17..142 of consensus"
repeat_region 11391..11694
/note="AluX repeat: matches 1..308 of consensus"
repeat_region 11704..11753
/note="25 copies 2 mer tt 78% conserved"
repeat_region 11759..12783
/note="L1PA5 repeat: matches 5094..6140 of consensus"
repeat_region 13649..13933
/note="AluX repeat: matches 1..306 of consensus"
repeat_region 14804..14987
/note="WIR repeat: matches 72..262 of consensus"
repeat_region 15471..15509
/note="MER4B repeat: matches 500..538 of consensus"
repeat_region 15958..16389
/note="L1PA7 repeat: matches 5697..6140 of consensus"
repeat_region 16394..16695
/note="AluY repeat: matches 1..301 of consensus"
repeat_region 16974..17101
/note="L2 repeat: matches 2581..2710 of consensus"
repeat_region 17300..17329
/note="15 copies 2 mer ga 86% conserved"
repeat_region 18508..18682
/note="AluY repeat: matches 137..311 of consensus"
repeat_region 18946..19246
/note="AluX repeat: matches 1..310 of consensus"
repeat_region 19389..19472
/note="WIR repeat: matches 102..193 of consensus"
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/note="AluX repeat: matches 1..296 of consensus"
repeat_region 20918..21170
/note="L1M3C repeat: matches 1811..2072 of consensus"
repeat_region 21171..21458
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repeat_region 21459..21570
/note="L1M3C repeat: matches 2072..2181 of consensus"

repeat_region 21598..21649
/note="LIMB7 repeat: matches 4373..4429 of consensus"
repeat_region 21650..21954
/note="AluY repeat: matches 1..305 of consensus"
repeat_region 21955..21982
/note="LIMB7 repeat: matches 4429..4458 of consensus"
repeat_region 21983..22288
/note="AluSg repeat: matches 1..304 of consensus"
repeat_region 22289..22408
/note="LIMB7 repeat: matches 4458..4552 of consensus"
repeat_region 22410..22456
/note="AluG repeat: matches 88..136 of consensus"
repeat_region 22466..22629
/note="LIMB7 repeat: matches 4541..4707 of consensus"
repeat_region 22630..22799
/note="AluG repeat: matches 137..302 of consensus"
repeat_region 22800..23494
/note="LIMB7 repeat: matches 4707..5415 of consensus"
repeat_region 23495..23758
/note="AluSx repeat: matches 3..254 of consensus"
repeat_region 23759..24538
/note="LIMB7 repeat: matches 5415..6165 of consensus"
repeat_region 24588..24718
/note="LIM4 repeat: matches 4526..4659 of consensus"
repeat_region 24894..25081
/note="MER2 repeat: matches 184..345 of consensus"
repeat_region 25082..25204
/note="LIM4 repeat: matches 6020..6142 of consensus"
repeat_region 25205..25377
/note="MER2 repeat: matches 3..184 of consensus"
repeat_region 26101..26224
/note="MER5B repeat: matches 43..178 of consensus"
repeat_region 27509..27789
/note="AluG repeat: matches 1..284 of consensus"
repeat_region 27910..28027
/note="FLAM_C repeat: matches 1..119 of consensus"
repeat_region 28109..28650
/note="MER68A repeat: matches 1..564 of consensus"
repeat_region 28785..29102
/note="AluG repeat: matches 1..308 of consensus"
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/note="complement(29236..29760)"
repeat_region 29297..29368
/note="match: GSS: Em:AQ768592"
repeat_region 29315..29370
/note="36 copies 2 mer ta 73% conserved"
repeat_region 29612..29786
/note="L2 repeat: matches 2177..2356 of consensus"
repeat_region 29902..30026
/note="L2 repeat: matches 2617..2750 of consensus"
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/note="match: GSS: Em:B33090"
repeat_region 33733..34033
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repeat_region 34034..34144
/note="LIM2 repeat: matches 6039..6154 of consensus"
misc_feature 35305..35536
/note="match: GSS: Em:B14851"
repeat_region 36148..36288
/note="MIR repeat: matches 53..190 of consensus"
repeat_region 36895..36957

Query Match 77.7%; Score 20.2; DB 89; Length 176689;
Best Local Similarity 88.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CTCCTTGGGCTGGCTCTCTC 26
|||||
Db 15862 CTCCTTGGGCTCTCTCTC 15838

RESULT 13
AL139331/C

LOCUS AL139331 180547 bp DNA PRI 01-NOV-2000
DEFINITION Human DNA sequence from clone RP11-328M4 on chromosome 6, complete sequence.
ACCESSION AL139331
VERSION AL139331.19 GI:11120999
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
Babbage/A.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT
On Nov 8, 2000 this sequence version replaced gi:11042268.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone conigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RP11-328M4 is from the library RPCT-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-328M4. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true right end of clone RP11-328M4 is at 180547 in this sequence. The true left end of clone RP5-1092C14 is at 101202 in this sequence. The true right end of clone RP1-149M18 is at 100 in this sequence.
FEATURES
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/db_xref="taxon:9606"
/chromosome="6"
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/clone_lib="RPCT-11.2"
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/note="MIR repeat: matches 63..165 of consensus"
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complement(1604..2086)
/note="match: GSS: Em:B81842"
2931..3236
/note="AluSg repeat: matches 1..309 of consensus"
3784..3827
/note="11 copies 4 mer ctct 93% conserved"
4072..4143
/note="4 copies 18 mer 79% conserved"
4510..4688
/note="MIR repeat: matches 22..224 of consensus"
4811..5120
/note="AluSg repeat: matches 3..312 of consensus"
5387..5403

ORGANISM Mus musculus
 Eumetazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 238521)
 Bechtold-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
 Bouffard, G.C., Dietrich, N.L., Eagle, W.O., Gupta, J., Ho, S.-L.,
 Huang, M.C., Idol, J., Lee-Lin, S.-Q., Maduro, O.L., Maduro, V.B.,
 Mastriano, S.D., McCloskey, J.C., McDowell, J., Ojodu, M.A., Pearson, R.,
 Stantirpop, S., Summers, T.J., Thomas, J.W., Thomas, P.J.,
 Tjongson, E.E., Touchman, J.W., Tran, J.T., Vogt, J.L., Walker, M.A.,
 Wetherby, K.D. and Green, E.D.
 NISC Mouse Sequencing Initiative
 Unpublished
 2 (bases 1 to 238521)
 Green, E.D.
 Direct Submission
 Submitted (11-AUG-2000) NIH Intramural Sequencing Center, 8717
 Grovemont Circle, Gaithersburg, MD 20877, USA
 COMMENT
 ----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: http://www.nisc.nih.gov
 Contact: nisc_mouse@nih.gov
 ----- Project Information
 Center project name: tf
 Center clone name: 011P24
 ----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 225819 bases at least Q40
 Consensus quality: 229481 bases at least Q30
 Consensus quality: 231007 bases at least Q20
 Insert size: 216000; agarose-ftp
 Insert size: 248000; pulse-field-gel
 Insert size: 236521; sum-of-coverage
 Quality coverage: 5.18x in Q20 bases; agarose-ftp
 Quality coverage: 4.51x in Q20 bases; pulse-field-gel
 Quality coverage: 4.73x in Q20 bases; sum-of-coverage

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 21 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1
 * 3197: contig of 3197 bp in length
 * 3198 3297: gap of unknown length
 * 3298 5529: contig of 2232 bp in length
 * 5530 5629: gap of unknown length
 * 5630 9534: contig of 3905 bp in length
 * 9535 9634: gap of unknown length
 * 9635 12112: contig of 2478 bp in length
 * 12113 12212: gap of unknown length
 * 12213 17291: contig of 5079 bp in length
 * 17292 17391: gap of unknown length
 * 17392 23721: contig of 6330 bp in length
 * 23722 23821: gap of unknown length
 * 23822 29985: contig of 6164 bp in length
 * 29986 30085: gap of unknown length
 * 30086 34329: contig of 4244 bp in length
 * 34330 34429: gap of unknown length
 * 34430 40695: contig of 6266 bp in length
 * 40696 40795: gap of unknown length
 * 40796 45075: contig of 4280 bp in length
 * 45076 45175: gap of unknown length
 * 45176 53329: contig of 7954 bp in length
 * 53330 53329: gap of unknown length
 * 53329 57922: contig of 4693 bp in length
 * 57923 58022: gap of unknown length
 * 58023 67177: contig of 9155 bp in length

FEATURES
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 /strain="C57BL6/J"
 /db_xref="taxon:10090"
 /chromosome="6"
 /clone="RP23-11P24"
 /clone_11b="RP23 mouse BAC library 23"
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 3298. 5529
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 5630. 9534
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 9635. 12112
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 12213. 17291
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 17392. 23721
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 23822. 29985
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 34430. 40695
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 134808. 160231
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 160332. 194122
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 194223. 238521
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 BASE COUNT 65360 a 53528 c 51800 g 65780 t 2053 others
 ORIGIN
 Query Match 77.7%; Score 20.2; DB 76; Length 238521;

Best Local Similarity 88.0%; Pred. No. 51;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 CTCCTTGGGCTGCTGCTCTC 26
||||| |||||||||
Db 121501 CTCCTGCTCTGCTGCTCTTC 121525

RESULT 15
AC073819 259978 bp DNA HTG 29-JUN-2000
LOCUS AC073819 Mus musculus clone RP23-75K9, WORKING DRAFT SEQUENCE, 24 unordered
DEFINITION pieces.
AC073819
AC073819.1 GI:8810436
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 259978)
DOE Joint Genome Institute.
Sequencing of Mouse
Unpublished
2 (bases 1 to 259978)
DOE Joint Genome Institute.
Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1765921
Center clone name: RPCI-23_75K9

Summary Statistics
Consensus quality: 239199 bases at least Q40
Consensus quality: 247804 bases at least Q30
Consensus quality: 249411 bases at least Q20
Estimated insert size: 226000; agarose-fp estimation
Estimated insert size: 257678; sum-of-contigs estimation
Quality coverage: 8.27 in Q20 bases; agarose-fp estimation
Quality coverage: 7.25 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1125: contig of 1125 bp in length
* 1126 1225: gap of unknown length
* 1226 2493: contig of 1268 bp in length
* 2494 2593: gap of unknown length
* 2594 3997: contig of 1404 bp in length
* 3998 4097: gap of unknown length
* 4098 5249: contig of 1152 bp in length
* 5250 5349: gap of unknown length
* 5350 6498: contig of 1149 bp in length
* 6499 6598: gap of unknown length
* 6599 7624: contig of 1026 bp in length
* 7625 7724: gap of unknown length
* 7725 9063: contig of 1339 bp in length
* 9064 9164: gap of unknown length
* 9164 10221: contig of 1058 bp in length
* 10222 10321: gap of unknown length
* 10322 11353: contig of 1032 bp in length
* 11354 11453: gap of unknown length
* 11454 12531: contig of 1078 bp in length

* 12532 12631: gap of unknown length
* 12632 13643: contig of 1012 bp in length
* 13644 13743: gap of unknown length
* 13744 15668: contig of 1825 bp in length
* 15669 15668: gap of unknown length
* 15669 17969: contig of 2301 bp in length
* 17970 18069: gap of unknown length
* 18070 19876: contig of 1807 bp in length
* 19877 19976: gap of unknown length
* 19977 23634: contig of 3658 bp in length
* 23635 23734: gap of unknown length
* 23735 30157: contig of 6423 bp in length
* 30158 30257: gap of unknown length
* 30258 38411: contig of 8154 bp in length
* 38412 38511: gap of unknown length
* 38512 45576: contig of 7065 bp in length
* 45577 45676: gap of unknown length
* 45677 45677: gap of unknown length
* 45677 57485: contig of 11809 bp in length
* 57486 57585: gap of unknown length
* 57586 76237: contig of 18652 bp in length
* 76238 76337: gap of unknown length
* 76338 104363: contig of 28026 bp in length
* 104364 104463: gap of unknown length
* 104464 143001: contig of 38538 bp in length
* 143002 143101: gap of unknown length
* 143102 191668: contig of 48567 bp in length
* 191669 191768: gap of unknown length
* 191769 259978: contig of 68210 bp in length.
FEATURES
source
1..259978
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="RPCI mouse BAC library 23"
BASE COUNT 63143 a 63765 c 65171 g 65593 t 2306 others
ORIGIN

Query Match 77.7%; Score 20.2; DB 75; Length 259978;
Best Local Similarity 88.0%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TCTCCTTGGGCTGCTGCTCTC 25
||||| |||||||||
Db 60113 TTCTTTTGGGCTGCTGCTCTC 60137

Search completed: April 20, 2001, 00:00:03
Job time: 9480 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:48 ; Search time 547.68 Seconds
(without alignments):
27.714 Million cell updates/sec

Title: US-09-016-464-13

Perfect score: 26

Sequence: 1 TCTCCCTGGGCTCTGCTCTCTC 26

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_0401.*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT.*
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10: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT.*
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13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	100.0	26	18	T76097	Human histidine de
2	26	100.0	26	20	X53902	Histidine decarbox
3	26	100.0	26	21	F19467	Human histidine de
4	26	100.0	26	21	A33345	Low adenosine anti
5	26	100.0	171	20	X54577	Histidine decarbox
6	26	100.0	171	21	F20146	Human histidine de
7	26	100.0	171	21	A34024	Human adenosine re
8	26	100.0	2355	21	F21309	Human low adenosin
9	26	100.0	2355	21	A35187	Human adenosine re
10	26	100.0	2396	21	F21310	Human low adenosin
11	26	100.0	2396	21	A35188	Human adenosine re

c 12	26	100.0	32351	21	F21307	Human low adenosin
c 13	26	100.0	32351	21	A35185	Human adenosine re
c 14	26	100.0	40298	21	F21311	Human low adenosin
c 15	26	100.0	40298	21	A35189	Human adenosine re
c 16	26	100.0	114955	20	X53491	Human adenosine Al
c 17	19.4	74.6	1144	20	X02117	Human FEN-1 DNA tr
c 18	19.4	74.6	1144	20	X02107	Human FEN-1 CDNA
c 19	19.2	73.8	628	21	Z80283	Human colon cancer
c 20	19.2	73.8	1241	21	C57832	Arachidonic acid m
c 21	19.2	73.8	1241	21	C37026	Arabidopsis thalia
c 22	19.2	73.8	2483	21	A39511	Human tumour prote
c 23	18.6	71.5	1215	21	C48517	Arabidopsis thalia
c 24	18.6	71.5	1219	21	C36133	Arabidopsis thalia
c 25	18.6	71.5	2509	21	C93515	Human secreted pro
c 26	18.6	71.5	273254	21	C81914	Chlamydia pneumoni
c 27	18.4	70.8	1930	20	X02108	Mouse FEN-1 CDNA
c 28	18.4	70.8	2033	20	X02111	Human FEN-1 genom
c 29	18	69.2	53	19	V59245	DNA 53mer circle s
c 30	18	69.2	53	19	V59246	Stem loop RNA mult
c 31	18	69.2	53	19	V12931	Oligonucleotide SE
c 32	18	69.2	53	19	V12932	Oligonucleotide SE
c 33	18	69.2	53	20	X30035	RNA oligonucleotid
c 34	18	69.2	457	21	C38313	Zea mays DNA fragm
c 35	18	69.2	608	21	C44139	Zea mays DNA fragm
c 36	18	69.2	3350	17	T08553	Oncogene R-ras mut
c 37	18	69.2	16862	20	X58060	Genomic DNA for Hu
c 38	17.8	68.5	403	14	061334	Human brain Expres
c 39	17.8	68.5	2035	11	003452	Recombinant molecu
c 40	17.8	68.5	2035	11	003710	Gene encoding huma
c 41	17.8	68.5	2035	11	052651	Sequence encoding
c 42	17.8	68.5	122186	22	C89560	Human histone deac
c 43	17.6	67.7	530	21	F08631	Fusarium venenatum
c 44	17.6	67.7	929	21	F17999	Lung cancer associ
c 45	17.6	67.7	2233	15	066045	Wnt clone contg. t

ALIGNMENTS

RESULT 1	
ID T76097	standard; DNA; 26 BP.
AC T76097;	
DT 12-SEP-1997	(first entry)
DE Human histidine decarboxylase antisense oligonucleotide HUMHDCAS1.	
XX Asthma; airway epithelium; adenosine free; cystic fibrosis;	
XX chronic obstructive pulmonary disease; bronchitis; ss.	
KW	
XX	
OS Synthetic.	
XX	
XX W09640162-Al.	
PN	
XX	
PD 19-DEC-1996.	
XX	
PF 06-JUN-1996;	96WO-US09306.
XX	
PR 07-JUN-1995;	95US-047497.
XX	
PA (UYEC-) UNIV EAST CAROLINA.	
XX	
PI Metzger WJ, Nyce JW;	
XX	
DR WPI; 1997-051871/05.	
PT Treatment of airway diseases such as asthma - by topically applying	
PT adenosine-free antisense oligo:nucleotide to airway epithelium of	
PT subject	
XX	
PS Claim 5; Page 25; 71pp; English.	

CC The present invention describes low adenosine (A) content antisense

CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impaired respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.

SO Sequence 26 BP: 0 A; 11 C; 5 G; 10 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Gaps 0;
Matches 26; Conservative 0; Indels 0;

OY 1 TCTCCCTTGCGCTGCGCTCTTC 26
|||||
Db 1 tctcccttggtctgctctcttc 26

RESULT 4
ID A33345 standard; DNA: 26 BP.
XX A33345;

DT 28-JUL-2000 (first entry)

DE Low adenosine antisense oligonucleotide SEQ ID NO:1034.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiallergic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS WO200009525-A2.

PN 24-FEB-2000.

PD 03-AUG-1999; 99WO-US17712.

PF 03-AUG-1998; 98US-0095212.

PR (UYEC-) UNIV EAST CAROLINA.

PA Nyce JW;

XX PI

XX WP1: 2000-205971/18.

DR New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension, or
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -

PS Claim 18; Page 394; 1343pp: English.

XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiallergic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33922) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.

SO Sequence 26 BP: 0 A; 11 C; 5 G; 10 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Gaps 0;
Matches 26; Conservative 0; Indels 0;

OY 1 TCTCCCTTGCGCTGCGCTCTTC 26
|||||
Db 1 tctcccttggtctgctctcttc 26

RESULT 5
ID X54577 standard; DNA: 171 BP.
XX X54577;

DT 05-JUL-1999 (first entry)

DE Histidine decarboxylase receptor antisense oligonucleotide.

XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impaired respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.

OS Synthetic.

PN WO9913886-A1.

XX OS

PD 25-MAR-1999.
 XX 17-SEP-1998; 98MO-US19419.
 PR 09-JUN-1998; 98US-0093972.
 PR 17-SEP-1997; 97US-0059160.
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX NYCE JW;
 DR WPI: 1999-229400/19.
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 XX
 PS Disclosure: Page 45; 120pp; English.
 CC The specification describes antisense oligonucleotides (X52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have
 CC metastasized to the lungs, including breast and prostate cancer.
 CC
 XX Sequence 171 BP: 0 A; 70 C; 35 G; 62 T; 4 other;
 SO
 Query Match 100.0%; Score 26; DB 20; Length 171;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TCTCCCTGGGCTGCTGCTCTTC 26
 Db 1 tctccctgggctcgtcgtcctcttc 26
 RESULT 6
 F20146 100.0%; Score 26; DB 20; Length 171;
 ID F20146 standard; DNA: 171 BP.
 XX F20146;
 XX 14-MAR-2001 (first entry)
 XX
 DE Human histidine decarboxylase polynucleotide fragment #1713.
 XX Low adenosine antisense oligonucleotide: phosphorothioate; allergy;
 KW human: airway disorder: bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antialstematic; analgesic; hypotensive; cyostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.

XX WO200062736-A2.
 PN 26-OCT-2000.
 PD 24-MAR-2000; 2000MO-US08020.
 XX 06-APR-1999; 99US-0127958.
 PR (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX NYCE JW;
 DR WPI: 2000-679539/66.
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX Claim 14; Page 141; 1592pp; English.
 PS
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antialstematic, hypotensive and cyostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 CC
 XX Sequence 171 BP: 0 A; 70 C; 35 G; 62 T; 4 other;
 SO
 Query Match 100.0%; Score 26; DB 21; Length 171;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TCTCCCTGGGCTGCTGCTCTTC 26
 Db 1 tctccctgggctcgtcgtcctcttc 26
 RESULT 7
 A34024 100.0%; Score 26; DB 21; Length 171;
 ID A34024 standard; DNA: 171 BP.
 XX A34024;
 XX 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:1713.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1999; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW.
 XX
 DR WPI: 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Disclosure: Page 478; 1343pp: English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A3313 to A35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A23233
 CC to A33922) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 XX
 SQ Sequence 171 BP; 0 A; 70 C; 35 G; 62 T; 4 other;

Query Match 100.0%; Score 26; DB 21; Length 171;
 Best Local Similarity 100.0%; Pred. No. 0.14; 0;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTCTGGCTCCTTCTC 26
 ||||||||||||||||||||||||||||
 DB 1 tctcccttggtcctgtcctctcttc 26

RESULT 8
 F21309/c

ID F21309 standard; DNA; 2355 BP.
 XX
 AC F21309;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human low adenosine antisense oligonucleotide related sequence #2876.
 KW
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary vasoconstriction; impaired respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW.
 XX
 DR WPI: 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure: Page 1303-1304; 1592pp: English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impaired respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infectious, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 2355 BP; 556 A; 622 C; 619 G; 558 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 2355;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTCGGCTCCTTC 26
 ||||||||||||||||||
 DB 52 TCTCCCTGGGCTCGGCTCCTTC 27

RESULT 9
 A35187/c
 ID A35187 standard; DNA: 2355 BP.
 AC A35187;
 XX
 XX 28-JUL-2000 (first entry)
 DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:61.
 XX
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KM phosphorothioate; impaired respiration; inflammation; allergy;
 KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KM antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;
 KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 XX Homo sapiens.
 OS
 XX MO200009525-A2.
 PN
 XX 24-FEB-2000.
 PD
 XX 03-AUG-1999; 99WO-US17712.
 PF
 XX 03-AUG-1998; 98US-0095212.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX Nyce JW;
 PI
 XX WPI: 2000-205971/18.
 DR
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischaemia or
 PT cancers -
 XX
 XX Disclosure: Page 1220-1221; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytosstatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. A32313 to A35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences

CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323 to A33992) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 XX
 XX Sequence 2355 BP; 556 A; 622 C; 619 G; 558 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 2355;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTCGGCTCCTTC 26
 ||||||||||||||||||
 DB 52 TCTCCCTGGGCTCGGCTCCTTC 27

RESULT 10
 F21310/c
 ID F21310 standard; DNA: 2396 BP.
 AC F21310;
 XX
 XX 14-MAR-2001 (first entry)
 DE Human low adenosine antisense oligonucleotide related sequence #2877.
 XX
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosstatic;
 KM respiratory obstruction; pulmonary obstruction; impaired respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200062736-A2.
 PN
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX (NYCE/) NYCE J W.
 PA
 XX Nyce JW;
 PI
 XX WPI: 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 XX Disclosure: Page 1304-1305; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (1) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (1) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytosstatic activities. The antisense oligonucleotides and (1) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes,

CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. P18434 to P21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
CC
CC
SQ Sequence 2396 BP; 558 A; 637 C; 636 G; 565 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 2396;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTCCCTTGCGCTGCTCCTTC 26
|||||
Db 103 TCTCCCTTGCGCTGCTCCTTC 78

RESULT 11
A35188/c
ID A35188 standard; DNA: 2396 BP.

AC A35188;

DT 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:62.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.

PN WO200009525-A2.

XX 24-FEB-2000.

PD 03-AUG-1999; 99WO-US17712.

PF 03-AUG-1999; 98US-0095212.

PR 03-AUG-1998; 98US-0095212.

XX (UYEC-) UNIV EAST CAROLINA.

XX NYCE JW;

DR WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers

PS Disclosure: Page 1221; 1343pp; English.

CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ON reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A33313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
CC
CC
SQ Sequence 2396 BP; 558 A; 637 C; 636 G; 565 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 2396;

Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTCCCTTGCGCTGCTCCTTC 26
|||||
Db 103 TCTCCCTTGCGCTGCTCCTTC 78

RESULT 12
F21307/c
ID F21307 standard; DNA: 32351 BP.

AC F21307;

DT 14-MAR-2001 (first entry)

DE Human low adenosine antisense oligonucleotide related sequence #2874.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

OS Homo sapiens.

PN WO200062736-A2.

XX 26-OCT-2000.

PD 24-MAR-2000; 2000WO-US08020.

PF 06-APR-1999; 99US-0127958.

PR (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX NYCE JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -

PS Disclosure: Page 1295-1303; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antisthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating factors and antibodies, antibody receptors, cytokines and
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impaired respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
XX present invention.

XX Sequence 32351 BP; 8594 A; 7026 C; 7405 G; 9326 T; 0 other;

XX Query Match 100.0%; Score 26; DB 21; Length 32351;
XX Best Local Similarity 100.0%; Pred. No. 0.17;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTGGCTCCTTC 26

DB 7384 TCTCCCTGGGCTGGCTCCTTC 7359

XX RESULT 13
XX A35185/c
XX A35185 standard; DNA: 32351 BP.

AC A35185;

XX 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:59.

XX Human: adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antisthmatic; cytostatic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US17712.

XX 03-AUG-1998; 98US-0095212.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX Disclosure: Page 1212-1219; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antisthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
XX sequence listing.

XX Sequence 32351 BP; 8594 A; 7027 C; 7405 G; 9325 T; 0 other;

XX Query Match 100.0%; Score 26; DB 21; Length 32351;
XX Best Local Similarity 100.0%; Pred. No. 0.17;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTGGGCTCCTTC 26

DB 7384 TCTCCCTGGGCTGGGCTCCTTC 7359

XX RESULT 14
XX F21311/c
XX F21311 standard; DNA: 40298 BP.

AC F21311;

XX 14-MAR-2001 (first entry)

XX Human low adenosine antisense oligonucleotide related sequence #2878.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;
XX respiratory obstruction; pulmonary obstruction; impaired respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE) NYCE J W.
 PI Nyce JW;
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure; Page 1305-1315; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergies,
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 40298 BP; 10485 A; 9119 C; 9484 G; 11210 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 40298;
 Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TCTCCCTTGGGCTCTGGCTCCTTCTC 26
 |||||||
 Db 38005 TCTCCCTTGGGCTCTGGCTCCTTCTC 37980

RESULT 15
 A35189/c

ID A35189 standard; DNA; 40298 BP.
 XX
 AC A35189;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:63.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Disclosure; Page 1221-1231; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cyostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC sarcomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A32313 to A35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
 CC to A33992) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 CC
 XX
 SQ Sequence 40298 BP; 10485 A; 9121 C; 9482 G; 11210 T; 0 other;

Query Match 100.0%; Score 26; DB 21; Length 40298;
 Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Apr 20 10:22:54 2001

us-09-016-464-13.rng

Page 10

QY 1 TCTCCCTTGGGCTCTGGCTCTCTC 26
| | | | | | | | | | | | | | | |
Db 38005 TCTCCCTTGGGCTCTGGCTCTCTC 37980

Search completed: April 20, 2001, 00:12:52
Job time: 10014 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:24:46 ; Search time 7150.85 Seconds
(without alignments)
0.531 Million cell updates/sec

Title: US-09-016-464-13

Perfect score: 26
Sequence: 1 TCTCCCTGGGCTCTGCTCCTCTC 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
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187: gb.est118:*
188: gb.est119:*
189: gb.est120:*

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Result No.	Score	Match	Length	ID	Description
1	23.4	90.0	503	105	AL041199 DKE2p4341
2	20.2	77.7	232	161	BB595186 BB595186
3	20.2	77.7	377	30	AV427578 AV427578
4	20.2	77.7	409	29	AV412582 AV412582
5	20.2	77.7	412	30	AV521996 AV521996
6	20.2	77.7	413	30	AV419700 AV419700
7	20.2	77.7	428	30	AV417461 AV417461
8	20.2	77.7	468	144	BF177639 BF177639
9	20.2	77.7	1635	174	BG155667 BG155667
10	20	76.9	366	149	BF543175 BF543175
11	19.6	75.4	230	170	BF874051 BF874051
12	19.6	75.4	294	213	AO892704 HS-3156_B
13	19.6	75.4	399	146	BF283917 BF283917
14	19.6	75.4	406	105	AL375792 AL375792
15	19.6	75.4	411	1	AA062246 AA062246
16	19.6	75.4	416	104	AI989162 AI989162
17	19.6	75.4	506	168	BF711186 BF711186
18	19.6	75.4	512	22	AI595539 AI595539

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C	19	19.6	75.4	514	207	AA0475779	AA0475779.CITBT-El-
C	20	19.6	75.4	516	175	C95971	C95971.C95971.Marc
C	21	19.6	75.4	536	205	AQ366531	AQ366531.HS-5037.B
C	22	19.6	75.4	544	146	BF283918	BF283918.ESF448509
C	23	19.6	75.4	562	175	C95778	C95778.C95778.Marc
C	24	19.6	75.4	569	118	AA657451	AA657451.110667.MA
C	25	19.6	75.4	611	73	AU081627	AU081627.Matchanti
C	26	19.6	75.4	632	175	C96030	C96030.C96030.Marc
C	27	19.4	74.6	222	117	AM581548	AM581548.RC1-PR000
C	28	19.4	74.6	235	114	AM373141	AM373141.RC3-BF050
C	29	19.4	74.6	297	7	AA471223	AA471223.PMY2202.K
C	30	19.4	74.6	373	112	AM188148	AM188148.x392h10.x
C	31	19.4	74.6	384	164	BE258717	BE258717.601107502
C	32	19.4	74.6	415	114	AM373138	AM373138.RC3-BF050
C	33	19.4	74.6	436	9	AA626820	AA626820.ab52f12.r
C	34	19.4	74.6	455	204	AO281416	AO281416.RPC111-78
C	35	19.4	74.6	496	122	AA991481	AA991481.RC1-BM000
C	36	19.4	74.6	500	5	AA305950	AA305950.ESF176942
C	37	19.4	74.6	514	165	BE276873	BE276873.601178437
C	38	19.4	74.6	561	145	BF238768	BF238768.601904357
C	39	19.4	74.6	590	144	BE263450	BE263450.601190023
C	40	19.4	74.6	590	166	BE408229	BE408229.601302559
C	41	19.4	74.6	611	166	BE388740	BE388740.601283812
C	42	19.4	74.6	627	164	BE257409	BE257409.601109247
C	43	19.4	74.6	660	164	BE255166	BE255166.601115702
C	44	19.4	74.6	685	164	BE263976	BE263976.601192252
C	45	19.4	74.6	698	143	BF034100	BF034100.601456446

ALIGNMENTS

RESULT 1
LOCUS AL041199/c
DEFINITION DKFZP434I1516.t1 434 (synonym: htes3) Homo sapiens cDNA clone
AL041199
AL041199.1 GI:5410134
EST
Homo sapiens

REFERENCE 1 (bases 1 to 503)
AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehler, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Koehler K

MIPS
Am Kiofersplitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No sl sequence available.
This clone (DKFZP434I1516) is available at the RZPD in Berlin:
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

FEATURES

source
1..503
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP434I1516"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT 126 a 109 c 160 g 106 t 2 others
ORIGIN

Query Match
Best Local Similarity 92.3%; Pred. No. 35;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTCCCTGGCTGCTGCTTCCTC 26
DB 405 TCTCCCTGGCTGCTGCTTCCTTC 380

RESULT 2

BB595186 232 bp mRNA EST 30-NOV-2000
LOCUS BB595186 RIKEN full-length enriched, adult male corpus striatum Mus
DEFINITION musculus cDNA clone C03005A11 5', mRNA sequence.
ACCESSION BB595186
VERSION BB595186.1 GI:11491788

KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 232)
AUTHORS Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P.,
Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A.,
Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka,
T., Toya, T., Watabiki, A., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Aizawa, K. et al. 2000)

Unpublished (2000)
TITLE YOSHIDA, Y.
JOURNAL Contact: Yoshida Hayashizaki
COMMENT Genome Exploration Research Group, Life Science Tsukuba Center,
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rcc.riken.go.jp,
URL: http://genome.rcc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagao, S., Sasaki,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermocatalysis of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Iizawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rcc.riken.go.jp) for
further details.

FEATURES

source
1..232
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C03005A11"
/clone_lib="RIKEN full-length enriched, adult male corpus
striatum"
/sex="male"
/tissue_type="corpus striatum"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was

Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES
SOURCE

1. 412
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone_1lb="AP270d11f"
/clone_1lb="Arabidopsis thaliana aboveground organs two to six-week old"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 113 a 101 c 61 g 137 t
ORIGIN

Query Match 77.7%; Score 20.2; DB 30; Length 412;
Best Local Similarity 88.0%; Pred. No. 5.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CTCCTTGGGCTGCGCTCTTC 26
||| ||||| ||||| ||||| |||||
Db 214 CTCCTTGGGCTGCGCTCTTC 238

RESULT 6
AV419700/c

LOCUS AV419700 413 bp mRNA EST 23-MAY-2000
DEFINITION AV419700 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MM4172a12_r 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS

AV419700.1 GI:7748877
EST
SOURCE
ORGANISM

Lotus japonicus.
Lotus japonicus.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.

1 (bases 1 to 413)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a
legume, Lotus japonicus

JOURNAL
MEDLINE
COMMENT
Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES

1. 413
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone_1lb="MM4172a12_r"
/clone_1lb="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; Isolate=Miyakojima MG-20"
Location/Qualifiers

BASE COUNT 120 a 98 c 92 g 103 t
ORIGIN

Query Match 77.7%; Score 20.2; DB 30; Length 413;
Best Local Similarity 88.0%; Pred. No. 5.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCTCCCTTGGGCTGCGCTCTTC 25
||| | ||||| ||||| ||||| |||||
Db 362 TCTTCTTGGGCTGCGCTCTTC 338

RESULT 7

AV417461/c

LOCUS AV417461 428 bp mRNA EST 23-MAY-2000
DEFINITION AV417461 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MM4144g03_r 5', mRNA sequence.

ACCESSION AV417461
VERSION AV417461.1 GI:7746639
KEYWORDS
SOURCE
ORGANISM

Lotus japonicus.
Lotus japonicus.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
1 (bases 1 to 428)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a
legume, Lotus japonicus

JOURNAL
MEDLINE
COMMENT
Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES
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1. 428
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone_1lb="MM4144g03_r"
/clone_1lb="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; Isolate=Miyakojima MG-20"
Location/Qualifiers

BASE COUNT 127 a 101 c 99 g 101 t
ORIGIN

Query Match 77.7%; Score 20.2; DB 30; Length 428;
Best Local Similarity 88.0%; Pred. No. 5.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCTCCCTTGGGCTGCGCTCTTC 25
||| | ||||| ||||| ||||| |||||
Db 257 TCTTCTTGGGCTGCGCTCTTC 233

RESULT 8
BF177639/c

LOCUS BF177639 468 bp mRNA EST 31-OCT-2000
DEFINITION BF177639 588-bp Ljirnp Lambda Hybrid2 two-hybrid library Lotus
japonicus cDNA clone LP588-32-h2 5' similar to mRNA for elongation
factor 1b gamma, mRNA sequence.

ACCESSION BF177639
VERSION BF177639.1 GI:11065330
KEYWORDS
SOURCE
ORGANISM

Lotus japonicus.
Lotus japonicus.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
1 (bases 1 to 468)
Poulsen, C. and Poedenphant, L.
Expressed sequence tags from Mesorhizobium loti infected roots of
Lotus japonicus

JOURNAL
COMMENT
Unpublished (1999)
Contact: Poulsen, C.; Poedenphant, L.
Laboratory of Gene Expression, Department of Molecular and
Structural Biology
University of Aarhus
Gustav Wieds Vej 10C, DK-8000 Aarhus C, Denmark
Tel: +45 89425007
Fax: +45 86201222
Email: CHP@bio.au.dk
Seq primer: PADG14 5'-primer CCA CTA TGG ATG ATG TAT ATA AC

AUTHORS	Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T., Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and Hood L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 3156 row: D column: 14 Seq primer: M13 Reverse Class: BAC ends High quality sequence stop: 294. Location/Qualifiers 1..294 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="plate=3156 COL=14 Row=D" /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male" /note="Organ: sperm; Vector: pBelobAC11; BAC clones in E-Coli DH10B"
BASE COUNT	70 a 84 c 76 g 64 t
ORIGIN	
Query Match	75.4%; Score 19.6; DB 213; Length 294;
Best Local Similarity	84.6%; Pred. No. 9.2e+02;
Matches	22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy	1 TCCTCCCTGGGCTGTGCCTCTTC 26 1 111111111
Db	261 TCCTCCCTTCTCCGTGGCTCTTC 236
RESULT 13	
BF283917	
LOCUS	BF283917 399 bp mRNA EST 28-NOV-2000
DEFINITION	EST444508 Rat Gene Index, normalized rat, Rattus norvegicus CDNA
RATTUS NORVEGICUS	Rattus norvegicus CDNA clone RGIDJ01 3' sequence, mRNA sequence.
ACCESSION	BF283917
VERSION	BF283917.1 GI:11214987
KEYWORDS	EST.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus Phylum: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 399) Malek R.L., Cho J., Lee Y., Karamycheva S., Parvizli B., Pertea G., Sultana R., Tsai J., White J., Quackenbush J. and Lee N.H. Generation of ESTs from Normalized Rat Embryo, Bento Soares Unpublished (2000) Other_ESTs: EST448509 EST349096 EST349097 Contact: Lee, NH The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information. Location/Qualifiers 1..399 /organism="Rattus norvegicus" /db_xref="taxon:10116"
FEATURES	
SOURCE	

```

/clone="RGIEJ01"
/clone.lib="Rat Gene Index, normalized rat, Rattus
noveboracensis cDNA"
/tissue.type="mixed tissue"
/lab_host="DH5-alpha"
/notes="Vector: pTZ19; Site_1: EcoRI; Site_2: NotI;
combination of RCV, RBR, RLI, RPL, RLU, REM, RMU, RSP
, RHE, RPC, RPN"
BASE COUNT      71 a      100 c      107 g      121 t
ORIGIN

Query Match      75.4%; Score 19.6; DB 146; Length 399;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TCTCCCTGGGCTGCTGCTCTTC 26
|||||  |||  |||  |||  |||  |||
Db 357 TCTCCCTGCTGCTGCTGCTCTTC 382

RESULT 14
AL375792 406 bp mRNA EST 03-AUG-2000
LOCUS MCB19B01F1 MBB Medicago truncatula cDNA clone MCB19B01 T3, mRNA
DEFINITION sequence.
ACCESSION AL375792
VERSION AL375792.1 GI:9675544
KEYWORDS barrel medic.
SOURCE Eukarya; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
REFERENCE 1 (bases 1 to 406)
AUTHORS Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jallou,O.,
Nebel,A., Carreau,Y., Chataigner,O., Kahn,D., Glaninazzi-Pearson
,V. and Gamas,P.
TITLE Medicago truncatula ESTs from Sinorhizobium meliloti-induced root
nodules
JOURNAL Unpublished (2000)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seque@genoscope.cns.fr Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
http://sequence.toulouse.inra.fr/Mtruncatula.html).
FEATURES
SOURCE location/Qualifiers
1. 406
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MCB19B01"
/clone.lib="MCBB"
/tissue.type="symbiotic root nodules"
/dev_stage="harvested 4 days post inoculation with
Sinorhizobium meliloti"
/notes="Vector: pBluescript psk, Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber on
nitrogen-rich medium for 21 days. Three days before
inoculation with Sinorhizobium meliloti, the medium was
replaced by N-free medium. Root nodules (+ short adjacent
root segments) were harvested 4 days post inoculation.
cDNA was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zap XR vector from
Stratagene and packaged using GigaPack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-exciated from phage stocks using Exsakit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de

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Sequence (Genoscope, Evry, France)."
BASE COUNT      91 a      104 c      99 g      112 t
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Query Match      75.4%; Score 19.6; DB 105; Length 406;
Best Local Similarity 84.6%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TCTCCCTGGGCTGCTGCTCTTC 26
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Db 372 TCTCTCGGCTGCTGCTCTTC 347

RESULT 15
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LOCUS m15d06.r1 Strataene mouse testis (#937308) Mus musculus cDNA
DEFINITION clone IMAGE:515915 5', mRNA sequence.
ACCESSION AA062246
VERSION AA062246.1 GI:1556045
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 411)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,D., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMT Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMT Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:309763
Seq primer: -28m13 rev1 EF from Amersham
High quality sequence stop: 387.
FEATURES
SOURCE location/Qualifiers
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/organism="Mus musculus"
/strain="Inbred CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:515915"
/clone.lib="Stratagene mouse testis (#937308)"
/sex="males"
/tissue.type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
/notes="Organ: testis; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
01igo dt. Average insert size: 1.0 kb; Uni-ZAP XR Vector;
-5' adaptor sequence: 5' GATTGCGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTGTGTGTGTGTGTGTGT 3'"
BASE COUNT      110 a      111 c      143 g      47 t
ORIGIN

Query Match      75.4%; Score 19.6; DB 1; Length 411;
Best Local Similarity 84.6%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TCTCCCTGGGCTGCTGCTCTTC 26
|||||  |||  |||  |||  |||  |||
Db 109 TCTGCTTGGCTGCTGCTGCTCTTC 84

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Fri Apr 20 10:22:58 2001

us-09-016-464-13.rst

Page 9

Search completed: April 19, 2001, 23:24:49
Job time: 8166 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:34 ; Search time 280.46 seconds
(without alignments)
16.187 Million cell updates/sec

Title: US-09-016-464-13

Perfect score: 26
Sequence: 1 TCTCCCTGGGCTCTGCTCTCTCTC 26

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA:*
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6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	19.4	74.6	1144	2	US-08-455-968E-28
C 3	18.4	70.8	1930	2	US-08-455-968E-4
C 4	18.4	70.8	2033	2	US-08-455-968E-9
C 5	18	69.2	53	3	US-08-910-632-40
C 6	18	69.2	53	3	US-08-910-632-41
C 7	18	69.2	53	3	US-08-805-631A-40
C 8	18	69.2	53	3	US-08-805-631A-41
C 9	18	69.2	3350	1	US-08-247-946A-2
C 10	18	69.2	3350	5	PCT-US95-06420-2
C 11	17.6	67.7	2694	3	US-08-975-703-5
C 12	17.2	66.2	1023	3	US-08-554-385-4
C 13	17.2	66.2	1100	2	US-08-950-449A-18
C 14	17.2	66.2	1200	1	US-08-011-398B-3
C 15	17.2	66.2	1200	1	US-08-464-051-3
C 16	17.2	66.2	1200	2	US-08-462-498-3
C 17	17.2	66.2	1381	2	US-08-950-449A-13
C 18	17.2	66.2	1423	1	US-08-469-421-13
C 19	17.2	66.2	1423	1	US-08-250-975-13
C 20	17.2	66.2	1423	1	US-08-605-002A-13
C 21	17.2	66.2	1423	5	PCT-US94-10529-13
C 22	17.2	66.2	1539	4	US-08-286-904-1
C 23	17.2	66.2	3774	2	US-08-950-449A-11
C 24	17.2	66.2	3813	1	US-08-469-421-11
C 25	17.2	66.2	3813	1	US-08-250-975-11
C 26	17.2	66.2	3813	2	US-08-605-002A-11
C 27	17.2	66.2	3813	5	PCT-US94-10529-11

C 28	17.2	66.2	4545	6	5183884-3	Patent No. 5183884
C 29	17.2	66.2	4905	1	US-07-978-895-3	Sequence 3, Appl1
C 30	17.2	66.2	4905	1	US-08-473-119-3	Sequence 3, Appl1
C 31	17.2	66.2	4905	2	US-08-475-352-3	Sequence 3, Appl1
C 32	17.2	66.2	50341	1	US-08-247-901C-1	Sequence 1, Appl1
C 33	17.2	66.2	50341	2	US-09-075-904-1	Sequence 1, Appl1
C 34	17	65.4	620	4	US-09-040-984-67	Sequence 67, Appl1
C 35	17	65.4	2255	2	US-08-741-134-1	Sequence 1, Appl1
C 36	17	65.4	2706	4	US-09-066-046-23	Sequence 23, Appl1
C 37	17	65.4	3014	2	US-08-808-982-1	Sequence 1, Appl1
C 38	17	65.4	3073	4	US-08-975-762-41	Sequence 41, Appl1
C 39	17	65.4	5187	2	US-08-540-406-3	Sequence 9, Appl1
C 40	17	65.4	5187	2	US-08-540-406-9	Sequence 9, Appl1
C 41	17	65.4	5187	3	US-08-656-055-3	Sequence 9, Appl1
C 42	17	65.4	5187	3	US-08-656-055-9	Sequence 9, Appl1
C 43	17	65.4	5187	4	US-08-954-668-3	Sequence 9, Appl1
C 44	17	65.4	5187	4	US-08-954-668-9	Sequence 9, Appl1
C 45	17	65.4	5187	5	PCT-US95-13233-3	Sequence 3, Appl1

ALIGNMENTS

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RESULT 1
US-08-455-968E-2/C
; Sequence 2, Application US/08455968E
; Patent No. 5874283
;
GENERAL INFORMATION:
; APPLICANT: Harrington, John L.
; APPLICANT: Hsieh, Chih-Lin
; APPLICANT: Lieber, Michael
; TITLE OF INVENTION: Mammalian Flap-Specific Endonuclease
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,968E
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 18985-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
;
INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
;
US-08-455-968E-2

Query Match          74.6%; Score 19.4; DB 2; Length 1144;
Best Local Similarity 95.2%; Pred. No. 8.9;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCCCTGGGCTCTGCTCTT 23
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Db      1086 TCCCTGGGCTCTGCTCTT 1066
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RESULT 2
US-08-455-968E-28/C
; Sequence 28, Application US/08455968E
; Patent No. 5874283
; GENERAL INFORMATION:
; APPLICANT: Harrington, John L.
; APPLICANT: Hsieh, Chih-Lin
; APPLICANT: Lieber, Michael
; TITLE OF INVENTION: Mammalian Flap-Specific Endonuclease
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,968E
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 18985-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (polynucleotide)
US-08-455-968E-28

Query Match          74.6%; Score 19.4; DB 2; Length 1144;
Best Local Similarity 95.2%; Pred. No. 8.9;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 TCCCTGGGCTGCTCCTT 23
DB 1086 TCCCTGGGCTGCTCCTT 1066

RESULT 3
US-08-455-968E-4/C
; Sequence 4, Application US/08455968E
; Patent No. 5874283
; GENERAL INFORMATION:
; APPLICANT: Harrington, John L.
; APPLICANT: Hsieh, Chih-Lin
; APPLICANT: Lieber, Michael
; TITLE OF INVENTION: Mammalian Flap-Specific Endonuclease
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,968E
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 18985-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1930 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-455-968E-4

Query Match          70.8%; Score 18.4; DB 2; Length 1930;
Best Local Similarity 95.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 CCCTTGGGCTGCTCCTT 23
DB 1079 CCCTTGGGCTGCTCCTT 1060

RESULT 4
US-08-455-968E-9/C
; Sequence 9, Application US/08455968E
; Patent No. 5874283
; GENERAL INFORMATION:
; APPLICANT: Harrington, John L.
; APPLICANT: Hsieh, Chih-Lin
; APPLICANT: Lieber, Michael
; TITLE OF INVENTION: Mammalian Flap-Specific Endonuclease
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,968E
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 18985-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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FEATURE:
NAME/KEY: CDS
LOCATION: 104..1237
US-08-455-968E-9

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Best Local Similarity 95.0%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCCTTGSGCTGCGCTTC 23
DB 1182 CCCTTGSGCTGCGCTTC 1163

RESULT 5
US-08-910-632-40/C
Sequence 40, Application US/08910632B
Patent No. 6077668
GENERAL INFORMATION:
APPLICANT: KOOL, ERIC T.
TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
FILE REFERENCE: 220.00010130
CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER FILING DATE: 1997-02-26
EARLIER APPLICATION NUMBER: 08/393,439
EARLIER FILING DATE: 1995-02-23
EARLIER APPLICATION NUMBER: 08/047,860
EARLIER FILING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 40
LENGTH: 53
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA 53mer circle
US-08-910-632-40

Query Match 69.2%; Score 18; DB 3; Length 53;
Best Local Similarity 80.8%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCTCCCTTGSGCTGCGCTTC 26
DB 45 TCTCTAGGAGATCTCTCTTC 20

RESULT 6
US-08-910-632-41
Sequence 41, Application US/08910632B
Patent No. 6077668
GENERAL INFORMATION:
APPLICANT: KOOL, ERIC T.
TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
FILE REFERENCE: 220.00010130
CURRENT APPLICATION NUMBER: US/08/910,632B
CURRENT FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER FILING DATE: 1997-02-26
EARLIER APPLICATION NUMBER: 08/393,439
EARLIER FILING DATE: 1995-02-23
EARLIER APPLICATION NUMBER: 08/047,860
EARLIER FILING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 53
TYPE: RNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: stem-loop RNA multimer which binds HIV-1 gag RNA
US-08-910-632-41

Query Match 69.2%; Score 18; DB 3; Length 53;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 12; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCTCCCTTGSGCTGCGCTTC 26
DB 18 ucucucaggaaggaucucucucuc 43

RESULT 7
US-08-805-631A-40/C
Sequence 40, Application US/08805631A
Patent No. 6096880
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6096880th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,631A
FILING DATE: 26-FEB-97
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-805-631A-40

Query Match 69.2%; Score 18; DB 3; Length 53;
Best Local Similarity 80.8%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCTCCCTTGSGCTGCGCTTC 26
DB 45 TCTCTAGGAGATCTCTCTTC 20

RESULT 8
US-08-805-631A-41

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: FLOPPY DISK
3  COMPUTER: IBM PC COMPATIBLE
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: WORDPERFECT 5.1
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/247,946A
8  FILING DATE: 24-MAY-1994
9  CLASSIFICATION: 536
10 ATTORNEY/AGENT INFORMATION:
11 NAME: DOROTHY R. AUTH
12 REGISTRATION NUMBER: 36,434
13 REFERENCE/DOCKET NUMBER: 2026-4150
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: (212) 758-4800
16 TELEFAX: (212) 751-6849
17
18 INFORMATION FOR SEQ ID NO: 2:
19
20 SEQUENCE CHARACTERISTICS:
21
22 LENGTH: 3350
23 TYPE: Nucleic acid
24 STRANDEDNESS: Double
25 TOPOLOGY: Linear
26 MOLECULE TYPE: cDNA
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28 HYPOTHETICAL: NO
29 ORIGINAL SOURCE:
30 ORGANISM: Human
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33 DEVELOPMENTAL STAGE:
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35 HAPLOTYPE:
36 TISSUE TYPE:
37 CELL TYPE:
38 CELL LINE:
39 ORGANELLE:
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41 FEATURE:
42 NAME/KEY: Human R-ras gene
43 LOCATION:
44 IDENTIFICATION METHOD:
45 OTHER INFORMATION: exons 2-6.
46
47 US-08-247-946A-2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-534-385-4

Query Match 66.2%; Score 17.2; DB 3; Length 1023;
Best Local Similarity 86.4%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 125 TCTCCAGTGGCTGTGCGCCCT 146

RESULT 13
US-08-950-449A-18
Sequence 18, Application US/08950449A
Patent No. 5955366
GENERAL INFORMATION:
APPLICANT: Lee, John C.
APPLICANT: Adams, Jerry L.
APPLICANT: Gallagher, Timothy F.
APPLICANT: Green, David W.
APPLICANT: Heys, J. Richard
APPLICANT: McDonnell, Peter
APPLICANT: McNulty, Dean E.
APPLICANT: Strickler, James E.
APPLICANT: Young, Peter R.
TITLE OF INVENTION: Drug Binding Protein
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property/P.O. Box
STREET: 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950.449A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,175
FILING DATE: 17-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hecht, Elizabeth J.
REGISTRATION NUMBER: P-41,824
REFERENCE/DOCKET NUMBER: P50195-1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5009
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-950-449A-18

Query Match 66.2%; Score 17.2; DB 2; Length 1100;
Best Local Similarity 86.4%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TCTCCCTGGGCTGTGCTCCT 22
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DB 93 TCTCCAGTGGCTGTGCGCCCT 114

RESULT 14
US-08-011-398B-3
Sequence 3, Application US/08011398B
Patent No. 5512473
GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/011.398B
FILING DATE: 29 JAN 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/160001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-011-398B-3

Query Match 66.2%; Score 17.2; DB 1; Length 1200;
Best Local Similarity 86.4%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 334 TCTCCAGTGGCTGTGCGCCCT 355

RESULT 15
US-08-464-051-3
Sequence 3, Application US/08464051
Patent No. 5780262

GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
City: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,051
FILING DATE: 05 JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/160002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-051-3

Query Match 66.2%; Score 17.2; DB 1; Length 1200;
Best Local Similarity 86.4%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTCTGGCTCT 22
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DB 334 TCTCAGTGGGCTCTGGCGCCT 355

Search completed: April 20, 2001, 00:03:35
Job time: 9672 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 03:21:16 : Search time 1165 seconds

(without alignments)
12.125 Million cell updates/sec

Title: US-09-016-464-13

Perfect score: 26

Sequence: 1 TCTCCCTTGAGCTCTGCTCCTCTC 26

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 13168883 seqs, 2603265903 residues

Total number of hits satisfying chosen parameters: 26337766

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	26	100.0	26	US-08-474-497-13	Sequence 13, Appl
2	26	100.0	26	US-09-016-464-13	Sequence 13, Appl
3	26	100.0	26	US-09-509-152A-1034	Sequence 1034, Ap
4	26	100.0	171	US-09-509-152A-1713	Sequence 1713, Ap
5	26	100.0	302	US-09-533-804-2087	Sequence 2087, Ap
6	26	100.0	2650	US-60-172-373-146	Sequence 146, App
7	26	100.0	2929	US-09-726-807-2787	Sequence 2787, Ap
8	20.8	80.0	463	US-60-213-362-6264	Sequence 6264, Ap
9	20.8	80.0	463	US-60-234-630-9433	Sequence 9433, Ap
10	20.2	77.7	406	US-09-619-643-824	Sequence 824, App
11	20.2	77.7	406	US-60-146-907-788	Sequence 788, App
12	20	76.9	465	US-09-565-309A-16215	Sequence 16215, A
13	19.6	75.4	192	US-09-654-617-312473	Sequence 312473,
14	19.6	75.4	192	US-09-684-016-312473	Sequence 312473,
15	19.6	75.4	405	PCT-US01-01334-5504	Sequence 5504, Ap
16	19.6	75.4	681	US-60-162-247-1020	Sequence 1020, Ap
17	19.6	75.4	767	US-09-733-089-2801	Sequence 2801, Ap
18	19.6	75.4	1455	US-60-138-103-22921	Sequence 22921, A
19	19.6	75.4	2612	US-09-404-550-1286	Sequence 1286, Ap
20	19.6	75.4	6284	US-60-242-679-501	Sequence 501, App
21	19.6	75.4	13274	PCT-US01-01338-2428	Sequence 2428, Ap
22	19.6	75.4	16519	US-60-213-846-510	Sequence 510, App
23	19.6	75.4	22753	US-60-243-468-510	Sequence 510, App
24	19.6	75.4	171584	US-09-528-237A-21	Sequence 21, Appl
25	19.6	75.4	186871	US-60-212-664-104	Sequence 104, App
26	19.4	74.6	345	US-09-515-128-10259	Sequence 10259, A
27	19.4	74.6	486	US-09-534-855-4872	Sequence 4872, Ap
28	19.4	74.6	500	US-09-534-855-4869	Sequence 4869, Ap
29	19.4	74.6	557	US-09-534-855-4870	Sequence 4870, Ap
30	19.4	74.6	1113	US-60-164-285-4322	Sequence 4322, Ap
31	19.4	74.6	1144	US-08-455-968B-2	Sequence 2, Appl1
32	19.4	74.6	1144	US-08-455-968B-28	Sequence 28, Appl1
33	19.4	74.6	1144	US-08-455-968B-2	Sequence 28, Appl1
34	19.4	74.6	1872	US-09-205-070-6679	Sequence 6679, Ap
35	19.4	74.6	2241	US-09-699-998-8857	Sequence 8857, Ap
36	19.4	74.6	2241	US-09-710-281-4363	Sequence 4363, Ap
37	19.4	74.6	2241	US-09-710-282-3863	Sequence 3863, Ap
38	19.4	74.6	2241	US-09-717-350-8836	Sequence 5836, Ap
39	19.4	74.6	2241	US-09-726-174-4569	Sequence 4569, Ap
40	19.4	74.6	2241	US-09-726-788-6011	Sequence 6011, Ap
41	19.4	74.6	2241	US-09-726-806-4697	Sequence 4697, Ap
42	19.4	74.6	2241	US-09-726-807-3319	Sequence 3319, Ap
43	19.4	74.6	2241	US-60-213-360-4404	Sequence 4404, Ap

ALIGNMENTS

RESULT 1
US-08-474-497-13
Sequence 13, Application US/08474497
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: Method of Treatment of Lung Diseases
TITLE OF INVENTION: Using Antisense Oligonucleotides
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: NC
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,497
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-474-497-13

Query Match 100.0%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTCCCTGGGCTGGCTGCTTCTC 26
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DB 1 TCTCCCTGGGCTGGCTGCTTCTC 26

RESULT 2
US-09-016-464-13
Sequence 13, Application US/09016464
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: Method of Treatment of Lung Diseases
TITLE OF INVENTION: Using Antisense Oligonucleotides
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: NC
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,464
FILING DATE: 30-Jan-1998
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,497
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-016-464-13

Query Match 100.0%; Score 26; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTCCCTGGGCTGGCTGCTTCTC 26
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DB 1 TCTCCCTGGGCTGGCTGCTTCTC 26

RESULT 3
US-09-509-152A-1034
Sequence 1034, Application US/09509152A
GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-408-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1034:
SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1034:
US-09-509-152A-1034

Query Match 100.0%; Score 26; DB 19; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTCTGCTCCTTCTC 26
|||||
Db 1 TCTCCCTGGGCTCTGCTCCTTCTC 26

RESULT 4
US-09-509-152A-1713
; Sequence 1713, Application US/09509152A
; GENERAL INFORMATION:
; APPLICANT: NYCE, JONATHAN W.
; TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
; FORMULATIONS, KITS & APPLICATIONS
; NUMBER OF SEQUENCES: 2419
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 CLARKE DRIVE
; CITY: CRANBURY
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/509,152A
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,160
; FILING DATE: 1997-09-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 1713:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1713:
US-09-509-152A-1713

Query Match 100.0%; Score 26; DB 19; Length 171;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTCTGCTCCTTCTC 26
|||||
Db 1 TCTCCCTGGGCTCTGCTCCTTCTC 26

RESULT 5
US-09-533-804-2087/c

; Sequence 2087, Application US/09533804
; GENERAL INFORMATION:
; APPLICANT: Sellhammer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING LYASES
; FILE REFERENCE: PD-1004 CIP
; CURRENT APPLICATION NUMBER: US/09/533,804
; CURRENT FILING DATE: 2000-03-24
; PRIOR APPLICATION DATA removed - refer to PALM or File Wrapper
; NUMBER OF SEQ ID NOS: 5491
; SOFTWARE: PERL Program
; SEQ ID NO 2087
; LENGTH: 302
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu01349116
US-09-533-804-2087

Query Match 100.0%; Score 26; DB 20; Length 302;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTCTGCTCCTTCTC 26
|||||
Db 77 TCTCCCTGGGCTCTGCTCCTTCTC 52

RESULT 6
US-60-172-373-146/c
; Sequence 146, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 146
; LENGTH: 2650
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 274904.2
; NAME/KEY: unsure
; LOCATION: 182, 2641-2642, 2646
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-146

Query Match 100.0%; Score 26; DB 49; Length 2650;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTCTGCTCCTTCTC 26
|||||
Db 332 TCTCCCTGGGCTCTGCTCCTTCTC 307

RESULT 7
US-09-726-807-2787/c

```
; Sequence 2787, Application US/09726807
; GENERAL INFORMATION:
; APPLICANT: Gearling, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Kinsbury, Gillian A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2053-001
; CURRENT APPLICATION NUMBER: US/09/726,807
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/166,040
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 4076
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2787
; LENGTH: 2929
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2929)
; OTHER INFORMATION: n = A,T,C or G
US-09-726-807-2787
```

```
Query Match          100.0%; Score 26; DB 29; Length 2929;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TCTCCCTGGGCTGCTGGCTCTTCTC 26
    ||||||||||||||||||||||||
DB 402 TCTCCCTGGGCTGCTGGCTCTTCTC 377
```

```
RESULT 8
US-60-213-362-6264
; Sequence 6264, Application US/60213362
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0016 P
; CURRENT APPLICATION NUMBER: US/60/213,362
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8429
; SOFTWARE: PERL Program
; SEQ ID NO 6264
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 400391.1
; NAME/KEY: unsure
; LOCATION: 85-144, 300, 338-411, 449
; OTHER INFORMATION: a, t, c, g, or other
US-60-213-362-6264
```

```
Query Match          80.0%; Score 20.8; DB 53; Length 463;
Best Local Similarity 91.7%; Pred. No. 5.3e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 CTCCTTGAGCTGCTGCTCTTCT 25
    ||||||||||||||||||||||||
DB 169 ctgtcttgagctgctgctcttct 192
```

```
RESULT 9
US-60-234-690-9433
```

```
; Sequence 9433, Application US/60234690
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0021 P
; CURRENT APPLICATION NUMBER: US/60/234,690
; CURRENT FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 12060
; SOFTWARE: PERL Program
; SEQ ID NO 9433
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 400391.1
; NAME/KEY: unsure
; LOCATION: 300, 338-411, 449
; OTHER INFORMATION: a, t, c, g, or other
US-60-234-690-9433
```

```
Query Match          80.0%; Score 20.8; DB 55; Length 463;
Best Local Similarity 91.7%; Pred. No. 5.3e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 CTCCTTGAGCTGCTGCTCTTCT 25
    ||||||||||||||||||||||||
DB 169 ctgtcttgagctgctgctcttct 192
```

```
RESULT 10
US-09-619-643-824/C
; Sequence 824, Application US/09619643
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated wi
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51230)B
; CURRENT APPLICATION NUMBER: US/09/619,643
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 824
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3115-015-P1-K1-E8
US-09-619-643-824
```

```
Query Match          77.7%; Score 20.2; DB 23; Length 406;
Best Local Similarity 88.0%; Pred. No. 8.8e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 1 TCTCCCTTGAGCTGCTGCTCTTCT 25
    ||||||||||||||||||||||||
DB 27 TCTCCCTTGAGCTGCTGCTCTTCT 3
```

```
RESULT 11
US-60-146-907-788/C
; Sequence 788, Application US/60146907
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: NOCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51365)A
```

```
; CURRENT APPLICATION NUMBER: US/60/146,907
; CURRENT FILING DATE: 1999-08-02
; NUMBER OF SEQ ID NOS: 3607
; SEQ ID NO 788
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3115-015-P1-K1-E8
US-60-146-907-788
```

```
Query Match          77.7%; Score 20.2; DB 46; Length 406;
Best Local Similarity 88.0%; Pred. No. 8.8e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 TCTCCCTTGCGCTGCTGCTCTTCT 25
    1 ||||| ||||| ||||| |||||
DB 27 TGTCCCTTGCGCTGCGCTCTTCT 3
```

```
RESULT 12
US-09-565-309A-16215/C
; Sequence 16215, Application US/09565309A
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-0853P
; CURRENT APPLICATION NUMBER: US/09/565,309A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 68449
; SEQ ID NO 16215
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(465)
; OTHER INFORMATION: any n = a, g, c, t, unknown, or other
; NAME/KEY: misc.feature
; LOCATION: (1)..(465)
; OTHER INFORMATION: 20549;108898 (Clone Number:Unique Sequence Identifier)
US-09-565-309A-16215
```

```
Query Match          76.9%; Score 20; DB 22; Length 465;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 20; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 CTCCTTGCGCTGCTGCTCTTCT 25
    1 ||||| ||||| ||||| |||||
DB 73 CTTCTTGCGCTGCTGCTCTTCT 50
```

```
RESULT 13
US-09-654-617-312473/C
; Sequence 312473, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 312473
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Zea mays
US-09-654-617-312473
```

```
Query Match          75.4%; Score 19.6; DB 25; Length 192;
Best Local Similarity 84.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 TCTCCCTTGCGCTGCGCTCTTCTC 26
    1 ||||| ||||| ||||| |||||
DB 178 TGTCCCTTGCGCTGCTGCTCTTCTC 153
```

```
RESULT 14
US-09-684-016-312473/C
; Sequence 312473, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 312473
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Zea mays
US-09-684-016-312473
```

```
Query Match          75.4%; Score 19.6; DB 27; Length 192;
Best Local Similarity 84.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 TCTCCCTTGCGCTGCGCTCTTCTC 26
    1 ||||| ||||| ||||| |||||
DB 178 TGTCCCTTGCGCTGCTGCTCTTCTC 153
```

```
RESULT 15
PCT-US01-01354-5504/C
; Sequence 5504, Application PC/TUS0101354
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC004PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01354
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 42506
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5504
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-01354-5504
```

```
Query Match          75.4%; Score 19.6; DB 1; Length 405;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 TCTCCCTTGCGCTGCGCTCTTCTC 26
    1 ||||| ||||| ||||| |||||
DB 249 TGTCCCTTGCGCTGCTGCTCTTCTC 224
```

Search completed: April 20, 2001, 03:21:18
Job time: 14165 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:15:19 ; Search time 101.94 Seconds
(without alignments)
35.293 Million cell updates/sec

Title: US-09-016-464-13

Perfect score: 26
Sequence: 1 TCTCCCTTGGGCTCTGCTCCTTCTC 26

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 seqs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending-Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCF_NEM_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEM_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEM_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEM_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEM_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEM_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	26	US-09-543-679A-1034	Sequence 1034, Ap
2	26	100.0	171	US-09-543-679A-1713	Sequence 1713, Ap
3	26	100.0	2355	US-09-543-679A-2876	Sequence 2876, Ap
4	26	100.0	2396	US-09-543-679A-2877	Sequence 2877, Ap
5	26	100.0	32351	US-09-543-679A-2874	Sequence 2874, Ap
6	26	100.0	40298	US-09-543-679A-2878	Sequence 2878, Ap
7	19.2	73.8	18710	US-60-248-505-124	Sequence 124, App
8	19.2	73.8	18711	US-60-248-505-466	Sequence 466, App
9	18.6	71.5	32696	US-60-248-505-281	Sequence 281, App
10	17.6	67.7	545	US-09-487-566A-2440	Sequence 2440, Ap
11	17.6	67.7	19387	US-60-248-505-223	Sequence 223, App
12	17.6	67.7	56642	US-60-248-505-263	Sequence 263, App
13	17.6	67.7	56643	US-60-248-505-572	Sequence 572, App
14	17.2	66.2	1539	US-09-543-679A-2678	Sequence 2678, Ap
15	17.2	66.2	1539	US-09-543-679A-2732	Sequence 2732, Ap
16	17.2	66.2	3089	US-09-543-679A-2680	Sequence 2680, Ap
17	17.2	66.2	84272	US-60-248-505-65	Sequence 65, Appl
18	17.2	66.2	117931	US-60-248-505-322	Sequence 322, Appl
19	17.2	66.2	219335	US-60-248-505-496	Sequence 496, Appl
20	17.2	66.2	219672	US-60-248-505-57	Sequence 57, Appl
21	17	65.4	495	US-08-276-163D-8027	Sequence 8027, A
22	17	65.4	498	US-08-276-163D-13234	Sequence 13234, A
23	17	65.4	500	US-09-813-206-216	Sequence 216, App
24	17	65.4	2046	US-09-813-206-816	Sequence 816, App
25	17	65.4	3847	US-60-248-505-1370	Sequence 1370, Ap
26	17	65.4	22081	US-60-248-505-38	Sequence 38, Appl
27	17	65.4	143068	US-09-543-679A-2672	Sequence 2672, Ap

C 28	17	65.4	143068	5	US-09-543-679A-2839	Sequence 2839, Ap
C 29	17	65.4	152740	5	US-09-543-679A-2840	Sequence 2840, Ap
C 30	17	65.4	160609	6	US-60-248-505-48	Sequence 48, Appl
C 31	16.8	64.6	408	5	US-09-739-449-2364	Sequence 2364, Ap
C 32	16.8	64.6	99568	6	US-60-248-505-54	Sequence 54, Appl
C 33	16.6	63.8	508	4	US-08-276-163D-2367	Sequence 2367, Ap
C 34	16.6	63.8	761	5	US-09-813-206-929	Sequence 929, App
C 35	16.6	63.8	1079	5	US-09-809-391-215	Sequence 215, App
C 36	16.6	63.8	1153	5	US-09-809-391-41	Sequence 41, Appl
C 37	16.6	63.8	3734	5	US-09-543-679A-2827	Sequence 2827, Ap
C 38	16.6	63.8	4683	5	US-09-543-679A-2828	Sequence 2828, Ap
C 39	16.6	63.8	21140	6	US-60-248-505-144	Sequence 144, App
C 40	16.6	63.8	21141	6	US-60-248-505-404	Sequence 404, App
C 41	16.6	63.8	21693	6	US-60-248-505-659	Sequence 659, App
C 42	16.6	63.8	123654	6	US-60-248-505-41	Sequence 41, Appl
C 43	16.4	63.1	331	4	US-08-276-163D-4490	Sequence 4490, Ap
C 44	16.4	63.1	350	5	US-09-543-679A-2726	Sequence 2726, Ap
C 45	16.4	63.1	847	5	US-09-739-449-1846	Sequence 1846, Ap

ALIGNMENTS

RESULT 1
US-09-543-679A-1034
; Sequence 1034, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-APR-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 1034:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1034:
US-09-543-679A-1034

Query Match 100.0%; Score 26; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2877:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2877:
US-09-543-679A-2877

Query Match
Best Local Similarity 100.0%; Score 26; DB 5; Length 2396;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTGCTGCTCTTC 26
Db 103 TCTCCCTGGGCTGCTGCTCTTC 78

RESULT 5
US-09-543-679A-2874/C
; Sequence 2874, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICITION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2874:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32351 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2874:
US-09-543-679A-2874
```

```
Query Match
Best Local Similarity 100.0%; Score 26; DB 5; Length 32351;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTGCTGCTCTTC 26
Db 7384 TCTCCCTGGGCTGCTGCTCTTC 7359

RESULT 6
US-09-543-679A-2878/C
; Sequence 2878, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICITION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2878:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40298 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2878:
US-09-543-679A-2878

Query Match
Best Local Similarity 100.0%; Score 26; DB 5; Length 40298;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCCCTGGGCTGCTGCTCTTC 26
Db 38005 TCTCCCTGGGCTGCTGCTCTTC 37980

RESULT 7
US-60-248-505-124/C
; Sequence 124, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
```

```

; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 18710
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(18710)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-505-124
```

```

Query Match          73.8%; Score 19.2; DB 6; Length 18710;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 TCCTTGGGCTGCTGCTCTCTC 26
    1 111111111111111111111111
DB 452 TCCTGGGGCCCTGCTCTCTC 429
```

```

RESULT 8
US-60-248-505-466/c
; Sequence 466, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 18711
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(18711)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-505-466
```

```

Query Match          73.8%; Score 19.2; DB 6; Length 18711;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 TCCTTGGGCTGCTGCTCTCTC 26
    1 111111111111111111111111
DB 453 TCCTGGGGCCCTGCTCTCTC 430
```

```

RESULT 9
US-60-248-505-281
; Sequence 281, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FASTSEQ for Windows Version 4.0
```

```

; SEQ ID NO 281
; LENGTH: 32696
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(32696)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-505-281
```

```

Query Match          71.5%; Score 18.6; DB 6; Length 32696;
Best Local Similarity 84.0%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 TCTCCCTTGGGCTGCTGCTCTCTC 25
    11111111111111111111111111
DB 10570 tctccctggtcactctgctcctt 10594
```

```

RESULT 10
US-09-487-566A-2440
; Sequence 2440, Application US/09487566A
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 44
; FILE REFERENCE: PO-44
; CURRENT APPLICATION NUMBER: US/09/487,566A
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/116,668
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 5508
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2440
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (309)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (365)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (376)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (390)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (425)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (444)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (447)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (458)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (466)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (489)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (518)
```


; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (531)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-487-566A-2440

Query Match 67.7%; Score 17.6; DB 5; Length 545;
Best Local Similarity 83.3%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TCCTCCCTGGGCTCTGGCTCTTC 24
11 ||||| ||||| ||||| |||||
Db 256 tcctgcttgagcactgctccttc 279

RESULT 11
US-60-248-505-223
; Sequence 223, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 19387
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(19387)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-505-223

Query Match 67.7%; Score 17.6; DB 6; Length 19387;
Best Local Similarity 83.3%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 TCCTGGGCTCTGGCTCTCTTC 26
||||| ||||| ||||| |||||
Db 12021 tccttgagctgctccttc 12044

RESULT 12
US-60-248-505-263
; Sequence 263, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 56642
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(56642)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-505-263

Query Match 67.7%; Score 17.6; DB 6; Length 56643;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CTCCTGGGCTCTGGCTCTCT 25
||||| ||||| ||||| |||||
Db 13933 ctccctggcctggcactct 13956

RESULT 13
US-60-248-505-572
; Sequence 572, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 572
; LENGTH: 56643
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(56643)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-505-572

Query Match 67.7%; Score 17.6; DB 6; Length 56643;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CTCCTGGGCTCTGGCTCTCT 25
||||| ||||| ||||| |||||
Db 13934 ctccctggcctggcactct 13957

RESULT 14
US-09-543-679A-2678
; Sequence 2678, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICION, LONG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIDENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2678:
SEQUENCE CHARACTERISTICS:
LENGTH: 1539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2678
US-09-543-679A-2678

Query Match 66.2%; Score 17.2; DB 5; Length 1539;
Best Local Similarity 86.4%; Pred. No. 74;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCTCCCTGGGCTGCGCTCT 22
||||| ||||| ||||| ||||| |||||
Db 376 TCTCCAGTGGCTCTGGCGCCT 397

RESULT 15
US-09-543-679A-2732
Sequence 2732, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2732:
SEQUENCE CHARACTERISTICS:
LENGTH: 1539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2732
US-09-543-679A-2732

Query Match 66.2%; Score 17.2; DB 5; Length 1539;

Best Local Similarity 86.4%; Pred. No. 74;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TCTCCCTGGGCTGCGCTCT 22
||||| ||||| ||||| ||||| |||||
Db 376 TCTCCAGTGGCTCTGGCGCCT 397

Search completed: April 20, 2001, 00:15:24
Job time: 9461 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:00:03 ; Search time 2028.86 Seconds
(without alignments)
63.738 Million cell updates/sec

Title: US-09-016-464-14

Perfect score: 21

Sequence: 1 CTGCTCTCTGGGGGCTCTCTG 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
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91: gb_vl34:*
92: gb_vl35:*
93: gb_vl36:*
94: gb_vl37:*
95: gb_vl38:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	768	88	AF206666	AF206666 Homo sapi
2	21	100.0	884	88	AF206665	AF206665 Homo sapi
3	21	100.0	1081	9	AR080462	AR080462 Sequence
4	21	100.0	1081	93	HUMTRX3A	M33493 Human trypt
5	21	100.0	1128	9	AR080461	AR080461 Sequence
6	21	100.0	1128	93	HUMTRX2A	M33492 Human trypt
7	21	100.0	1137	9	AR080460	AR080460 Sequence
8	21	100.0	1137	93	HUMTRX1A	M33491 Human trypt
9	21	100.0	1143	93	HUMBTX1A	M37488 Human beta-
10	21	100.0	1145	93	S55551	S55551 beta-trypt
11	21	100.0	1154	9	AR080459	AR080459 Sequence

C	12	C	12	21	100.0	1154	93	HUMTRY
C	13	C	13	21	100.0	12221	9	AXO14344
C	14	C	14	21	100.0	1455	88	AF099147
C	15	C	15	21	100.0	2197	93	M33494
C	16	C	16	21	100.0	2280	88	AF099143
C	17	C	17	21	100.0	2575	88	AF098327
C	18	C	18	21	100.0	5441	88	AF098328
C	19	C	19	21	100.0	5456	88	AF099144
C	20	C	20	21	100.0	30228	91	HS303A1
C	21	C	21	21	100.0	30228	91	HS303A1
C	22	C	22	21	100.0	37718	83	HS357D8
C	23	C	23	18.4	87.6	66254	89	AL137791
C	24	C	24	18.4	87.6	111916	72	AC035143
C	25	C	25	18.4	87.6	137862	80	AL565780
C	26	C	26	18.4	87.6	167013	92	AL565780
C	27	C	27	18.4	87.6	177874	81	AL450472
C	28	C	28	18.4	87.6	178046	81	AL456459
C	29	C	29	18.4	87.6	188018	97	AC021525
C	30	C	30	18	85.7	388	92	HSMBCT1
C	31	C	31	18	85.7	56320	86	AC008168
C	32	C	32	17.8	84.8	1466	94	AF028739
C	33	C	33	17.8	84.8	1476	94	AF037065
C	34	C	34	17.8	84.8	1537	94	AL4012084
C	35	C	35	17.8	84.8	3730	15	YSJRXJ2HOM
C	36	C	36	17.8	84.8	37045	86	AC007787
C	37	C	37	17.8	84.8	50814	73	AC055816
C	38	C	38	17.8	84.8	68121	94	AF001917
C	39	C	39	17.8	84.8	75630	64	AC016210
C	40	C	40	17.8	84.8	80436	64	AC016200
C	41	C	41	17.8	84.8	108333	94	AP001293
C	42	C	42	17.8	84.8	149779	80	AL455383
C	43	C	43	17.8	84.8	152036	79	AL139374
C	44	C	44	17.8	84.8	156594	78	AL136108
C	45	C	45	17.8	84.8	161933	69	AC024704

ALIGNMENTS

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		/product="mast cell alpha II tryptase"							
		/protein_id="AAG3696.1"							
		/db_xref="GI:11493900"							
		/translation="AYAAPAVQALQAGIVGQEPAPRSKPMQVSLFVRDRYMHMFC							
		GGSLLHPQWVLTAAHGLCPVOLREOHLVYODLLVSRITVHPGFYIIOTGADIALLE							
		LEEVNITSRRVHTWMLPASEFTPPGMCWCWVGMDVNDDELPPFPLKQVYIMT							
		NHICDAYHLGATGDDVRIITRDMLCAGNRRDSCGDSGGLVCKVNGVTLQAGVY							
		SWDSCADPNRPFGIYTRVYTLDMTHHVPKRP"							
BASE COUN	146 a	256 c	237 g	129 t					
ORIGIN									
Query Match	100.0%	Score 21;	DB 88;	Length 768;					
Best Local Similarity	100.0%	Pred. No. 7.2;							
Matches 21; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0.		
Oy	1	CTTGCTCGGGGGGCGCTCCTG	21						
Db	78	CTTGCTCCTGGGGCGCTCCTG	58						
RESULT	2								
AF206665/c	AF206665	884 bp	mRNA	PRI	01-DEC-2000				
LOCUS	Homo sapiens mast cell alpha II tryptase mRNA, complete cds,								
DEFINITION	alternatively spliced.								
ACCESSION	AF206665								
VERSION	AF206665.1								
KEYWORDS	GI:11493897								
SOURCE	human.								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								

```

RESULT      1
AF206666/c

LOCUS       AF206666               768 bp    mRNA    PRI      01-DEC-2000
DEFINITION  Homo sapiens mast cell alpha II tryptase mRNA, partial cds,
ACCESSION  AF206666
VERSION    AF206666
KEYWORDS
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 768)
            Wang,H.W., McNeill,H.P., Thomas,P.S., Murphy,B.N., Webster,M.J.,
            Hettler,Richl,A., Kling,G., Heywood,G.J., Huang,C., Stevens,R.L. and
            Hunt,J.B.
            Molecular cloning and characterization of novel human tryptase
            cDNAs and splicing variants
            Unpublished
            2 (bases 1 to 768)
            Hunt,J.B., Wang,H.W., Thomas,H.P. and McNeill,H.P.
            Direct Submission
            Submitted (19-NOV-1999) Pathology, University of New South Wales,
            High St., Kensington, NSW 2052, Australia
            Location/Qualifiers
                1..768
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                /db_xref="taxon:9606"
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                /note="alternatively spliced"

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JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 2 (bases 1 to 884)
 Hunt,J.E., Wang,H.W., Thomas,H.P. and McNeill,H.P.
 Direct Submission
 Submitted (19-NOV-1999) Pathology, University of New South Wales,
 High St., Kensington, NSW 2052, Australia
 Location/Qualifiers
 1. 884
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 /db_xref="taxon:9606"
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 11. 838
 /note="serine protease; alternatively spliced; similar to
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 /db_xref="GI:11493898"
 /translation="MLSLLLLALPVLASPAYAAPVQALQAGIVGCGEAPRSKMP
 QVSLRSBDRYMHFCGSLIRPQWLTFAALGDPVDKATLRLVQLRQHLIYDQDLT
 PVSILTIYPOPIYIOTGADILLLELEFPVNTSSVHTVMTALPPASFTPPGMCWTG
 GDVNDERLPPRPFLKQYKVPYIMENICDARYHGATYIGDVRITIRDMLCAGNTRR
 SCQDSGRLPGKNGTWLQAGVSMDEGCAQPNRPGIYITVTIYLLDIWHIVPKRP

Qy 1 CTTGCTCTGCGGGGCTCCTG 21
|||||
Db 133 CTTGCTCTGCGGGGCTCCTG 113

RESULT 3
LOCUS AR080462 1081 bp DNA PAT 31-AUG-2000
DEFINITION Sequence 17 from patent US 5968782.
ACCESSION AR080462
VERSION AR080462.1 GI:10007197
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1081)
AUTHORS Stevens,R.L.
TITLE Mast cell protease that cleaves fibrinogen
JOURNAL Patent: US 5968782-A 17 19-OCT-1999;
FEATURES
source 1.1081
/organism="unknown"
BASE COUNT 181 a 398 c 317 g 185 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1081;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTGCTCTGCGGGGCTCCTG 21
|||||
Db 100 CTTGCTCTGCGGGGCTCCTG 80

RESULT 4
LOCUS HUMTRY3A 1081 bp mRNA PRI 03-AUG-1993
DEFINITION Human tryptase-III mRNA, 3' end.
ACCESSION M33493
VERSION M33493.1 GI:339984
KEYWORDS serine protease; tryptase-III.
SOURCE Human adult skin, cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1081)
AUTHORS Vanderslice,P., Ballinger,S.M., Tam,E.K., Goldstein,S.M.,
Craik,C.S. and Caughey,G.H.
TITLE Human mast cell tryptase: Multiple cDNAs and genes reveal a
multigene serine protease family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815 (1990)
MEDLINE 90251647
COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad.
Sci. U.S.A. (1990) In press] kindly submitted
by P.Vanderslice, 02-APR-1990.
FEATURES
source 1.1081
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/db_xref="taxon:9606"
<1.805
/note="tryptase-III"
/codon_start=2
/protein_id="AAA36780.1"
/db_xref="GI:339985"
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RYMHFCGSLHPQWVLTAAHCVPDVKDLAALRVQLREOHLVYODOLLPVSRIVH
POFYTAOIGADIALLELEPVPVSSVHVHTLPPASEFPFGMPGCVTGMGVNDER
LPPPRIGOVKPYIMENHTCDAKYHIGATGCDVRIYRDMICAGTTRDSCGDSG
PLVCKVNGTWLAGVYSGEGCAQDPKREITRYIVYIDMHHIVFKK"

BASE COUNT 181 a 398 c 317 g 185 t
ORIGIN

Query Match 100.0%; Score 21; DB 93; Length 1081;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGCTCTGCGGGGCTCCTG 21
|||||
Db 100 CTTGCTCTGCGGGGCTCCTG 80

RESULT 5
LOCUS AR080461 1128 bp DNA PAT 31-AUG-2000
DEFINITION Sequence 15 from patent US 5968782.
ACCESSION AR080461
VERSION AR080461.1 GI:10007196
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1128)
AUTHORS Stevens,R.L.
TITLE Mast cell protease that cleaves fibrinogen
JOURNAL Patent: US 5968782-A 15 19-OCT-1999;
FEATURES
source 1.1128
/organism="unknown"
BASE COUNT 190 a 409 c 329 g 200 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1128;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTTGCTCTGCGGGGCTCCTG 21
|||||
Db 121 CTTGCTCTGCGGGGCTCCTG 101

RESULT 6
LOCUS HUMTRY2A 1128 bp mRNA PRI 03-AUG-1993
DEFINITION Human tryptase-II mRNA, 3' end.
ACCESSION M33492
VERSION M33492.1 GI:339982
KEYWORDS serine protease; tryptase-II.
SOURCE Human adult skin, cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1128)
AUTHORS Vanderslice,P., Ballinger,S.M., Tam,E.K., Goldstein,S.M.,
Craik,C.S. and Caughey,G.H.
TITLE Human mast cell tryptase: Multiple cDNAs and genes reveal a
multigene serine protease family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815 (1990)
MEDLINE 90251647
COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad.
Sci. U.S.A. (1990) In press] kindly submitted
by P.Vanderslice, 02-APR-1990.
FEATURES
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VSRIIVHPOFYTAQIGADIALLELEPVKVVSSHVHTVTLPPASETFPPGMPQWVGWG
 DVDNDERLPPPEPLKQVPIWENHICDAKYHLGAYTGDVRIVRDDMLCAQNTRRDS
 CGDGGGGLVCKVNGTWTWLAGVSVWEGCAQNPBGITRYVTYTLDMIHVYVKKRP"
 POLYA_signal 1121..1126
 BASE COUNT 190 a 409 c 329 g 200 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGCTCTCTGGGGGCTCTCTG 21
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 Db 121 CTTGCTCTCTGGGGGCTCTCTG 101

RESULT 7
 AR080460/c 1137 bp DNA PAT 31-AUG-2000
 LOCUS AR080460
 DEFINITION Sequence 13 from patent US 5968782.
 ACCESSION AR080460
 VERSION AR080460.1 GI:10007195
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1137)
 AUTHORS Stevens,R.L.
 TITLE Mast cell protease that cleaves fibrinogen
 JOURNAL Patent: US 5968782-A 13 19-OCT-1999;
 FEATURES Location/Qualifiers

source 1..1137
 /organism="unknown"
 BASE COUNT 196 a 410 c 328 g 203 t
 ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1137;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGCTCTCTGGGGGCTCTCTG 21
 |||
 Db 119 CTTGCTCTCTGGGGGCTCTCTG 99

RESULT 8
 HUMTRYIA/c 1137 bp mRNA PRI 03-AUG-1993
 LOCUS HUMTRYIA Human tryptase-I mRNA, 3' end.
 DEFINITION M33491
 ACCESSION M33491.1 GI:339980
 VERSION M33491.1
 KEYWORDS serine protease; tryptase-I.
 SOURCE Human adult skin, cDNA to mRNA.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1137)
 AUTHORS Vanderslice,P., Ballinger,S.M., Tam,E.K., Goldstein,S.M.,
 Craik,C.S. and Caughey,G.H.
 TITLE Human mast cell tryptase: Multiple cDNAs and genes reveal a
 multigene serine protease family
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815 (1990)
 MEDLINE 90251647

FEATURES
 source 1..1137
 Location/Qualifiers

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 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 119 CTTGCTCTCTGGGGGCTCTCTG 99

RESULT 9
 HUMTRYP/c 1143 bp mRNA PRI 31-OCT-1994
 LOCUS HUMTRYP Human beta-tryptase mRNA, complete cds.
 DEFINITION M37488
 ACCESSION M37488.1 GI:179583
 VERSION M37488.1
 KEYWORDS beta-tryptase; mast cell serine protease; tryptase.
 SOURCE Human adult lung mast cell, cDNA to mRNA, clone 10.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1143)
 AUTHORS Miller,J.S., Moxley,G. and Schwartz,L.B.
 TITLE Cloning and characterization of a second complementary DNA for
 human tryptase
 JOURNAL J. Clin. Invest. 86 (3), 864-870 (1990)

MEDLINE 90369005
 COMMENT Draft entry and computer-readable sequence for [J. Clin. Invest.
 (1990) in press] kindly submitted
 by L.B. Schwartz, 06-AUG-1990.

FEATURES
 source 1..1143
 Location/Qualifiers

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 /tissue_type="lung"
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6..95
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 /note="G00-125-891"
 /product="beta-tryptase"
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 /gene="TPS2"
 /note="TPS2"
 6..833
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 96..830
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mat_peptide


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BASE COUNT      197 a      410 c      332 g      204 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 21; DB 93; Length 1143;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  CTTGCTCTGCGGGGCTCCTG 21
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        128 CTTGCTCTGCGGGGCTCCTG 108

RESULT 10
LOCUS      S55551      1145 bp      mRNA      PRI      08-MAY-1993
DEFINITION beta-tryptase [human, basophil cell line KU812, mRNA, 1145 nt].
ACCESSION      S55551
VERSION      S55551.1 GI:265666
KEYWORDS
SOURCE      human basophil cell line KU812.
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE      1 (bases 1 to 1145)
JOURNAL      Blom, T. and Hellman, L.
MEDLINE      Characterization of a tryptase mRNA expressed in the human basophil
REMARK      cell line KU812
          Scand. J. Immunol. 37 (2), 203-208 (1993)
          9316209
          Genbank staff at the National Library of Medicine created this
          entry [NCBI g1bbsq 125219] from the original journal article.

FEATURES
source      1..1145
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BASE COUNT      195 a      412 c      336 g      202 t
ORIGIN

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  CTTGCTCTGCGGGGCTCCTG 21
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RESULT 11
LOCUS      AR080459/c      1154 bp      DNA      PAT      31-AUG-2000
DEFINITION Sequence 11 from patent US 5968782.
ACCESSION      AR080459
VERSION      AR080459.1 GI:10007194
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 1154)

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AUTHORS      Stevens, R.L.
TITLE      Mast cell protease that cleaves fibrinogen
JOURNAL      Patent: US 5968782-A 11-19-OCT-1999;
FEATURES
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BASE COUNT      203 a      411 c      330 g      210 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 21; DB 9; Length 1154;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  CTTGCTCTGCGGGGCTCCTG 21
        |||
        140 CTTGCTCTGCGGGGCTCCTG 120

RESULT 12
LOCUS      HUMTRY/c      1154 bp      mRNA      PRI      07-FEB-1996
DEFINITION Human tryptase mRNA, complete cds.
ACCESSION      M30038
VERSION      M30038.1 GI:1182066
KEYWORDS      serine protease; tryptase.
SOURCE      Human cDNA to mRNA.
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE      1 (bases 1 to 1154)
JOURNAL      Miller, J.S., Westin, E.H. and Schwartz, L.B.
MEDLINE      Cloning and characterization of complementary DNA for human
REMARK      tryptase
          J. Clin. Invest. 84 (4), 1188-1195 (1989)
          90009311
          2 (bases 1 to 1154)
          Schwartz, L.B.
          Direct Submission
          Submitted (15-MAR-1990) Lawrence B. Schwartz, Medicine, Virginia
          Commonwealth University, Richmond, VA 23298, USA
          On Feb 7, 1996 this sequence version replaced gi:339978.

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            GDVNDDEPLRPFPKLVKQVPRIMENHICDAKYHILGADVRIYRDMLCAGNSORD
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BASE COUNT      203 a      411 c      330 g      210 t
ORIGIN

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Best Local Similarity 100.0%; Score 21; DB 93; Length 1154;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 140 CTTGCTCTGCGGCGCTCCTG 120

RESULT 13

AX014344/c

LOCUS

DEFINITION

AX014344

VERSION

AX014344.1

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 1221)

Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and

Pilarsky, C.

Human nucleic acid sequences of normal uterus tissue

Patent: WO 9954353-A 53 28-OCT-1999;

SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN

BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GFS FUER GENOMFORSCHUNG

(DE); PILARSKI CHRISTIAN (DE)

Location/Qualifiers

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BASE COUNT

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ORIGIN

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGCGCTCCTG 21

Db 172 CTTGCTCTGCGGCGCTCCTG 152

RESULT 14

AF099147/c

LOCUS

DEFINITION

AF099147

VERSION

AF099147.1

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 1455)

Pallaoro, M., Fejzo, M.S., Shayesteh, L., Blount, J.L. and Caughey, G.H.

Characterization of genes encoding known and novel human mast cell

tryptases on chromosome 16p13.3

J. Biol. Chem. 274 (6), 3355-3362 (1999)

99121069

2 (bases 1 to 1455)

Pallaoro, M., Fejzo, M.S., Shayesteh, L., Blount, J.L. and Caughey, G.H.

Direct Submission

Submitted (19-OCT-1998) CVRI, UCSF, 90 Medical Center Way, San

Francisco, CA 94143, USA

Location/Qualifiers

1..1455

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/db_xref="taxon:9606"

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CDs

MRNA

CDs

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BASE COUNT

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGCGCTCCTG 21

Db 446 CTTGCTCTGCGGCGCTCCTG 426

RESULT 15

M33494/c

LOCUS

DEFINITION

M33494

VERSION

M33494.1

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 2197)

Vanderslice, P., Ballinger, S.M., Tam, E.K., Goldstein, S.M.,

Craik, C.S. and Caughey, G.H.

Human mast cell tryptase: Multiple cDNAs and genes reveal a

multigene serine protease family

Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815 (1990)

90251647

2 (bases 1 to 2197)

Caughey, G. H.

Direct Submission

Submitted (25-NOV-1998) University of California at San Francisco,

San Francisco, CA, USA

Sequence update by submitter

On Nov 25, 1998 this sequence version replaced gi:339976.

Draft entry and computer-readable sequence for [Proc. Natl. Acad.

Sci. U.S.A. (1990) In press] kindly submitted

by P.Vanderslice 02-APR-1990.

Location/Qualifiers

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197..201

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/note="intron A"

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CDs

MRNA

CDs

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:52 ; Search time 547.68 Seconds
(without alignments)
22.384 Million cell updates/sec

Title: US-09-016-464-14

Perfect score: 21
Sequence: 1 CTGCTCTCGGGGGCCCTCG 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT.*
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20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	18 T76103	Human beta tryptas
2	21	100.0	21	18 T76106	Human tryptase-I a
3	21	100.0	21	20 X53911	Human tryptase-I a
4	21	100.0	21	20 X53908	Human beta tryptas
5	21	100.0	21	21 F19473	Human beta tryptas
6	21	100.0	21	21 F19476	Human tryptase-I p
7	21	100.0	21	21 A33351	Low adenosine anti
8	21	100.0	21	21 A33354	low adenosine anti
9	21	100.0	123	20 X54581	Human beta tryptas
10	21	100.0	123	21 F20150	Human beta tryptas
11	21	100.0	123	21 A34028	Human adenosine re

12	21	100.0	132	20 X54585	Human tryptase-I a
13	21	100.0	132	21 F20154	Human tryptase-I p
14	21	100.0	132	21 A34032	Human adenosine re
c 15	21	100.0	735	21 Z40172	Human beta-tryptas
c 16	21	100.0	771	21 Z40175	Human beta-tryptas
c 17	21	100.0	1081	19 V44331	Human mast cell tr
c 18	21	100.0	1081	19 V42713	Human mast cell tr
c 19	21	100.0	1081	21 F21082	Human low adenosin
c 20	21	100.0	1081	21 A34960	Human adenosine re
c 21	21	100.0	1128	19 V44330	Human mast cell tr
c 22	21	100.0	1128	19 V42712	Human mast cell tr
c 23	21	100.0	1137	19 V44329	Human mast cell tr
c 24	21	100.0	1137	19 V42711	Human mast cell tr
c 25	21	100.0	1137	21 F21079	Human low adenosin
c 26	21	100.0	1137	21 A34957	Human adenosine re
c 27	21	100.0	1143	21 F21077	Human low adenosin
c 28	21	100.0	1143	21 A34955	Human adenosine re
c 29	21	100.0	1145	21 F21078	Human low adenosin
c 30	21	100.0	1145	21 A34956	Human adenosine re
c 31	21	100.0	1154	19 V44328	Human mast cell tr
c 32	21	100.0	1154	19 V42710	Human mast cell tr
c 33	21	100.0	1154	21 F21081	Human low adenosin
c 34	21	100.0	1154	21 A34959	Human adenosine re
c 35	21	100.0	1221	20 Z41376	Human normal uteru
c 36	21	100.0	2197	21 F21080	Human low adenosin
c 37	21	100.0	2197	21 A34958	Human adenosine re
c 38	21	100.0	2218	20 V33911	Nucleotide sequenc
c 39	21	100.0	2259	20 V33910	Human low adenosin
c 40	21	100.0	2280	21 F21083	Human low adenosin
c 41	21	100.0	2280	21 A34961	Human adenosine re
c 42	21	100.0	5441	21 F21074	Human low adenosin
c 43	21	100.0	5441	21 A34952	Human adenosine re
c 44	21	100.0	6225	20 X55273	Human enzyme-relat
45	21	100.0	6225	21 F20843	Human multiple tar

ALIGNMENTS

RESULT 1
T76103 standard; DNA: 21 BP.
AC T76103;
XX
DT 12-SEP-1997 (first entry)
XX
DE Human beta tryptase antisense oligonucleotide HUMETRYPASI.
XX
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS Synthetic.
XX
PM W09640162-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09306.
XX
PR 07-JUN-1995; 95US-0474497.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Metzger 'WJ, Nyce JW;
XX
DR WPI; 1997-051871/05.
XX
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
XX
PS Claim 5; Page 26; 71pp; English.

XX A method for treating airway disease in a subject has been produced.
 CC which involves the topical administration of an essentially adenosine
 CC free antisense oligonucleotide (ON) to the airway epithelium of the
 CC subject. The present sequence is an antisense oligonucleotide
 CC HUMTRPA1 specific for the human beta tryptase. The method can be
 CC used to treat airway diseases such as cystic fibrosis, asthma,
 CC chronic obstructive pulmonary disease, bronchitis and other
 CC airway diseases characterised by an inflammatory response. By
 CC eliminating adenosine from the antisense ON, its liberation upon
 CC antisense degradation is prevented, thereby preventing adenosine-
 CC induced bronchoconstriction in patients with hyper-reactive airways.
 CC
 XX Sequence 21 BP: 0 A: 8 C: 7 G: 6 T: 0 other:

Query Match 100.0%; Score 21; DB 18; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGGCTCGGGGGCTCTCTG 21
 Db 1 ctgctcctggggcctcctg 21

RESULT 2

T76106
 ID T76106 standard; DNA: 21 BP.

AC T76106;

DT 12-SEP-1997 (first entry)

DE Human tryptase-I antisense oligonucleotide HUMTRPA1.

DE Asthma; airway epithelium; adenosine free; cystic fibrosis;

KW chronic obstructive pulmonary disease; bronchitis; ss.

XX Synthetic.

OS W09640162-A1.

PN 19-DEC-1996.

PD 06-JUN-1996; 96MO-US09306.

PE 07-JUN-1995; 95US-0474497.

PR (UYEC-) UNIV EAST CAROLINA.

PA Metzger WJ, Nyce JW;

PI WPI: 1997-051871/05.

DR Treatment of airway diseases such as asthma - by topically applying

PT adenosine-free antisense oligo:nucleotide to airway epithelium of

PT subject

XX Claim 5; Page 26; 71pp; English.

XX A method for treating airway disease in a subject has been produced.

CC which involves the topical administration of an essentially adenosine

CC free antisense oligonucleotide (ON) to the airway epithelium of the

CC subject. The present sequence is an antisense oligonucleotide

CC HUMTRPA1 specific for the human tryptase-I. The method can be

CC used to treat airway diseases such as cystic fibrosis, asthma,
 CC chronic obstructive pulmonary disease, bronchitis and other
 CC airway diseases characterised by an inflammatory response. By
 CC eliminating adenosine from the antisense ON, its liberation upon
 CC antisense degradation is prevented, thereby preventing adenosine-
 CC induced bronchoconstriction in patients with hyper-reactive airways.
 CC
 XX Sequence 21 BP: 0 A: 8 C: 7 G: 6 T: 0 other:

Query Match 100.0%; Score 21; DB 18; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CTGGCTCGGGGGCTCTCTG 21
 Db 1 ctgctcctggggcctcctg 21

RESULT 3

X53911
 ID X53911 standard; DNA: 21 BP.

AC X53911;

DT 05-JUL-1999 (first entry)

DE Human tryptase-I antisense oligonucleotide fragment.

DE Antisense oligonucleotide; multiple target; antisense treatment;

KW impaired respiration; inflammation; lung disease;

KW pulmonary vasoconstriction; inflammation; allergic rhinitis;

KW acute asthma; allergy; asthma; impeded respiration;

KW respiratory distress syndrome; pain; cystic fibrosis;

KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;

KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;

KW colon cancer; breast cancer; lung cancer; pancreatic cancer;

KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;

KW prostate cancer; ss.

XX Synthetic.

OS W09913886-A1.

PN 25-MAR-1999.

PD 17-SEP-1998; 98MO-US19419.

PE 09-JUN-1998; 98US-0093972.

PR 17-SEP-1997; 97US-0059160.

PA (UYEC-) UNIV EAST CAROLINA.

PI Nyce JW;

PI WPI: 1999-229400/19.

DR New antisense oligonucleotides used in treatment of, e.g. pulmonary

PT vasoconstriction

XX Disclosure; Page 45; 120pp; English.

XX The specification describes antisense oligonucleotides (X52869-X55271)

CC directed against at least 2 mRNAs selected from target genes, coding and

CC non-coding regions of RNAs corresponding to target genes, gene

CC initiation codons, genomic flanking regions, intron-exon borders, the

CC 5'-end, the 3'-end and the juxta-section between coding and non-coding

CC regions and all segments of RNAs encoding proteins associated with one

CC or more diseases, conditions or mixtures. The antisense oligonucleotides

CC may be derived from sequences X55272-74. These multiple target

CC oligonucleotides (specifically X55180-271) can be used for the antisense

CC treatment of diseases and conditions. Typical diseases and conditions

CC are those associated with impaired respiration and inflammation,

CC including lung diseases, pulmonary vasoconstriction, inflammation,

CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,

CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary

CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive

CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,

CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic

CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic

CC metastases, as well as all types of cancers which may metastasize or have

CC metastasized to the lungs, including breast and prostate cancer.
XX Sequence 21 BP; 0 A; 8 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGCTCTGCGGGGCGCTCTG 21
1 cttgctctcctg99g9cctcctg 21

RESULT 4
X53908
ID X53908 standard; DNA; 21 BP.

AC X53908;
XX
DT 05-JUL-1999 (first entry)
XX

DE Human beta tryptase antisense oligonucleotide fragment.

KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.

OS Synthetic.

XX WO913886-A1.

XX 25-MAR-1999.

XX 17-SEP-1998; 98WO-US19419.

XX 09-JUN-1998; 98US-0093972.

XX 17-SEP-1997; 97US-0059160.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 1999-229400/19.

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction

XX Disclosure; Page 45; 120pp; English.

XX The specification describes antisense oligonucleotides (X52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences X55272-74. These multiple target
CC oligonucleotides (specifically X55180-271) can be used for the antisense
CC treatment of diseases and conditions. Typical diseases and conditions
CC are those associated with impaired respiration and inflammation,
CC including lung diseases, pulmonary vasoconstriction, inflammation,
CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,

CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC metastases, as well as all types of cancers which may metastasize or have
CC metastasized to the lungs, including breast and prostate cancer.

SQ Sequence 21 BP; 0 A; 8 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGCTCTGCGGGGCGCTCTG 21
1 cttgctctcctg99g9cctcctg 21

RESULT 5
F19473
ID F19473 standard; DNA; 21 BP.

AC F19473;
XX

DT 14-MAR-2001 (first entry)
XX

DE Human beta tryptase polynucleotide fragment #1040.

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

OS Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

XX 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -

XX Claim 14; Page 141; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and

CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.

CC
XX
SQ Sequence 21 BP; 0 A; 8 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCCTGGGGGCGCTCTCTG 21
1 |||||||
DB 1 cttgctcctgggggctcctctg 21

RESULT 6
F19476
ID F19476 standard; DNA: 21 BP.

AC F19476;

DT 14-MAR-2001 (first entry)

XX Human trypsinase-I polynucleotide fragment #1043.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary obstruction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.

XX Homo sapiens.

OS
XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US08020.

XX 06-APR-1999; 99US-0127958.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX NYCE JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -

XX Claim 14; Page 141; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.

CC
XX
SQ Sequence 21 BP; 0 A; 8 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCCTGGGGGCGCTCTCTG 21
1 |||||||
DB 1 cttgctcctgggggctcctctg 21

RESULT 7
A33351
ID A33351 standard; DNA: 21 BP.

XX A33351;

XX 28-JUL-2000 (first entry)

XX Low adenosine antisense oligonucleotide SEQ ID NO:1040.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphorothioate; impaired respiration; inflammation; allergy;
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KM antiallergic; antiaesthetic; cytostatic; analgesic; impaired airway;
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS
XX WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US17712.

XX 03-AUG-1998; 98US-0095212.

XX (UYEC-) UNIV EAST CAROLINA.

XX	Nyce JW;
PI	
XX	WI; 2000-205971/18.
XX	
PT	New antisense oligonucleotides useful for treating e.g. pulmonary
PT	vasoconstriction, inflammation, allergies, asthma, hypertension,
PT	bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT	cancers -
XX	
PS	Claim 18; Page 395; 1343pp; English.
XX	
CC	The present invention describes a new composition comprising an antisense
CC	oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC	nucleic acids involved in bronchoconstriction, allergies, and/or
CC	inflammation. The ON can have anti-inflammatory, antiallergic,
CC	antianasthmatic, cyostatic and analgesic activities. The compositions are
CC	useful for the treatment of diseases associated with inflammation,
CC	impaird always, including lung disease and diseases whose secondary
CC	effects afflict the lungs of a subject. They can be used for treating
CC	e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC	impeded respiration, respiratory distress syndrome, pain, cystic
CC	fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC	pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC	carcinomas, and cancers which may metastasise to the lungs, including
CC	breast and prostate cancer. The reduction of the adenosine content of the
CC	ONS reduces side effects. The A-containing ONS break down with the
CC	release of deoxyadenosine which activates adenosine receptors causing
CC	bronchoconstriction and inflammation. A3313 to A35312 represent the
CC	nucleotide sequences given in the sequence listing from the present
CC	invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC	185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC	differ from the previously named sequences. SEQ ID NO:11 to 1680 (A3233
CC	to A33992) are specifically claimed ONS from the present invention.
CC	N.B. Sequences given in the disclosure of the present invention do not
CC	match up with their corresponding SEQ ID NO: sequences given in the
CC	sequence listing.
XX	
SQ	Sequence 21 BP; 0 A; 8 C; 7 G; 6 T; 0 other;
XX	
Query Match	100.0%; Score 21; DB 21; Length 21;
Best Local Similarity	100.0%; Pred. No. 2.3;
Matches 21; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 GTTGCTCTGGGCGCTCTCTG 21
Db	1 ctgtgcctcggggcctcctg 21
RESULT	8
ID	A33354
AC	A33354 standard; DNA; 21 BP.
XX	A33354:
XX	
DT	28-JUL-2000 (first entry)
XX	
DE	Low adenosine antisense oligonucleotide SEQ ID NO:1043.
XX	
KW	Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW	phosphorothioate; impaired respiration; inflammation; allergy;
KW	allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW	antiallergic; antianasthmatic; cytostatic; analgesic; impaired airway;
KW	lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW	respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW	pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW	cancer; leukemia; lymphoma; carcinoma; metastasis; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200009525-A2.
XX	

PD 24-FEB-2000.

XX PF 03-AUG-1999; 99WO-US17712.

XX PR 03-AUG-1998; 98US-0095212.

XX PA (UYEC-) UNIV EAST CAROLINA.

XX P1 Nyce JW;

XX DR WPI; 2000-205971/18.

XX PT New antisense oligonucleotides useful for treating e.g. pulmonary

PT vasoconstriction, inflammation, allergies, asthma, hypertension,

PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers -

PS Claim 18; Page 395; 1343pp; English.

XX The present invention describes a new composition comprising an antisense

CC oligonucleotide (ON) with low adenosine (up to 15%), which targets

CC nucleic acids involved in bronchoconstriction, allergies, and/or

CC inflammation. The ON can have antiinflammatory, antiallergic,

CC antiasthmatic, cytostatic and analgesic activities. The compositions are

CC useful for the treatment of diseases associated with inflammation,

CC impaired airways, including lung disease and diseases whose secondary

CC effects afflict the lungs of a subject. They can be used for treating

CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,

CC impeded respiratory, respiratory distress syndrome, pain, cystic

CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive

CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,

CC carcinomas, and cancers which may metastasize to the lungs, including

CC breast and prostate cancer. The reduction of the adenosine content of the

CC ON reduces side effects. The A-containing ONs break down with the

CC release of deoxyadenosine which activates adenosine receptors causing

CC bronchoconstriction and inflammation. A32313 to A35312 represent the

CC nucleotide sequences given in the sequence listing from the present

CC invention, which correspond to SEQ ID NO:1 to 185, and then the last

CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences

CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323

CC to A33992) are specifically claimed ONs from the present invention.

CC N.B. Sequences given in the disclosure of the present invention do not

CC match up with their corresponding SEQ ID NO: sequences given in the

CC sequence listing.

XX SQ Sequence 21 BP: 0 A; 8 C; 7 G; 6 T; 0 other;

OY Query Match 100.0%; Score 21; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. NO. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0

DG 1 CTGTCTCGGGGGGCCTCTG 21
|||||
Db 1 ctgtctcctggggcctcctg 21

RESULT 9

ID X54581 X54581 standard; DNA; 123 BP.

XX X54581;

DT 05-JUL-1999 (first entry)

DE Human beta tryptase antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;

KM	immunosuppressive; antialstematic; analgesic; hypotensive; cytostatic;
KM	respiratory obstruction; pulmonary obstruction; impeded respiration;
KM	respiratory hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM	pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM	cancer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200062736-A2.
XX	
PD	26-OCT-2000.
XX	
PF	24-MAR-2000; 2000WO-US08020.
XX	
PR	06-APR-1999; 99US-0127958.
XX	
PA	(UYEC-) UNIV EAST CAROLINA.
XX	(NYCE/) NYCE J W.
PI	
XX	Nyce JW;
XX	
DR	WPI: 2000-679539/66.
XX	
PT	Low adenosine (A) content antisense oligonucleotides which do not
Pr	trigger adenosine receptors during metabolism, useful e.g. for treating
Pr	cancers and respiratory obstructions -
XX	
PS	Claim 14; Page 141; 1592pp: English.
XX	
XX	The present invention describes low adenosine (A) content antisense
CC	oligonucleotides and compositions (I) comprising them. In the antisense
CC	oligonucleotides the A is replaced by a 'universal' or alternative base.
CC	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC	immunosuppressive, antialstematic, hypotensive and cytostatic activities.
CC	The antisense oligonucleotides and (I) can be used to down-regulate the
CC	expression and or activity of target polypeptides associated with
CC	lung/respiratory disorders and malignancies, such as stimulating and
CC	activating peptide factors and transmitters, transcription factors,
CC	immunoglobulins and antibodies, antibody receptors, cytokines and
CC	chemokines, endogenously produced specific and non-specific enzymes,
CC	binding proteins, adhesion molecules and their receptors, cytokine and
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central
CC	nervous system (CNS) and peripheral nervous and non-nervous system
CC	receptors, CNS and peripheral nervous and non-nervous system peptide
CC	transmitters, defensins, growth factors, vasoactive peptides and
CC	receptors, binding proteins and malignancy associated proteins. The
CC	antisense oligonucleotides may be used in this way to treat disorders
CC	including respiratory obstruction (especially pulmonary obstruction
CC	and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC	and/or surfactant hypoproduction which are associated with a disease or
CC	condition selected from pulmonary vasoconstriction, inflammation,
CC	allergies, asthma, impeded respiration, respiratory distress syndrome
CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC	and/or cancer. nt844 to nt2153 represent human polynucleotide fragments
CC	and antisense oligonucleotides used in the exemplification of the
CC	present invention.
XX	
SQ	Sequence 123 BP; 0 A; 43 C; 49 G; 19 T; 12 other;
Query Match 100.0%; Score 21; DB 21; Length 123;	
Best Local Similarity 100.0%; Pred. No. 2,4;	
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CTTGCTCCTGGGGGCTCTG 21
db	1 cttgctcctgggggctctctg 21

RESULT 11
A34028 ID A34028 standard; DNA; 123 BP.
XX
AC A34028;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:1717.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphodiesterase; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytosolic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
OS Homo sapiens.
XX
PN MO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PI Nyce JW;
XX
DR WPI: 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischaemia or
PT cancers -
XX
XX Disclosure; Page 478; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytosolic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A3313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32333
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
XX Sequence 123 BP; 0 A; 43 C; 49 G; 19 T; 12 other;

Query Match 100.0%; Score 21; DB 21; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTGCTCTCGGGGCGCTCG 21
|||||
Db 1 ctgctccctg999gctcctcg 21
RESULT 12
X54585 ID X54585 standard; DNA; 132 BP.
XX
AC X54585;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human typtase-I antisense oligonucleotide fragment.
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impaired respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
OS Synthetic.
XX
XX
XX WO9913886-A1.
XX
PN 25-MAR-1999.
XX
PD 17-SEP-1998; 98WO-US19419.
XX
PF 09-JUN-1998; 98US-0093972.
XX
PR 17-SEP-1997; 97US-0059160.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PI Nyce JW;
XX
DR WPI: 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
XX
PS Disclosure; Page 45; 120pp; English.
XX
CC The specification describes antisense oligonucleotides (X52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences X55272-74. These multiple target
CC oligonucleotides (specifically X55180-271) can be used for the antisense
CC treatment of diseases and conditions. Typical diseases and conditions
CC are those associated with impaired respiration and inflammation,
CC including lung diseases, pulmonary vasoconstriction, inflammation,
CC allergic rhinitis, acute asthma, allergies, asthma, impaired respiration,
CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC metastases, as well as all types of cancers which may metastasize or have
CC metastasized to the lungs, including breast and prostate cancer.
XX
XX Sequence 132 BP; 0 A; 48 C; 48 G; 21 T; 15 other;

Query Match 100.0%; Score 21; DB 20; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGGCCTCCTG 21
|||||
DB 1 ctgtcctcctg99gctcctg 21

RESULT 13
F20154
ID F20154 standard; DNA; 132 BP.
XX
AC F20154;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human tryptase-I polynucleotide fragment #1721.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antisthmatic; analgesic; hypotensive; cytosstatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNITV EAST CAROLINA.
XX
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI: 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Claim 14; Page 141; 1592pp; English.

CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antisthmatic, hypotensive and cytosstatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors and vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction

CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 132 BP; 0 A; 48 C; 48 G; 21 T; 15 other;

Query Match 100.0%; Score 21; DB 21; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGGCCTCCTG 21
|||||
DB 1 ctgtcctcctg99gctcctg 21

RESULT 14
A34032
ID A34032 standard; DNA; 132 BP.
XX
AC A34032;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:1721.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antisthmatic; cytosstatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNITV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI: 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure: Page 479; 1343pp; English.

CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antisthmatic, cytosstatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating

CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONS reduces side effects. The A-containing ONS break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A3313 to A35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
 CC to A33992) are specifically claimed ONS from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 XX
 SQ Sequence 132 BP; 0 A; 48 C; 48 G; 21 T; 15 other;

Query Match 100.0%; Score 21; DB 21; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGTGGGGCCTCCTG 21
 ||||||||||||||||
 DB 1 cttgctctgtggggcctcctg 21

RESULT 15
 240172/c
 ID 240172 standard; DNA: 735 BP.
 XX

240172;

18-FEB-2000 (first entry)

Human beta-tryptase coding sequence.

DE Human beta-tryptase coding sequence.
 XX
 XX Beta-tryptase; human; DNA expression construct; protein production;
 KW combinatorial library screening; X ray crystallography; antigen;
 KW antibody generation; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO9960139-A1.
 PN
 XX
 XX 25-NOV-1999.
 PD
 XX
 XX 29-OCT-1998; 98WO-US22994.
 PF
 XX
 XX 15-MAY-1998; 98US-0079970.
 PR
 XX
 XX (PROM-) PROMEGA CORP.
 PA
 XX
 XX Mafitt MA, Niles AL, Haak-Frendscho M;
 PI
 XX
 XX WPI: 2000-053300/04.
 DR
 XX
 XX P-PSDB: Y55010.
 DR

PT New DNA expression construct for production of enzymatically active
 PT recombinant human beta-tryptase -
 XX
 XX
 XX Claim 4; Page 40-41; 50pp; English.
 PS

CC This sequence encodes the human beta-tryptase. The invention relates to a
 CC DNA expression construct comprising (5' to 3') a promoter linked to a
 CC signal sequence which is linked to a sequence encoding human
 CC beta-tryptase. The DNA construct is useful for transforming host cells to
 CC express, post translationally process and secrete enzymatically active
 CC human tryptase. The method is useful for the production of large amounts
 CC of tryptase with defined specifications. The transformant is useful for

CC pharmacological studies, combinatorial library screens and X ray
 CC crystallographic studies. The tryptase produced allows for the
 CC development of tryptase agonists and/or antagonists, is useful as an
 CC antigen to generate antihuman tryptase antibodies in various animals,
 CC can be used in screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists etc. and to assay for the presence of tryptase in
 CC biological or other solutions. Tryptase inhibitors, antagonists, agonists
 CC etc. may be useful as therapeutics. The tryptase does not require any
 CC post-expression or post-purification modifications or manipulations to
 CC initiate tryptase activity and it has enzymatic activity which compares
 CC favourably with cadaveric tryptase. The availability of enzymatically
 CC active tryptase facilitates the large scale screening of combinatorial
 CC libraries for specific tryptase inhibitors as potential therapeutics and
 CC advances the understanding of the biological significance of tryptase in
 CC mast cell mediated diseases. The tryptase can be used to detect low
 CC levels of tryptase.
 XX
 SQ Sequence 735 BP; 141 A; 245 C; 229 G; 120 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGTGGGGCCTCCTG 21
 ||||||||||||||||
 DB 33 CTTGCTCTGTGGGGCCTCCTG 13

Search completed: April 20, 2001, 00:12:52
 Job time: 10014 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:24:49 ; Search time 7150.85 Seconds
(without alignments)
0.429 Million cell updates/sec

Title: US-09-016-464-14

Perfect score: 21

Sequence: 1 CTTGCTCCTGGGGCCTCCTCG 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: gb_est3:*
4: gb_est4:*
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7: gb_est7:*
8: gb_est8:*
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227: gb_gss27:*
228: gb_gss28:*
229: gb_gss29:*
230: gb_gss30:*
231: gb_gss31:*
232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	351	155	R09803	R09803 yf28e04.r1
2	21	100.0	512	168	BF724180	BF724180 bx01p02.y
3	18.4	87.6	431	7	AA463316	AA463316 zx71e05.r
4	18	85.7	263	147	BF356271	BF356271 RC4-HT088
5	17.8	84.8	400	215	AZ079087	AZ079087 RPCI-23-4
6	17.8	84.8	481	2	AA087428	AA087428 mn96g09.r
7	17.8	84.8	514	170	BF890958	BF890958 RPCI-23-3
8	17.8	84.8	517	216	AZ084692	AZ084692 RPCI-23-3
9	17.8	84.8	526	143	BF080484	BF080484 231396.MA
10	17.8	84.8	526	170	BF891052	BF891052 PM3-MT011
11	17.8	84.8	626	166	BE380256	BE380256 601270206
12	17.8	84.8	669	169	BF782735	BF782735 602107582
13	17.8	84.8	737	147	BF385487	BF385487 602047031
14	17.8	84.8	749	150	BF584872	BF584872 602098742
15	17.8	84.8	856	169	BF785352	BF785352 602111589
16	17.8	84.8	881	147	BF385236	BF385236 602047558
17	17.8	84.8	912	147	BF384546	BF384546 602046815
18	17.8	84.8	913	144	BF140807	BF140807 601788368

19	17.8	84.8	941	169	BF789226	BF7892276	6020160661
20	17.8	84.8	946	145	BF235691	BF235692	602026830
21	17.8	84.8	955	169	BF785509	BF785509	602111884
22	17.8	84.8	1021	169	BF780244	BF780244	602103342
23	17.8	84.8	1053	144	BF164079	BF164079	601772810
24	17.4	82.9	172	8	AA51455	AA51455	n189a10.s
25	17.4	82.9	299	7	AA402894	AA402894	zuse6h01.s
26	17.4	82.9	323	118	AM647600	AM647600	EST326143
27	17.4	82.9	332	118	AM646571	AM646571	EST325561
28	17.4	82.9	339	171	BF948111	BF948111	CM0-NN115
29	17.4	82.9	404	118	AM647281	AM647281	EST35824
30	17.4	82.9	433	21	A1497173	A1497173	fb4h803.x
31	17.4	82.9	460	170	BF882571	BF882571	OV3-ET020
32	17.4	82.9	472	154	N33991	N33991	yx75d04.r1
33	17.4	82.9	510	154	N43015	N43015	yx08f04.r1
34	17.4	82.9	512	174	BF8231811	BF823181	naF31b01.
35	17.4	82.9	534	170	BF828564	BF828564	OV3-ET020
36	17.4	82.9	541	170	BF882563	BF882563	OV3-ET020
37	17.4	82.9	601	145	BF200352	BF200352	WHE2257.A
38	17.4	82.9	607	164	BE267062	BE267062	601193256
39	17.4	82.9	658	167	BE492999	BE492999	WHE0562.C
40	17.4	82.9	669	105	AL048057	AL048057	DFK2586F5
41	17	81.0	388	115	AM471929	AM471929	s117f11.y
42	17	81.0	956	150	BF579259	BF579259	602093430
43	17	81.0	963	174	BG258412	BG258412	602380212
44	16.8	80.0	148	115	AM412628	AM412628	uq45d06.y
45	16.8	80.0	177	9	AA590157	AA590157	vm19d03.r

ALIGNMENTS

AA5930157 vml3d03.1
 BC256412 60238001212
 BC256412 uq45006.y
 AA5145295 n19g8a01.s
 AA4028494 zuseb01.s
 AM647600 EST3261433
 AM649571 C50353561
 AM6494111 CMO-NN115
 AM647281 EST358242
 A1197173 fbb8a03.x
 BB888571 yq3-ET020
 N3391 yx75d04.r1
 N3015 yx08f04.r1
 BC213811 na3.f31201
 BB882564 yq3-ET020
 BB882563 yq3-ET020
 BB8200352 WHE257.A
 BE267062 601193256
 A4049059 WHE0562.C
 AL049807 DHE2586FC
 BF571929 s117r11.y
 AA579129 602093430
 BC256412 60238001212
 AA412628 uq45006.y
 AA5930157 vml3d03.1

						/dev_stage="20 week-post conception fetus"	
						/lab_host="DH10B (ampicillin resistant)"	
						/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)	
						with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;	
						1st strand cDNA was primed with a Pac I - oligo(dT) primer	
						[5' AACGCGAGACATTAATTAAGACATCTTT	

RESULT	1
LOCUS	R09803/c
DEFINITION	R09803 351 bp mRNA EST 06-APR-1995 y728e04.f1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:128190 5' similar to gb:S55551 BETA-TREYPLASE PRECURSOR (HUMAN)
ACCESSION	R09803
VERSION	R09803
KEYWORDS	EST.
SOURCE	R09803.1 GI:761759
ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 351)
AUTHORS	Hillier,L., Clark,N., Dubnque,T., Ellison,K., Hakkins,M., Holman ,M., Hulthan,M., Kucaba,T., Le,M., Lennon,G., Maira,M., Parsons,J., Rickin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston ,R., Williamson,A., Wohlmann,P. and Wilson,R. The Washu-Merck EST Project Unpublished (1995)
TITLE	Contact: Wilson RK
JOURNAL	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
COMMENT	Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 1273 High quality sequence stops: 115 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1273 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 115. Location/Qualifiers 1..351 /organism="Homo sapiens" /db_xref="GDB:480351" /db_xref="taxon:9606" /clone="IMAGE:128190" /clone_lib="Soares fetal liver spleen INFLS" /sex="male"
FEATURES	
source	

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 512)
AUTHORS	Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
TITLE	NEIBANK: EST analysis and bioinformatics for ocular genomics
JOURNAL	Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
COMMENT	Contact: Wistow G Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 01 row: h column: 02 Seq primer: M13RPI reverse primer (ABI). Location/Qualifiers 1..512 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="bx01h02" /clone_lib="Human Iris cDNA (Un-normalized, unamplified): Bx" /tissue_type="Iris" /dev_stage="Adult" /lab_host="EMDH10B" /note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetechn.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTAGTTCGATCGCAGCGCCGCC(1)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoRV sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing

BASE COUNT 83 a 176 c 167 g 84 t 2 others
 ORIGIN

Query Match 100.0%; Score 21; DB 168; Length 512;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGCTCTGGGGGCGCTCTG 21
 ||||||||||||||||||
 Db 130 CTGCTCTGGGGGCGCTCTG 110

RESULT 3
 AA463316 431 bp mRNA EST 10-JUN-1997
 LOCUS zx71e05.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
 DEFINITION IMAGE:796928 5', mRNA sequence.

ACCESSION AA463316
 VERSION AA463316.1 GI:2188200
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 431)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Kuababa, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wylie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997

TITLE Unpublished (1997)
 JOURNAL Contact: Wilson R
 COMMENT Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28m3 rev2 ET from Amersham.
 Location/Qualifiers
 1. 431

FEATURES
 source
 /organism="Homo sapiens"
 /db_xref="GDB:6041597"
 /db_xref="taxon:9606"
 /clone_image="796928"
 /clone_11b="Soares_total_fetus_Nb2HF8_9w"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 /note="Vector: pRTT3D-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from pooled 8-9 week
 (total) fetus material with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAGTGGAGCGCCCTTAATTTTCTTTTCTTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRTT3 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 91 a 133 c 130 g 77 t
 ORIGIN

Query Match 87.6%; Score 18.4; DB 7; Length 431;
 Best Local Similarity 95.0%; Pred. No. 5.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTGCTCTGGGGGCGCTCTG 21
 ||||||||||||||||||
 Db 329 TTGCTCTGGGGGCGCTCTG 348

RESULT 4
 BF356271/c 263 bp mRNA EST 22-NOV-2000
 LOCUS RC4-HT0888-250800-011-e08_1 HT0888 Homo sapiens cDNA, mRNA
 DEFINITION sequence.

ACCESSION BF356271
 VERSION BF356271.1 GI:11315345
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 263)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, M.J.R., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?LI-RC4et2-RC4-HT0888-
 250800-011-e08_1et3-2000-08-25et4-1)
 Seq primer: puc 18 forward
 High quality sequence stop: 176.
 Location/Qualifiers
 1. 263

FEATURES
 source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_11b="HT0888"
 /dev_stage="Adult"
 /note="Organ: head neck; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 65 a 91 c 75 g 32 t
 ORIGIN

Query Match 85.7%; Score 18; DB 147; Length 263;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTGCTCTGGGGGCGCTTC 19
 ||||||||||||||||||
 Db 184 TTGCTCTGGGGGCGCTTC 167

RESULT 5
 A2079087/c 400 bp DNA GSS 31-MAR-2000
 LOCUS RPI-23-400C11.rjb RPI-23 Mus musculus genomic clone
 DEFINITION RPI-23-400C11, DNA sequence.

ACCESSION A2079087
 VERSION A2079087.1 GI:7371986
 KEYWORDS GSS.
 SOURCE house mouse.

REFERENCE	TITLE	ORGANISM
1 (bases 1 to 400)	Mouse BAC End Sequences from Library RPCI-23	Mus musculus
Zhao,S., Niemman,M., Feldblyum,T., Malek,J., Shatsman,S., Akintet	Unpublished (1999)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.	Other_GSSS: RPCI-23-400C11.TVB	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
and Fraser,C.M.	Contact: Shaying Zhao	
	Department of Eukaryotic Genomics	
	The Institute for Genomic Research	
	9712 Medical Center Dr., Rockville, MD 20850, USA	
	Tel: 301 838 0200	
	Fax: 301 838 0208	
	Email: szhaoc@tigr.org	
	Clones are derived from the mouse BAC library RPCI-23. For BAC	
	library availability, please contact Pieter de Jong	
	(pieter@edjong.med.buffalo.edu). Clones may be purchased from	
	BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)	
	or from Resea ch Genetics (info@resgen.com). BAC end page:	
	http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html	
	Plate: 400 row: C column: 11	
	Seq primer: SP6	
	Class: BAC ends.	
FEATURES	Location/Qualifiers	
source	1..400	
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	/strain="C57BL/6J"	
	/db_xref="taxon:10090"	
	/clone="RPCI-23-400C11"	
	/clone_11b="RPCI-23"	
	/sex="Female"	
	/lab_host="DH10B"	
	/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1:	
	EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or	
	brain genomic DNA was isolated and partially digested	
	with a combination of EcoRI and EcoRI Methylase. Size	
	selected DNA was cloned into the pBAC3.6 vector at the	
	EcoRI sites. The ligation products were transformed into	
	DH10B electrocompetent cells (BRL Life Technologies).	
BASE COUNT	86 a 136 c 110 g 68 t	
ORIGIN		
Query Match	84.8%; Score 17.8; DB 215; Length 400;	
Best Local Similarity	90.5%; Pred. No. 9.9e+02;	
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0.		
0y 1 CTTGCTCTCGGGGCGCTCTG 21		
1		
Db 283 COTGCTCTCTGCGGCGCTCTG 263		
RESULT 6		
LOCUS	AA087428 481 bp mRNA EST 15-FEB-1997	
DEFINITION	mp6g09.r1 stragene mouse lung 937302 Mus musculus cDNA clone	
IMAGE:551968 5', mRNA sequence.		
ACCESSION	AA087428	
VERSION	AA087428.1 GI:1630669	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
	1 (bases 1 to 481)	
REFERENCE	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,	
AUTHORS	Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,	
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,	
	Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and	
	Waterston,R.	

[illegible]

QY 1 CTTGCTCCTGGGGCCTCTG 21
||||| ||||||| |||||||
Db 237 CTTGCCCTGGGGCTCTCTG 257

RESULT 10
BF891052 526 bp mRNA EST 18-JAN-2001
LOCUS PM3-MT0110-181000-003-f02 MT0110 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF891052
ACCESSION BF891052.1 GI:12282511
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 526)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?PL=PM3&f2=PM3-MT0110-
181000-003-f02&t3=2000-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 526.
Location/Qualifiers
1..526
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="MT0110"
/dev_stage="Adult"
/note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 105 a 158 c 116 g 147 t

ORIGIN

Query Match 84.8%; Score 17.8; DB 170; Length 526;
Best Local Similarity 90.5%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGCTCCTGGGGCCTCTG 21
||||| ||||||| |||||||
Db 264 CTTGCAGCTGGGGCCTCTG 284

RESULT 11
BE380256 626 bp mRNA EST 21-JUL-2000
LOCUS 601270206F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3599736 5',
DEFINITION

ACCESSION mRNA sequence.
BE380256
VERSION BE380256.1 GI:9325530
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 626)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM8782 row: k column: 01
High quality sequence stop: 533.
Location/Qualifiers
1..626
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_11b="IMAGE:3599736"
/clone_11b="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 89 a 219 c 162 g 156 t

ORIGIN

Query Match 84.8%; Score 17.8; DB 166; Length 626;
Best Local Similarity 90.5%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGCTCCTGGGGCCTCTG 21
||||| ||||||| |||||||
Db 410 CTTGCTCCTGGGGCCTCTG 430

RESULT 12
BF782735 669 bp mRNA EST 12-JAN-2001
LOCUS 602107582F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4235853
DEFINITION 5', mRNA sequence.
ACCESSION BF782735
VERSION BF782735.1 GI:12087771
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 669)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

Mammalia; Eutheria;

REFERENCE

1 (bases 1 to 856)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished (1999)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

EMAIL: Robert_Strausberg@nih.gov
 PHYSIO: Robert_Strausberg@nih.gov

Issue Procurement: Jeffrey E. Green, M.D.

CDNA Library Arrayed by the I M A C E Consortium

DNA Sequencing by: Instra Genomics Inc
 CEBA Arrayed by: The I.M.A.G.E. Consortium (LBNL)

Clone distribution: MGC clone distribution

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

ncpr://image.dni.gov
Data: I1A0853 row:

High quality sequence stop: 651.

LOCATION/QUALITY
1 856

1. : 850
/organisms="Mus musc

FEATURES

source

1.856

/organism="Mus musculus"

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/strain="FVB/N"
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/clone=1MAGE:423964/
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/clone_11D=-NC1_CGAP_K
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/ncce-organ: kidney; vector: pcmv-spec
site 3: salt: cloned unidirectionally

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Average insert size 1 75 kb Constructed by Life
 Sciences: built, cloned and directionally: Primer: Oligo dT

Technologies Note: this is a NCI CGAP Library 1" average insert size 1.75 kb. constructed by ERI

Accession No.	Year	Volume	Page	Author	Title	Notes
278 G	213 a	221 t				

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ORIGIN				

ORIGIN

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Best Local Similarity	90.5%;	Pred. No. 1e+03;		
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Matches 19; Conservative 0; Mismatches

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1 CTTGCTTCCTGGGGGCCCTCCCTC 21

[illegible]

Search completed: April 19, 2001, 23:24:52
Job time: 8169 sec

Job time: 8169 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:35 ; Search time 280.46 Seconds
(without alignments)
13.074 Million cell updates/sec

Title: US-09-016-464-14

Perfect score: 21

Sequence: 1 CTTGCTCTGGGGGCTCTCG 21

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/1na/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	100.0	1081	2	US-09-016-366A-22
C 2	21	100.0	1081	2	US-08-978-404B-17
C 3	21	100.0	1128	2	US-09-016-366A-20
C 4	21	100.0	1128	2	US-08-978-404B-15
C 5	21	100.0	1137	2	US-09-016-366A-18
C 6	21	100.0	1137	2	US-08-978-404B-13
C 7	21	100.0	1154	2	US-09-016-366A-16
C 8	21	100.0	1154	2	US-08-978-404B-11
C 9	21	100.0	2218	4	US-08-845-998-5
C 10	21	100.0	2218	4	US-09-206-537-5
C 11	21	100.0	2259	4	US-08-845-998-3
C 12	21	100.0	2259	4	US-09-206-537-3
C 13	17.4	82.9	7785	2	US-08-276-967-1
C 14	16.4	78.1	176373	4	US-09-128-155-17
C 15	16.2	77.1	1279	4	US-08-985-950-5
C 16	16.2	77.1	1728	4	US-08-985-950-7
C 17	16.2	77.1	1863	2	US-08-455-073A-3
C 18	16.2	77.1	2730	3	US-08-936-135-17
C 19	16.2	77.1	2781	3	US-08-936-135-19
C 20	15.8	75.2	849	3	US-08-807-300-2
C 21	15.8	75.2	1308	2	US-08-494-577-1
C 22	15.8	75.2	1308	2	US-08-795-868-1
C 23	15.8	75.2	2614	2	US-08-795-868-15
C 24	15.8	75.2	38506	4	US-09-320-878-19
C 25	15.8	75.2	176373	4	US-09-128-155-17
C 26	15.2	72.4	87	1	US-08-433-126A-166
C 27	15.2	72.4	87	1	US-08-433-126A-166

28	15.2	72.4	87	4	US-08-976-413A-166	Sequence 166, App
29	15.2	72.4	87	5	PCT-US96-06059-166	Sequence 166, App
C 30	15.2	72.4	1457	1	US-08-233-389C-2	Sequence 2, Appl
C 31	15.2	72.4	1457	2	US-08-801-863-2	Sequence 2, Appl
C 32	15.2	72.4	1457	2	US-08-486-596A-2	Sequence 2, Appl
C 33	15.2	72.4	1457	2	US-09-004-713-2	Sequence 2, Appl
C 34	15.2	72.4	1894	3	US-07-728-220C-1	Sequence 1, Appl
C 35	15.2	72.4	2542	4	US-08-941-445A-6	Sequence 6, Appl
C 36	15.2	72.4	2658	2	US-08-592-383-3	Sequence 3, Appl
C 37	15.2	72.4	2928	2	US-08-095-728B-3	Sequence 3, Appl
C 38	15.2	72.4	2928	2	PCT-US92-02320A-3	Sequence 3, Appl
C 39	15.2	72.4	2940	2	US-08-592-383-1	Sequence 3, Appl
C 40	15.2	72.4	2940	6	US-08-592-383-1	Sequence 1, Appl
C 41	15.2	72.4	3036	1	US-08-306-691B-52	Sequence 52, Appl
C 42	15.2	72.4	3036	2	US-08-095-728B-1	Sequence 1, Appl
C 43	15.2	72.4	3036	5	PCT-US92-02320A-1	Sequence 1, Appl
C 44	15.2	72.4	3511	3	US-08-892-747-13	Sequence 13, Appl
C 45	15.2	72.4	4131	3	US-08-353-784-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-016-366A-22/C
; Sequence 22, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1081 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-016-366A-22

Query Match 100.0%; Score 21; DB 2; Length 1081;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGCTCCTGGGGGCTCTG 21
| | | | | | | | | | | | | | |
Db 100 CTGCTCCTGGGGGCTCTG 80

RESULT 2

US-08-978-404B-17/C

Sequence 17, Application US/08978404B

Patent No. 5968782

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978.404B

FILING DATE: 25-NOV-97

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/032.354

FILING DATE: 04-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: B0801/7090

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX:

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 1081 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-978-404B-17

Query Match 100.0%; Score 21; DB 2; Length 1081;

Best Local Similarity 100.0%; Pred. No. 0.68; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0;

OY 1 CTGCTCCTGGGGGCTCTG 21

| | | | | | | | | | | | | | |

Db 100 CTGCTCCTGGGGGCTCTG 80

RESULT 3

US-09-016-366A-20/C

Sequence 20, Application US/09016366A

Patent No. 5955431

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

APPLICANT: Huang, Chifu

TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978.404B

FILING DATE: 25-NOV-97

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/032.354

FILING DATE: 04-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016.366A

FILING DATE: January 30, 1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037.090

FILING DATE: 05-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: B0801/7093

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX:

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1128 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-016-366A-20

Query Match 100.0%; Score 21; DB 2; Length 1128;

Best Local Similarity 100.0%; Pred. No. 0.68; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0;

OY 1 CTGCTCCTGGGGGCTCTG 21

| | | | | | | | | | | | | | |

Db 121 CTGCTCCTGGGGGCTCTG 101

RESULT 4

US-08-978-404B-15/C

Sequence 15, Application US/08978404B

Patent No. 5968782

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978.404B

FILING DATE: 25-NOV-97

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/032.354

FILING DATE: 04-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-15

Query Match 100.0%; Score 21; DB 2; Length 1128;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCCTG 21
|||||
Db 121 CTTGCTCTGGGGGCTCCTG 101

RESULT 5
US-09-016-366A-18/c
Sequence 18, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-016-366A-18

Query Match 100.0%; Score 21; DB 2; Length 1137;
Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTTGCTCTGGGGGCTCCTG 21
|||||
Db 119 CTTGCTCTGGGGGCTCCTG 99

RESULT 6
US-08-978-404B-13/c
Sequence 13, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-13

Query Match 100.0%; Score 21; DB 2; Length 1137;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCCTG 21
|||||
Db 119 CTTGCTCTGGGGGCTCCTG 99

RESULT 7
US-09-016-366A-16/c
Sequence 16, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-016-366A-16

Query Match 100.0%; Score 21; DB 2; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTG 21
|||||
Db 140 CTTGCTCTGGGGGCTCTG 120

RESULT 8
US-08-978-404B-11/C
Sequence 11, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-11

Query Match 100.0%; Score 21; DB 2; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTG 21
|||||
Db 140 CTTGCTCTGGGGGCTCTG 120

RESULT 9
US-08-845-998-5/C
Sequence 5, Application US/08845998
Patent No. 5879892
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2218 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: NB352/3
FEATURE:
NAME/KEY: CDS

LOCATION: 8..577
US-08-845-998-5

Query Match 100.0%; Score 21; DB 2; Length 2218;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCCTGGGGCCTCTG 21
130 CTTGCTCCTGGGGCCTCTG 110

RESULT 10
US-09-206-537-5/c
; Sequence 5, Application US/09206537
; Patent No. 6130052
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Coulie, Pierre G.
; APPLICANT: De Smet, Charles
; APPLICANT: Lucas, Sophie
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/845,998
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)720-3500
; TELEFAX: (617)720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: NVB352/3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 8..577
; US-09-206-537-5

Query Match 100.0%; Score 21; DB 4; Length 2218;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCCTGGGGCCTCTG 21

DB 130 CTTGCTCCTGGGGCCTCTG 110

RESULT 11
US-08-845-998-3/c
; Sequence 3, Application US/08845998
; Patent No. 5879892
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Coulie, Pierre G.
; APPLICANT: De Smet, Charles
; APPLICANT: Lucas, Sophie
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,998
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)720-3500
; TELEFAX: (617)720-2441
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2259 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 8..577
; US-08-845-998-3

Query Match 100.0%; Score 21; DB 2; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCCTGGGGCCTCTG 21
130 CTTGCTCCTGGGGCCTCTG 110

RESULT 12
US-09-206-537-3/c
; Sequence 3, Application US/09206537
; Patent No. 6130052
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Coulie, Pierre G.
; APPLICANT: De Smet, Charles
; APPLICANT: Lucas, Sophie
; APPLICANT: Boon, Thierry

```

; TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/845,998
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)720-3500
; TELEFAX: (617)720-2441
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2259 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 8..577
; US-09-206-537-3

Query Match          100.0%; Score 21; DB 4; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGTGGGGCCTCCTG 21
    ||||||||||||||||
DB 130 CTTGCTCTGTGGGGCCTCCTG 110

RESULT 13
US-08-276-967-1
; Sequence 1, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
; APPLICANT: Hardy, Daniel M.
; APPLICANT: Garders, David L.
; TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
; TITLE OF INVENTION: Sperm
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

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; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,967
; FILING DATE: Submitted Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSD:418\KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TEXAS: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-276-967-1

Query Match          82.9%; Score 17.4; DB 2; Length 7785;
Best Local Similarity 94.7%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCTCTGTGGGGCCTCCTG 21
    ||| ||||||||||||
DB 4337 TCGCTCTGTGGGGCCTCCTG 4355

RESULT 14
US-09-128-155-17
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT FILING DATE: 1998-08-03
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(176373)
; OTHER INFORMATION: n = A,T,C or G
; US-09-128-155-17

Query Match          78.1%; Score 16.4; DB 4; Length 176373;
Best Local Similarity 94.4%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTCTGTGGGGCCTCCTG 21
    ||||||||||||
DB 156949 gctcctg99gcttctg 156966

RESULT 15
US-08-985-950-5/c
; Sequence 5, Application US/08985950
; Patent No. 6140076
```

```

: GENERAL INFORMATION:
: APPLICANT: Adema, Gosse Jan
: TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DMAX Research Institute
: STREET: 901 California Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/985,950
: FILING DATE: 05-DEC-1997
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 60/041,279
: FILING DATE: 21-MARCH-1997
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 60/033,181
: FILING DATE: 16-DEC-1996
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 60/032,252
: FILING DATE: 06-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Edwin P.
: REGISTRATION NUMBER: 34,090
: REFERENCE/DOCKET NUMBER: DX0670K
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650)852-9196
: TELEFAX: (650)496-1204
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1279 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 155..1015
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1247
: OTHER INFORMATION: /note="nucleotide 1247 designated
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 218..1015
:
: US-08-985-950-5

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Best Local Similarity 85.7%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Q1 1 CTTGCTCTCTGGGGGCTCTCTG 21
||||| ||||||| |||||
Db 754 CTTGCTCTCTGGGGGCTCTCTG 734

Search completed: April 20, 2001, 00:03:38
Job time: 9675 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 03:21:18 ; Search time 1165 Seconds
(without alignments)
9.793 Million cell updates/sec.

Title: US-09-016-464-14
Perfect score: 21
Sequence: 1 CTGCTCCTGGGCGCTCCTG 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 13168883 seqs, 2603265903 residues

Total number of hits satisfying chosen parameters: 26337766

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	8 US-08-474-497-14	Sequence 14, Appl
2	21	100.0	21	8 US-08-474-497-15	Sequence 15, Appl
3	21	100.0	21	14 US-09-016-464-14	Sequence 14, Appl
4	21	100.0	21	14 US-09-016-464-15	Sequence 15, Appl
5	21	100.0	21	19 US-09-509-152A-1040	Sequence 1040, Ap
6	21	100.0	21	19 US-09-509-152A-1043	Sequence 1043, Ap
7	21	100.0	123	19 US-09-509-152A-1721	Sequence 1721, Ap
8	21	100.0	132	19 US-09-509-152A-1721	Sequence 1721, Ap
9	21	100.0	219	25 US-09-652-814-6418	Sequence 6418, Ap
10	21	100.0	253	20 US-09-535-886-32649	Sequence 32649, A
11	21	100.0	268	29 US-09-721-589-4001	Sequence 4001, A
12	21	100.0	310	53 US-60-213-800-537	Sequence 537, Ap
13	21	100.0	362	25 US-09-652-814-4508	Sequence 4508, Ap
14	21	100.0	383	16 US-09-235-076-6378	Sequence 6378, Ap
15	21	100.0	383	16 US-09-248-797-22402	Sequence 22402, A
16	21	100.0	383	17 US-09-332-782-6378	Sequence 6378, Ap
17	21	100.0	402	19 US-09-528-409-61113	Sequence 61113, A
18	21	100.0	415	16 US-09-293-972-32519	Sequence 32519, A
19	21	100.0	424	53 US-60-213-172-344	Sequence 344, App
20	21	100.0	424	53 US-60-213-173-344	Sequence 344, App
21	21	100.0	430	17 US-09-332-782-5548	Sequence 5548, Ap
22	21	100.0	430	19 US-09-515-654-5548	Sequence 5548, Ap
23	21	100.0	436	25 US-09-649-161-6734	Sequence 6734, Ap
24	21	100.0	439	53 US-60-213-800-99	Sequence 99, Appl
25	21	100.0	441	25 US-09-652-137-395	Sequence 295, App
26	21	100.0	454	19 US-09-528-409-70936	Sequence 70936, A
27	21	100.0	462	19 US-09-528-409-69188	Sequence 69188, A
28	21	100.0	469	19 US-09-516-092-113	Sequence 113, App
29	21	100.0	469	25 US-09-652-814-3761	Sequence 3761, App
30	21	100.0	480	16 US-09-248-797-21458	Sequence 21458, A
31	21	100.0	480	17 US-09-346-956-7982	Sequence 7982, Ap
32	21	100.0	485	19 US-09-528-409-71480	Sequence 71480, Ap
33	21	100.0	486	29 US-09-721-569-3268	Sequence 3268, Ap
34	21	100.0	487	16 US-09-234-611-19715	Sequence 19715, A
35	21	100.0	487	16 US-09-277-227-10408	Sequence 10408, A
36	21	100.0	487	20 US-09-649-161-2506	Sequence 2506, Ap
37	21	100.0	497	25 US-09-535-886-29605	Sequence 29605, A
38	21	100.0	560	22 US-09-577-410-192	Sequence 192, App
39	21	100.0	578	29 US-09-726-176-701	Sequence 701, App
40	21	100.0	595	29 US-09-736-119-263	Sequence 263, App
41	21	100.0	599	51 US-60-196-715-1	Sequence 1, Appl1
42	21	100.0	599	51 US-60-196-718-49	Sequence 49, Appl1
43	21	100.0	599	51 US-60-196-718-1809	Sequence 1809, Ap
44	21	100.0	599	51 US-60-196-718-1810	Sequence 1810, Ap
45	21	100.0	600	51 US-60-196-718-1876	Sequence 1876, Ap

ALIGNMENTS

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RESULT 1
US-08-474-497-14
; Sequence 14, Application US/08474497
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,497
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-497-14

Query Match          100.0%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGGCCTCTG 21
DB 1 CTTGCTCTGCGGGCCTCTG 21

RESULT 2
US-08-474-497-15
; Sequence 15, Application US/08474497
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,497
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-497-15

Query Match          100.0%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGGCCTCTG 21
DB 1 CTTGCTCTGCGGGCCTCTG 21

RESULT 3
US-09-016-464-14
; Sequence 14, Application US/09016464
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,464
; FILING DATE: 30-Jan-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,497
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-016-464-14

Query Match 100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTTGCTCTGCGGGGCTCTG 21

RESULT 4
US-09-016-464-15

Sequence 15, Application US/09016464
GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: Method of Treatment of Lung Diseases
Using Antisense Oligonucleotides

NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:

ADDRESS: Kenneth D. Sibley
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: NC

COUNTRY: USA
ZIP: 28234

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,464
FILING DATE: 30-Jan-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,497

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665

REFERENCE/DOCKET NUMBER: 5218-32
TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175

TELEX: 575102
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-016-464-15

Query Match 100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGGGCTCTG 21
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DB 1 CTTGCTCTGCGGGGCTCTG 21

RESULT 5
US-09-509-152A-1040

Sequence 1040, Application US/09509152A
GENERAL INFORMATION:

APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS

NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESS:

ADDRESS: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ

COUNTRY: USA
ZIP: 08512

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM compatible
OPERATING SYSTEM: DOS

SOFTWARE: ASCII
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160

FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1040:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1040:

US-09-509-152A-1040

Query Match 100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGGGCTCTG 21
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DB 1 CTTGCTCTGCGGGGCTCTG 21

RESULT 6
US-09-509-152A-1043

Sequence 1043, Application US/09509152A
GENERAL INFORMATION:

APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS

NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESS:

ADDRESS: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ

COUNTRY: USA
ZIP: 08512

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM compatible
OPERATING SYSTEM: DOS

SOFTWARE: ASCII
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000

CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1043:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1043
US-09-509-152A-1043

Query Match 100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCTG 21
DB 1 CTTGCTCTGGGGGCTCTG 21

RESULT 7
US-09-509-152A-1717
Sequence 1717, Application US/09509152A
GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1717:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1717:

US-09-509-152A-1717

Query Match 100.0%; Score 21; DB 19; Length 123;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCTG 21
DB 1 CTTGCTCTGGGGGCTCTG 21

RESULT 8
US-09-509-152A-1721
Sequence 1721, Application US/09509152A
GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1721:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1721:
US-09-509-152A-1721

Query Match 100.0%; Score 21; DB 19; Length 132;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCTG 21
DB 1 CTTGCTCTGGGGGCTCTG 21

RESULT 9
US-09-652-814-6418/c
Sequence 6418, Application US/09652814
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
THEREFOR

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FILE REFERENCE: 1600.1191-001
CURRENT APPLICATION NUMBER: US/09/652,814
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,109
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 10797
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6418
LENGTH: 219
TYPE: DNA
ORGANISM: Homo sapiens
US-09-652-814-6418
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Query Match          100.0%; Score 21; DB 25; Length 219;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CTTGCTCTGCGGGGCTCTCTG 21
|||||
DB 165 CTTGCTCTGCGGGGCTCTCTG 145
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RESULT 10
US-09-535-896-32649/c
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING HYDROLASES
FILE REFERENCE: PD-1003 CIP
CURRENT APPLICATION NUMBER: US/09/535,896
CURRENT FILING DATE: 2000-03-24
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 46268
SOFTWARE: PERL Program
SEQ ID NO 32649
LENGTH: 253
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu01313433
NAME/KEY: unsure
LOCATION: 13, 33, 35, 39, 73, 118
OTHER INFORMATION: a, t, c, g, or other
US-09-535-896-32649
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Query Match          100.0%; Score 21; DB 20; Length 253;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 CTTGCTCTGCGGGGCTCTCTG 21
|||||
DB 95 CTTGCTCTGCGGGGCTCTCTG 75
```

```
RESULT 11
US-09-721-589-4001/c
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Villevial, Jean-Luc
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.2045-001
CURRENT APPLICATION NUMBER: US/09/721,589
CURRENT FILING DATE: 2000-11-22
```

```
PRIOR APPLICATION NUMBER: 60/167,380
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 7017
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4001
LENGTH: 268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(268)
OTHER INFORMATION: n = A,T,C or G
US-09-721-589-4001
```

```
Query Match          100.0%; Score 21; DB 29; Length 268;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 CTTGCTCTGCGGGGCTCTCTG 21
|||||
DB 141 CTTGCTCTGCGGGGCTCTCTG 121
```

```
RESULT 12
US-60-213-800-537/c
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: C1000707
CURRENT APPLICATION NUMBER: US/60/213,800
CURRENT FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 657
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 537
LENGTH: 310
TYPE: DNA
ORGANISM: HUMAN
US-60-213-800-537
```

```
Query Match          100.0%; Score 21; DB 53; Length 310;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 CTTGCTCTGCGGGGCTCTCTG 21
|||||
DB 174 CTTGCTCTGCGGGGCTCTCTG 154
```

```
RESULT 13
US-09-652-814-4508/c
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.1191-001
CURRENT APPLICATION NUMBER: US/09/652,814
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,109
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 10797
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4508
LENGTH: 362
TYPE: DNA
ORGANISM: Homo sapiens
US-09-652-814-4508
```

Query Match 100.0%; Score 21; DB 25; Length 362;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCTG 21
 |||||
 DB 351 CTTGCTCTGGGGGCTCTG 331

RESULT 14

US-09-235-076-6378/c
 ; Sequence 6378, Application US/09235076
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/235,076
 ; CURRENT FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 6378
 ; LENGTH: 383
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-235-076-6378

Query Match 100.0%; Score 21; DB 16; Length 383;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCTG 21
 |||||
 DB 135 CTTGCTCTGGGGGCTCTG 115

RESULT 15

US-09-248-797-22402/c
 ; Sequence 22402, Application US/09248797
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-764
 ; CURRENT APPLICATION NUMBER: US/09/248,797
 ; CURRENT FILING DATE: 1999-02-12
 ; NUMBER OF SEQ ID NOS: 48909
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 22402
 ; LENGTH: 383
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-248-797-22402

Query Match 100.0%; Score 21; DB 16; Length 383;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCTG 21
 |||||
 DB 135 CTTGCTCTGGGGGCTCTG 115

Search completed: April 20, 2001, 03:21:19
 Job time: 14166 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:15:24 ; Search time 101.94 Seconds
(without alignments)
28.506 Million cell updates/sec

Title: US-09-016-464-14

Perfect score: 21

Sequence: 1 CTGGCTCTCGGGGCGCTCTG 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 segs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/1/pna/PCF_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being plotted,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	US-09-543-679A-1040	Sequence 1040, Ap
2	21	100.0	21	US-09-543-679A-1043	Sequence 1043, Ap
3	21	100.0	123	US-09-543-679A-1717	Sequence 1717, Ap
4	21	100.0	132	US-09-543-679A-1721	Sequence 1721, Ap
5	21	100.0	1081	US-09-543-679A-2649	Sequence 2649, Ap
6	21	100.0	1137	US-09-543-679A-2646	Sequence 2646, Ap
7	21	100.0	1143	US-09-543-679A-2644	Sequence 2644, Ap
8	21	100.0	1145	US-09-543-679A-2645	Sequence 2645, Ap
9	21	100.0	1154	US-09-543-679A-2648	Sequence 2648, Ap
10	21	100.0	2197	US-09-543-679A-2647	Sequence 2647, Ap
11	21	100.0	2280	US-09-543-679A-2650	Sequence 2650, Ap
12	21	100.0	5441	US-09-543-679A-2641	Sequence 2641, Ap
13	21	100.0	6225	US-09-543-679A-2410	Sequence 2410, Ap
14	21	100.0	17133	US-09-543-679A-3003	Sequence 3003, Ap
15	21	100.0	35459	US-09-543-679A-3003	Sequence 3003, Ap
16	18.4	87.6	678	US-09-811-284-49	Sequence 49, Appl
17	18.4	85.7	388	US-09-543-679A-2642	Sequence 2642, Ap
18	17	81.0	17	US-09-543-679A-1722	Sequence 1722, Ap
19	16.2	77.1	87137	US-60-248-505-20	Sequence 20, Appl
20	15.8	75.2	499	US-60-248-505-205	Sequence 205, Appl
21	15.4	73.3	105472	US-09-543-679A-1381	Sequence 1381, Ap
22	15.2	72.4	23	US-09-543-679A-1900	Sequence 1900, Ap
23	15.2	72.4	567	US-09-739-449-4507	Sequence 4507, Ap
24	15.2	72.4	903	US-09-543-679A-2467	Sequence 2467, Ap
25	15.2	72.4	8124	US-09-543-679A-3015	Sequence 3015, Ap
26	15.2	72.4	9372	US-09-543-679A-3015	Sequence 3015, Ap
27	15.2	72.4	9372	US-09-543-679A-3015	Sequence 3015, Ap

28	15.2	72.4	24057	6	US-60-248-505-408	Sequence 408, App
29	15.2	72.4	24990	6	US-60-248-505-467	Sequence 467, App
30	15.2	72.4	35459	5	US-09-543-679A-1003	Sequence 1003, App
31	15.2	72.4	63957	5	US-60-248-505-176	Sequence 176, App
32	15.2	72.4	84633	6	US-60-248-505-177	Sequence 177, App
33	15	71.4	312	4	US-08-276-163D-5991	Sequence 5491, App
34	14.8	70.5	255	4	US-08-276-163D-12658	Sequence 12658, A
35	14.8	70.5	315	5	US-09-739-449-1215	Sequence 1215, App
36	14.8	70.5	491	4	US-08-276-163D-11991	Sequence 11991, A
37	14.8	70.5	503	4	US-08-276-163D-12101	Sequence 12101, A
38	14.8	70.5	2245	5	US-09-543-679A-2971	Sequence 2971, App
39	14.8	70.5	31071	6	US-60-248-505-588	Sequence 588, App
40	14.8	70.5	32199	1	PCF-US01-01350-210	Sequence 210, App
41	14.8	70.5	38644	5	US-09-543-679A-2991	Sequence 2991, App
42	14.8	70.5	54477	6	US-60-248-505-143	Sequence 143, App
43	14.8	70.5	79470	6	US-60-248-505-175	Sequence 175, App
44	14.8	70.5	92585	6	US-60-248-505-383	Sequence 383, App
45	14.8	70.5	169998	5	US-09-676-610A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-543-679A-1040
Sequence 1040, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NICE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
INFORMATION FOR SEQ ID NO: 1040:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1040:
US-09-543-679A-1040
Query Match 100.0%; Score 21; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCTG 21
|||||
Db 1 CTTGCTCTGGGGGCTCTG 21

RESULT 2
US-09-543-679A-1043

; Sequence 1043, Application US/09543679A
; GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESSES:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543.679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1043:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1043:

Query Match 100.0%; Score 21; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCTG 21
|||||
Db 1 CTTGCTCTGGGGGCTCTG 21

RESULT 3
US-09-543-679A-1717

; Sequence 1717, Application US/09543679A
; GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESSES:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543.679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1717:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1717:

Query Match 100.0%; Score 21; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGGCTCTG 21
|||||
Db 1 CTTGCTCTGGGGGCTCTG 21

RESULT 4
US-09-543-679A-1721

; Sequence 1721, Application US/09543679A
; GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESSES:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Clarke Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543.679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958


```

; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 1721:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1721:
US-09-543-679A-1721

Query Match      100.0%; Score 21; DB 5; Length 132;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTGCTCTGGGGGCGCTCTG 21
        |||
Db      1 CTTGCTCTGGGGGCGCTCTG 21

RESULT 5
US-09-543-679A-2649/c
; Sequence 2649, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICITION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 2649:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1081 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2649
US-09-543-679A-2649
```

```

Query Match      100.0%; Score 21; DB 5; Length 1081;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTGCTCTGGGGGCGCTCTG 21
        |||
Db      100 CTTGCTCTGGGGGCGCTCTG 80

RESULT 6
US-09-543-679A-2646/c
; Sequence 2646, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICITION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 2646:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1137 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2646
US-09-543-679A-2646

Query Match      100.0%; Score 21; DB 5; Length 1137;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTGCTCTGGGGGCGCTCTG 21
        |||
Db      119 CTTGCTCTGGGGGCGCTCTG 99

RESULT 7
US-09-543-679A-2644/c
; Sequence 2644, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
```

COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2644:
SEQUENCE CHARACTERISTICS:
LENGTH: 1143 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2644
US-09-543-679A-2644

Query Match 100.0%; Score 21; DB 5; Length 1143;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCCTGGGGGCTCCTG 21
|||||
DB 128 CTGCTCCTGGGGGCTCCTG 108

RESULT 8
US-09-543-679A-2645/C
Sequence 2645, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2645:
SEQUENCE CHARACTERISTICS:
LENGTH: 1145 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2645
US-09-543-679A-2645

Query Match 100.0%; Score 21; DB 5; Length 1145;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCCTGGGGGCTCCTG 21
|||||
DB 130 CTGCTCCTGGGGGCTCCTG 110

RESULT 9
US-09-543-679A-2648/C
Sequence 2648, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2648:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2648
US-09-543-679A-2648

Query Match 100.0%; Score 21; DB 5; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCCTGGGGCCTCTG 21
|||||
DB 140 CTTGCTCCTGGGGCCTCTG 120

RESULT 10
US-09-543-679A-2647/c
Sequence 2647, Application US/09543679A

GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
OF AIRWAY DISORDERS ASSOCIATED WITH
COMPOSITIONS, KIT & METHOD FOR TREATMENT
NUMBER OF SEQUENCES: 3111
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
CORRESPONDENCE ADDRESS:
ADDRESS: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245

TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2647:
SEQUENCE CHARACTERISTICS:
LENGTH: 2197 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2647
US-09-543-679A-2647

Query Match 100.0%; Score 21; DB 5; Length 2197;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCCTGGGGCCTCTG 21
|||||
DB 734 CTTGCTCCTGGGGCCTCTG 714

RESULT 11

US-09-543-679A-2650/c
Sequence 2650, Application US/09543679A

GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESS: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245

TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2650:
SEQUENCE CHARACTERISTICS:
LENGTH: 2280 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2650
US-09-543-679A-2650

Query Match 100.0%; Score 21; DB 5; Length 2280;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCCTGGGGCCTCTG 21
|||||
DB 548 CTTGCTCCTGGGGCCTCTG 528

RESULT 12
US-09-543-679A-2641/c
Sequence 2641, Application US/09543679A

GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESS: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2641:
SEQUENCE CHARACTERISTICS:
LENGTH: 5441 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2641
US-09-543-679A-2641

Query Match 100.0%; Score 21; DB 5; Length 5441;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCTG 21
|||||
DB 2393 CTTGCTCTGGGGGCTCTCTG 2373

RESULT 13
US-09-543-679A-2410
Sequence 2410, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
OF AIRWAY DISORDERS ASSOCIATED WITH
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2410:
SEQUENCE CHARACTERISTICS:
LENGTH: 6225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2410:
US-09-543-679A-2410

Query Match 100.0%; Score 21; DB 5; Length 6225;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCTG 21
|||||
DB 1 CTTGCTCTGGGGGCTCTCTG 21

RESULT 14
US-09-543-679A-2651/C
Sequence 2651, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2651:
SEQUENCE CHARACTERISTICS:
LENGTH: 17133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2651
US-09-543-679A-2651

Query Match 100.0%; Score 21; DB 5; Length 17133;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTGCTCTGGGGGCTCTCTG 21

Db 15401 CTTGCTCTCTGGGGCCCTCTG 15381

```

RESULT 15
US-09-543-679A-3003
; Sequence 3003, Application US/09543679A
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICTION, LONG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 3003:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35459 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3003:
US-09-543-679A-3003

```

```

Query Match          100.0%; Score 21; DB 5; Length 35459;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTGCTCTCTGGGGCCCTCTG 21
   |||
Db 1 CTTGCTCTCTGGGGCCCTCTG 21

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Search completed: April 20, 2001, 00:15:26
Job time: 9463 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:00:05 ; Search time 2028.86 Seconds
(without alignments)
63.738 Million cell updates/sec

Title: US-09-016-464-15

Perfect score: 21

Sequence: 1 CTTGCTCTCGGGGCTCTCG 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pi1:*
13: gb_pi2:*
14: gb_pi3:*
15: gb_pi4:*
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17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
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31: em_htg_inv2:*
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91: em_pi44:*
92: em_pi45:*
93: em_pi46:*
94: em_pi47:*
95: em_pi48:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	768	88	AF206666 Homo sapi
2	21	100.0	884	88	AF206665 Homo sapi
3	21	100.0	1081	9	AR080462 Sequence
4	21	100.0	1081	93	AR080461 Human trypt
5	21	100.0	1128	9	AR080461 Sequence
6	21	100.0	1128	93	AR080461 Human trypt
7	21	100.0	1137	9	AR080460 Sequence
8	21	100.0	1137	93	AR080460 Human trypt
9	21	100.0	1143	93	M37488 Human beta-
10	21	100.0	1145	93	S55551 beta-trypt
11	21	100.0	1154	9	AR080459 Sequence

C 12	21	100.0	1154	93	HUMTRY	M30038 Human trypt
C 13	21	100.0	1221	9	AX014344	AX014344 Sequence
C 14	21	100.0	1455	88	AF099147	AF099147 Homo sapi
C 15	21	100.0	2197	93	M33494	M33494 Homo sapien
C 16	21	100.0	2280	88	AF099143	AF099143 Homo sapi
C 17	21	100.0	2375	88	AF098327	AF098327 Homo sapi
C 18	21	100.0	5441	88	AF098328	AF098328 Homo sapi
C 19	21	100.0	5456	88	AF099144	AF099144 Homo sapi
C 20	21	100.0	30228	91	HS303A1	AL031704 Human DNA
C 21	21	100.0	30228	91	HS303A1	AL031704 Human DNA
C 22	21	100.0	37718	83	HS357D8	AL031715 Homo sapi
C 23	21	100.0	66254	79	AL137791	AL137791 Human DNA
C 24	21	100.0	111916	82	AC035143	AC035143 Homo sapi
C 25	21	100.0	137862	90	AL356780	AL356780 Homo sapi
C 26	21	100.0	167013	92	HSDB28B9	AL121757 Human DNA
C 27	21	100.0	177874	81	AL450472	AL450472 Homo sapi
C 28	21	100.0	178046	80	AL356459	AL356459 Homo sapi
C 29	21	100.0	188018	67	AC021525	AC021525 Homo sapi
C 30	21	100.0	388	92	HSMBCT1	AF099145 Homo sapi
C 31	21	100.0	56320	86	AC008168	AC008168 Homo sapi
C 32	21	100.0	1466	94	AF028739	AF028739 Mus muscu
C 33	21	100.0	1479	94	AF037065	AF037065 Mus muscu
C 34	21	100.0	1537	94	AB012084	AB012084 Mus muscu
C 35	21	100.0	3730	15	YSJREX2HOM	L16238 Yarrowia.11
C 36	21	100.0	37045	86	AC007787	AC007787 Homo sapi
C 37	21	100.0	50814	73	AC055816	AC055816 Homo sapi
C 38	21	100.0	68121	94	AP001917	AP001917 Mus muscu
C 39	21	100.0	75630	64	AC016210	AC016210 Homo sapi
C 40	21	100.0	80436	64	AC016200	AC016200 Homo sapi
C 41	21	100.0	108333	94	AP001293	AP001293 Mus muscu
C 42	21	100.0	149779	80	AL355383	AL355383 Homo sapi
C 43	21	100.0	152036	79	AL139374	AL139374 Homo sapi
C 44	21	100.0	156394	78	AL136108	AL136108 Homo sapi
C 45	21	100.0	161933	69	AC024704	AC024704 Homo sapi

ALIGNMENTS

RESULT 1
AF206666/C 768 bp mRNA PRI 01-DEC-2000
LOCUS Homo sapiens mast cell alpha II tryptase mRNA, partial cds,
DEFINITION alternatively spliced.
ACCESSION AF206666
VERSION AF206666.1 GI:11493899
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 768)
Wang,H.W., McNeill,H.P., Thomas,P.S., Murphy,B.N., Webster,M.J.,
Hettiaratchi,A., King,G., Heywood,G.J., Huang,C., Stevens,R.L. and
Hunt,J.E.
TITLE Molecular cloning and characterization of novel human tryptase
cDNAs and splicing variants
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 768)
Hunt,J.E., Wang,H.W., Thomas,H.P. and McNeill,H.P.
JOURNAL Direct Submission
TITLE Submitted (19-NOV-1999) Pathology, University of New South Wales,
JOURNAL High St., Kensington, NSW 2052, Australia
FEATURES
SOURCE 1..768
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.3"
/tissue_type="lung"
/clone_lib="Invitrogen cat. number D6090-15"
CDS
<1..756
/note="alternatively spliced"

/codon_start=1
/product="mast cell alpha II tryptase"
/protein_id="AF35696.1"
/db_xref="GI:11493900"
/translation="AYAAPVQALQAGIVGQDAPRSKMPQVSLRDRYMMHFC
GSLIHQWVLAHCLGAPVOLREOHLYYQDLIPVSRILVHPFYIITGADALAE
LEEPVNISSRVHTVMPPEASETPFGMGVNDNDPLPPPLKQVYIME
NHICAKYHAGYGDVRIIRDDMLCAGNTRDSCQDSCGSLVCKVNGTWLQAGV
SWDECAQPNRPGIYRTYTLDRHHVPRKKP"
BASE COUNT 146 a 256 c 237 g 129 t
ORIGIN

Query Match 100.0% Score 21: DB 88; Length 768;
Best Local Similarity 100.0% Pred. No. 7.2;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGCGGGCCCTCTG 21
|||||
Db 78 CTTGCTCTGCGGGCCCTCTG 58

RESULT 2
AF206665/C 884 bp mRNA PRI 01-DEC-2000
LOCUS Homo sapiens mast cell alpha II tryptase mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF206665
VERSION AF206665.1 GI:11493897
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 884)
Wang,H.W., McNeill,H.P., Thomas,P.S., Murphy,B.N., Webster,M.J.,
Hettiaratchi,A., King,G., Heywood,G.J., Huang,C., Stevens,R.L. and
Hunt,J.E.
TITLE Molecular cloning and characterization of novel human tryptase
cDNAs and splicing variants
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 884)
Hunt,J.E., Wang,H.W., Thomas,H.P. and McNeill,H.P.
JOURNAL Direct Submission
TITLE Submitted (19-NOV-1999) Pathology, University of New South Wales,
JOURNAL High St., Kensington, NSW 2052, Australia
FEATURES
SOURCE 1..884
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.3"
/tissue_type="lung"
/clone_lib="Invitrogen cat. number D6090-15"
11..838
/note="serine protease; alternatively spliced; similar to
the product encoded by Genbank Accession Number AF098328"

CDS

BASE COUNT 162 a 297 c 276 g 149 t
ORIGIN

Query Match 100.0% Score 21: DB 88; Length 884;
Best Local Similarity 100.0% Pred. No. 7.1;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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OY      1  CTTGCTCTGTGGGGCCTCTG 21
          |||||||
Db      133 CTTGCTCTGTGGGGCCTCTG 113

RESULT  3
LOCUS   AR080462 1081 bp DNA
DEFINITION Sequence 17 from patent US 5968782.
ACCESSION AR080462
VERSION  AR080462.1 GI:10007197
KEYWORDS
SOURCE  Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 1081)
AUTHORS  Stevens,R.L.
TITLE    Mast cell protease that cleaves fibrinogen
JOURNAL  Patent: US 5968782-A 17 19-OCT-1999;
FEATURES
source   1. 1081
          /organism="unknown"
BASE COUNT 181 a 398 c 317 g 185 t
ORIGIN

Query Match          100.0%; Score 21; DB 9; Length 1081;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  CTTGCTCTGTGGGGCCTCTG 21
          |||||||
Db      100 CTTGCTCTGTGGGGCCTCTG 80

RESULT  4
LOCUS   HUMTRY3A 1081 bp mRNA
DEFINITION Human tryptase-III mRNA, 3' end.
ACCESSION M33493
VERSION  M33493.1 GI:339984
KEYWORDS serine protease; tryptase-III.
SOURCE   Human adult skin, cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1081)
AUTHORS  Vanderslice,P., Ballinger,S.M., Tam,E.K., Goldstein,S.M.,
          Craik,C.S. and Caughey,G.H.
TITLE    Human mast cell tryptase: Multiple cDNAs and genes reveal a
          multigene serine protease family
JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815 (1990)
COMMENT  Draft entry and computer-readable sequence for [Proc. Natl. Acad.
          Sci. U.S.A. (1990) in press] kindly submitted
          by P. Vanderslice, 02-Apr-1990.
FEATURES
source   1. 1081
          Location/Qualifiers
          /organism="Homo sapiens"
          /db_xref="taxon:9606"
          <1..805
          /note="tryptase-III"
          /codon_start=2
          /protein_id="AAA36780.1"
          /db_xref="GI:339985"
          /translation="LPVLASRAYAAPGALQRYGIVGGEAPRSKMPMPQVSLRYRD
          RYMHPCGSLIHPOWLTAAHCVGPDVKAALAEQHLVYQDQLPVSRIIVH
          POPYTAQIADALALEPEPVSSVHRTVTPRASETPPCMPCHVTGMDVNDER
          LPPEPLKQVNPIMENHICDKATHGATGVDRIVRDMLCAGTRRDSQGSQSG
          PLVCRVNGTWLDAGVSWGEGCAQPNRPDITRYVRYVYLDWIIHHYVPKP"
BASE COUNT 181 a 398 c 317 g 185 t
ORIGIN
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Query Match          100.0%; Score 21; DB 93; Length 1081;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  CTTGCTCTGTGGGGCCTCTG 21
          |||||||
Db      100 CTTGCTCTGTGGGGCCTCTG 80

RESULT  5
LOCUS   AR080461 1128 bp DNA
DEFINITION Sequence 15 from patent US 5968782.
ACCESSION AR080461
VERSION  AR080461.1 GI:10007196
KEYWORDS
SOURCE  Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 1128)
AUTHORS  Stevens,R.L.
TITLE    Mast cell protease that cleaves fibrinogen
JOURNAL  Patent: US 5968782-A 15 19-OCT-1999;
FEATURES
source   1. 1128
          /organism="unknown"
BASE COUNT 190 a 409 c 329 g 200 t
ORIGIN

Query Match          100.0%; Score 21; DB 9; Length 1128;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1  CTTGCTCTGTGGGGCCTCTG 21
          |||||||
Db      121 CTTGCTCTGTGGGGCCTCTG 101

RESULT  6
LOCUS   HUMTRY2A 1128 bp mRNA
DEFINITION Human tryptase-II mRNA, 3' end.
ACCESSION M33492
VERSION  M33492.1 GI:339982
KEYWORDS serine protease; tryptase-II.
SOURCE   Human adult skin, cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1128)
AUTHORS  Vanderslice,P., Ballinger,S.M., Tam,E.K., Goldstein,S.M.,
          Craik,C.S. and Caughey,G.H.
TITLE    Human mast cell tryptase: Multiple cDNAs and genes reveal a
          multigene serine protease family
JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815 (1990)
COMMENT  Draft entry and computer-readable sequence for [Proc. Natl. Acad.
          Sci. U.S.A. (1990) in press] kindly submitted
          by P. Vanderslice, 02-Apr-1990.
FEATURES
source   1. 1128
          Location/Qualifiers
          /organism="Homo sapiens"
          /db_xref="taxon:9606"
          <1..826
          /note="tryptase-II"
          /codon_start=2
          /protein_id="AAA36779.1"
          /db_xref="GI:339983"
          /translation="LNLILLALPVLASRAYAAPGALQRYGIVGGEAPRSKMPQ
          VSLRVHGPYMHFCGSLIHPOWLTAAHCVGPDVKAALAEQHLVYQDQLP
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VSRIIVHPOFYTAIGADIALLELEBPVKSVMHTVTLPPASETFPPGMPQWVTGMD
VDNDERLPPPEPLKOVKVPIMENHICDAKYHLGAYTGDVRIIVRDMILCAGNTRDS
CGDGSGLPVCKVNGTWLQAGVSMGECACQPNRGITRTVITYLDMIHVYPKRP"

polyA_signal 1121..1126
BASE COUNT 190 a 409 c 329 g 200 t
ORIGIN

Query Match 100.0%; Score 21; DB 93; Length 1128;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTCTGGGGCCCTCCTG 21
|||||
Db 121 CTTGCTCTCTGGGGCCCTCCTG 101

RESULT 7
LOCUS AR080460/c 1137 bp DNA PAT 31-AUG-2000
DEFINITION Sequence 13 from patent US 5968782.
ACCESSION AR080460
VERSION AR080460.1 GI:10007195
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1137)
AUTHORS Stevens,R.L.
TITLE Mast cell protease that cleaves fibrinogen
JOURNAL Patent: US 5968782-A 13 19-OCT-1999;
FEATURES
source 1..1137 /organism="unknown"
BASE COUNT 196 a 410 c 328 g 203 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1137;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTCTGGGGCCCTCCTG 21
|||||
Db 119 CTTGCTCTCTGGGGCCCTCCTG 99

RESULT 8
LOCUS HUMTRY1A/c 1137 bp mRNA PRI 03-AUG-1993
DEFINITION Human trypsinase-I mRNA, 3' end.
ACCESSION M33491
VERSION M33491.1 GI:339980
KEYWORDS serine protease; trypsinase-I.
SOURCE Human adult skin, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1137)
AUTHORS Vanderslice,P., Ballinger,S.M., Tam,E.K., Goldstein,S.M.,
Craik,C.S. and Caughey,G.H.
TITLE Human mast cell trypsinase: Multiple cDNAs and genes reveal a
multigene serine protease family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815 (1990)
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by P.Vanderslice, 02-Apr-1990.
FEATURES
source 1..1137
/organism="Homo sapiens"
/db_xref="taxon:9606"
<1..824
/note="trypsinase-I"

/codon_start=3
/protein_id="AAA36778.1"
/db_xref="GI:339981"
/translation="NLLILALPYLASRAYAAPAGQALQRVIGTGGQEARPSKRPQY
SLRVHGPYMHFCGSLIPQWVLPAAVCVPDKDLALRVQLREQHLVYQDQLPV
SRIIVHPOFYTAIGADIALLELEBPVKSVMHTVTLPPASETFPPGMPQWVTGMD
VDNDERLPPPEPLKOVKVPIMENHICDAKYHLGAYTGDVRIIVRDMILCAGNTRDS
CGDGSGLPVCKVNGTWLQAGVSMGECACQPNRGITRTVITYLDMIHVYPKRP"

polyA_signal 1119..1124
BASE COUNT 196 a 410 c 328 g 203 t
ORIGIN

Query Match 100.0%; Score 21; DB 93; Length 1137;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTCTGGGGCCCTCCTG 21
|||||
Db 119 CTTGCTCTCTGGGGCCCTCCTG 99

RESULT 9
LOCUS HUMTRY1P/c 1143 bp mRNA PRI 31-OCT-1994
DEFINITION Human beta-trypsinase mRNA, complete cds.
ACCESSION M37488
VERSION M37488.1 GI:179583
KEYWORDS beta-trypsinase; mast cell serine protease; trypsinase.
SOURCE Human adult lung mast cell, cDNA to mRNA, clone 10.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1143)
AUTHORS Miller,J.S., Moxley,G. and Schwartz,L.B.
TITLE Cloning and characterization of a second complementary DNA for
human trypsinase
JOURNAL J. Clin. Invest. 86 (3), 864-870 (1990)
COMMENT Draft entry and computer-readable sequence for [J. Clin. Invest.
(1990) in press] kindly submitted
by L.B.Schwartz, 06-AUG-1990.
FEATURES
source 1..1143
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="mast cell"
/tissue_type="lung"
/map="16"
<1..1143
/product="beta-trypsinase"
6..95
/gene="TPS2"
/note="G00-125-891"
/product="beta-trypsinase"
6..833
/gene="TPS2"
6..833
/gene="TPS2"
/codon_start=1
/db_xref="GDB:G00-125-891"
/product="beta-trypsinase"
/protein_id="AA51843.1"
/db_xref="GI:179584"
/translation="MLNLLALPYLASRAYAAPAGQALQRVIGTGGQEARPSKRPQY
SLRVHGPYMHFCGSLIPQWVLPAAVCVPDKDLALRVQLREQHLVYQDQLPV
SRIIVHPOFYTAIGADIALLELEBPVKSVMHTVTLPPASETFPPGMPQWVTGMD
VDNDERLPPPEPLKOVKVPIMENHICDAKYHLGAYTGDVRIIVRDMILCAGNTRDS
CGDGSGLPVCKVNGTWLQAGVSMGECACQPNRGITRTVITYLDMIHVYPKRP"

mat_peptide
/gene="TPS2"
/note="G00-125-891"
/product="beta-trypsinase"

BASE COUNT 197 a 410 c 332 g 204 t
ORIGIN

Query Match 100.0%; Score 21; DB 93; Length 1143;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCG 21
|||||
Db 128 CTTGCTCTGGGGGCTCTCG 108

RESULT 10
S55551 1145 bp mRNA PRI 08-MAY-1993
LOCUS beta-tryptase [human, basophil cell line KU812, mRNA, 1145 nt].
DEFINITION
ACCESSION S55551
VERSION S55551.1 GI:265666
KEYWORDS
SOURCE human basophil cell line KU812.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1145)
AUTHORS Blom, T. and Hellman, L.
TITLE Characterization of a tryptase mRNA expressed in the human basophil cell line KU812
JOURNAL Scand. J. Immunol. 37 (2), 203-208 (1993)
MEDLINE 9316209
REMARK Genbank staff at the National Library of Medicine created this entry [NCBI g1bbsq 125219] from the original journal article.

FEATURES
source 1..1145
/organism="Homo sapiens"
/db_xref="taxon:9606"
8..835
/gene="beta-tryptase"
/note="precursor"
8..835
/gene="beta-tryptase"
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/protein_id="AADI3876.1"
/db_xref="GI:4261576"
/translation="MLNLLILALPYLASRAYAAPAGALORVGIVGGOEAPRSKMP
QVSLRVHGRYMMHFGGSLIHPOWLTAAHCYPRYKDLAALRQLRECHLYQQL
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GDVNDDEPLPEPFLKQVKVPIEMNHICDAKYHLAGAYGDDVRIYDDMLCAGNRRD
SCQDSDGSLPCKVNGTWLQAGVSWDEGCAQPNRPGIYTRVYLYLDMIHVYRKP"

BASE COUNT 195 a 412 c 336 g 202 t
ORIGIN

Query Match 100.0%; Score 21; DB 93; Length 1145;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCG 21
|||||
Db 130 CTTGCTCTGGGGGCTCTCG 110

RESULT 11
AR080459 1154 bp DNA PAT 31-AUG-2000
LOCUS AR080459
DEFINITION Sequence 11 from patent US 5968782.
ACCESSION AR080459
VERSION AR080459.1 GI:10007194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1154)

AUTHORS Stevens, R.L.
TITLE Mast cell protease that cleaves fibrinogen
JOURNAL Patent: US 5968782-A 11 19-OCT-1999;
FEATURES
source 1..1154
/organism="unknown"
BASE COUNT 203 a 411 c 330 g 210 t
ORIGIN

Query Match 100.0%; Score 21; DB 9; Length 1154;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCG 21
|||||
Db 140 CTTGCTCTGGGGGCTCTCG 120

RESULT 12
HUMTRY/c 1154 bp mRNA PRI 07-FEB-1996
LOCUS HUMTRY
DEFINITION Human tryptase mRNA, complete cds.
ACCESSION M30038
VERSION M30038.1 GI:1182066
KEYWORDS serine protease; tryptase.
SOURCE Human cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1154)
AUTHORS Miller, J.S., Westin, E.H. and Schwartz, L.B.
TITLE Cloning and characterization of complementary DNA for human tryptase
JOURNAL J. Clin. Invest. 84 (4), 1188-1195 (1989)
MEDLINE 90009311
REFERENCE 2 (bases 1 to 1154)
AUTHORS Schwartz, L.B.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-1990) Lawrence B. Schwartz, Medicine, Virginia Commonwealth University, Richmond, VA 23298, USA 339978.
COMMENT On Feb 7, 1996 this sequence version replaced g1:339978.

FEATURES
source 1..1154
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/db_xref="taxon:9606"
/tissue="lung"
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/note="TRY mRNA"
18..107
/product="tryptase"
18..845
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/protein_id="AAA86934.1"
/db_xref="GI:1182067"
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QVSLRVHGRYMMHFGGSLIHPOWLTAAHCYPRYKDLAALRQLRECHLYQQL
PVSRTIVHPOFTTADIALLEEEPVKSSHYVTLPASETFPPGMPCWYTG
GDVNDDEPLPEPFLKQVKVPIEMNHICDAKYHLAGAYGDDVRIYDDMLCAGNRRD
SCQDSDGSLPCKVNGTWLQAGVSWDEGCAQPNRPGIYTRVYLYLDMIHVYRKP"

BASE COUNT 203 a 411 c 330 g 210 t
ORIGIN

Query Match 100.0%; Score 21; DB 93; Length 1154;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCG 21
|||||

DB	140	CTTGCTCCTGGGGGCTCCTG	120	
RESULT	13			
LOCUS	AX014344/c			
DEFINITION	Sequence 53 from Patent WO9594353.		PAT	07-SEP-2000
ACCESSION	AX014344			
VERSION	AX014344.1	GI:10040698		
KEYWORDS				
SOURCE				
ORGANISM	human.			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1221)			
AUTHORS	Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilsarsky,C.			
TITLE	Human nucleic acid sequences of normal uterus tissue			
JOURNAL	Patent: WO 9554353-A 53 28-OCT-1999;			
	SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL ENGAR (DE); HINZMANN			
	BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN			
	(DE); PILSARSKY CHRISTIAN (DE)			
FEATURES	location/Qualifiers			
source	1..1221			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
BASE COUNT	244 a 416 c 356 g 205 t			
ORIGIN				
Query Match	100.0%; Score 21; DB 9; Length 1221;			
Best Local Similarity	100.0%; Pred. No. 6.7;			
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0.			
QY	1 CTTGCTCCTGGGGGCTCCTG 21			
DB	172 CTTGCTCCTGGGGGCTCCTG 152			
RESULT	14			
LOCUS	AF099147/c			
DEFINITION	Homo sapiens mast cell MMP-7-like I protein gene, partial cds.			
ACCESSION	AF099147			
VERSION	AF099147.1	GI:4336620		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1455)			
AUTHORS	Pallaro,M., Fejzo,M.S., Shayesteh,L., Blount,J.L. and Caughey,G.H			
TITLE	Characterization of genes encoding known and novel human mast cell			
	tryptases on chromosome 16p13.3			
JOURNAL	J. Biol. Chem. 274 (6), 3355-3362 (1999)			
REFERENCE	99121069			
AUTHORS	2 (bases 1 to 1455)			
TITLE	Pallaro,M., Fejzo,M.S., Shayesteh,L., Blount,J.L. and Caughey,G.H			
JOURNAL	Direct Submission			
	Submitted (19-OCT-1998) CVRI, UCSF, 90 Medical Center Way, San			
	Francisco, CA 94143, USA			
FEATURES	location/Qualifiers			
source	1..1455			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/chromosome="16"			
	/map="16p13.3"			
	join(<171..221,385..556,666..931)			
	/product="mast cell MMP-7-like I protein"			
	join(171..221,385..556,666..931)			
	/note="serine protease"			
	/codon_start=1			
	/product="mast cell MMP-7-like I protein"			

BASE COUNT	250 a	472 c	489 g	244 t
ORIGIN				
Query Match	100.0%;	Score 21;	DB 88;	Length 1455;
Best Local Similarity	100.0%;	Pred. No. 6.4;		
Matches 21:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	CTTGCTCTGGGGCGCTCTG	21	
Db	446	CTTGCTCTGGGGCGCTCTG	426	
RESULT 15				
M33494/c				
LOCUS	M33494	2197 bp	DNA	PRI
DEFINITION	Homo sapiens	tryptase-I gene, complete cds.		04-DEC-1998
ACCESSION	M33494			
VERSION	M33494.1	GI:3927804		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
1 (bases 1 to 2197)				
Vanderslice,P., Baillinger,S.M., Tam,E.K., Goldstein,S.M.,				
Craik,C.S. and Caughey,G.H.				
Human mast cell tryptase: Multiple cDNAs and genes reveal a				
multigene serine protease family				
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815 (1990)				
JOURNAL	90251647			
2 (bases 1 to 2197)				
Caughey,G.H.				
Direct Submission				
Submitted (19-JUN-1990)				
University of California at San Francisco,				
San Francisco, CA, USA				
3 (bases 1 to 2197)				
Caughey,G.H.				
Direct Submission				
Submitted (25-NOV-1998)				
University of California at San Francisco,				
San Francisco, CA, USA				
REMARK				
Sequence update by submitter				
On Nov 25, 1998 this sequence version replaced gi:339976.				
Draft entry and computer-readable sequence for [Proc. Natl. Acad.				
Sci. U.S.A. (1990) In press] kindly submitted				
by P. Vanderslice 02-APR-1990.				
FEATURES				
Source	1. 2197			
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/db_xref="taxon:9606"				
/cell_type="mast"				
/tissue_type="skin"				
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/evidence=not_experimental				
197..201				
/evidence=not_experimental				
<225..247				
/number=1				
join<(225..247,458..518,673..844,954..1219,1346..1509,				
1595..2072)				
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248..457				
/note="Intron A"				
458..518				
/number=2				
join(458..518,673..844,954..1219,1346..1509,1595..1759)				

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/note="serine protease"
/codon_start=1
/product="trypsin-1"
/protein_id="AAC83172.1"
/db_xref="GI:33977"
/translation="MLNLLALLPVLASRAYAAPAPGOALQRVGIVGQEARPSKMP
QVSLRHGPRYMHFGGSLIHPOWLTAAHCVGPDVCDLALRVOLREOHLYODOL
PVSRIIVHPOFYTAQIGADIALLELEEVNYSHVHTVTLPPASEFPFGMPCWVIGW
GDVNDERLPPPEPLKQYKVPIMENHICDARYHLGAYTGDDVRIYRDMLCAGNTRD
SCGDGSGPLVKNGTWTQAGVYSMGSCAQPNRPGIYTRVITYLDWIIHIVPKK"
519..672
/note="intron B"
673..844
/number=3
845..953
/note="intron C"
954..1219
/number=4
1220..1345
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1346..1509
/number=5
1510..1594
/note="intron E"
1595..2072
/number=6
2073..379
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380..714
/number=8
715..1044
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1045..1374
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1375..1704
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1705..2034
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2035..2364
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2365..2694
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2695..3024
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3355..3684
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4675..5004
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5335..5664
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5665..5994
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5995..6324
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6325..6654
/number=26
6655..6984
/number=27
6985..7314
/number=28
7315..7644
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7645..7974
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7975..8304
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8305..8634
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8635..8964
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8965..9294
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9295..9624
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9625..9954
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9955..10284
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11605..11934
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17215..17544
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20845..21174
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21175..21504
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:52 ; Search time 547.68 Seconds
(without alignments)
22.384 Million cell updates/sec

Title: US-09-016-464-15

Perfect score: 21

Sequence: 1 CTGCTCTCGGGGCGCTCTG 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	21	100.0	21	18	T76103	Human beta tryptas
2	21	100.0	21	18	T76106	Human tryptase-I a
3	21	100.0	21	20	X53911	Human tryptase-I a
4	21	100.0	21	20	X53908	Human beta tryptas
5	21	100.0	21	21	F19473	Human beta tryptas
6	21	100.0	21	21	F19476	Human tryptase-I p
7	21	100.0	21	21	A33351	Low adenosine anti
8	21	100.0	21	21	A33354	Low adenosine anti
9	21	100.0	123	20	X54581	Human beta tryptas
10	21	100.0	123	21	F20150	Human beta tryptas
11	21	100.0	123	21	A34028	Human adenosine re

12	21	100.0	132	20	X54585	Human tryptase-I a
13	21	100.0	132	21	F20154	Human tryptase-I p
14	21	100.0	132	21	A34032	Human adenosine re
15	21	100.0	735	21	Z40172	Human beta-tryptas
16	21	100.0	771	21	Z40175	Human beta-tryptas
17	21	100.0	1081	19	V44331	Human mast cell tr
18	21	100.0	1081	19	V42713	Human mast cell tr
19	21	100.0	1081	21	F21082	Human low adenosin
20	21	100.0	1081	21	A34960	Human adenosine re
21	21	100.0	1128	19	V44330	Human mast cell tr
22	21	100.0	1128	19	V42712	Human mast cell tr
23	21	100.0	1137	19	V44329	Human mast cell tr
24	21	100.0	1137	19	V42711	Human mast cell tr
25	21	100.0	1137	21	F21079	Human low adenosin
26	21	100.0	1137	21	A34957	Human adenosine re
27	21	100.0	1143	21	F21077	Human low adenosin
28	21	100.0	1143	21	A34955	Human adenosine re
29	21	100.0	1145	21	F21078	Human low adenosin
30	21	100.0	1145	21	A34956	Human adenosine re
31	21	100.0	1154	19	V44328	Human mast cell tr
32	21	100.0	1154	19	V42710	Human mast cell tr
33	21	100.0	1154	21	F21081	Human low adenosin
34	21	100.0	1154	21	A34959	Human adenosine re
35	21	100.0	1121	20	Z41376	Human normal uteru
36	21	100.0	2197	21	F21080	Human low adenosin
37	21	100.0	2197	21	A34958	Human adenosine re
38	21	100.0	2218	20	V33911	Nucleotide sequenc
39	21	100.0	2259	20	V33910	Nucleotide sequenc
40	21	100.0	2280	21	F21083	Human low adenosin
41	21	100.0	2280	21	A34961	Human adenosine re
42	21	100.0	5441	21	F21074	Human low adenosin
43	21	100.0	5441	21	A34952	Human adenosine re
44	21	100.0	6225	20	X55273	Human enzyme-relat
45	21	100.0	6225	21	F20843	Human multiple tar

ALIGNMENTS

RESULT	1
ID	T76103 standard; DNA; 21 BP.
AC	T76103;
XX	
DT	12-SEP-1997 (first entry)
XX	
DE	Human beta tryptase antisense oligonucleotide HUMBTPTAS1.
KW	Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW	chronic obstructive pulmonary disease; bronchitis; ss.
XX	
OS	Synthetic.
XX	
PN	MO9640162-A1.
XX	
PD	19-DEC-1996.
XX	
PF	06-JUN-1996; 96WO-US09306.
XX	
PR	07-JUN-1995; 95US-0474497.
XX	
PA	(UYEC-) UNIV EAST CAROLINA.
XX	
PI	Metzger WJ, Nyce JW;
XX	
DR	WPI; 1997-051871/05.
XX	
PT	Treatment of airway diseases such as asthma - by topically applying
PT	adenosine-free antisense oligo:nucleotide to airway epithelium of
XX	subject
PS	Claim 5; Page 26; 71pp; English.

XX A method for treating airway disease in a subject has been produced.
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC HUMRRVASI specific for the human beta triptase. The method can be
CC used to treat airway diseases such as cystic fibrosis, asthma,
CC chronic obstructive pulmonary disease, bronchitis and other
CC airway diseases characterized by an inflammatory response. By
CC eliminating adenosine from the antisense ON, its liberation upon
CC antisense degradation is prevented, thereby preventing adenosine-
CC induced bronchoconstriction in patients with hyper-reactive airways.
SQ Sequence 21 BP: 0 A; 8 C; 7 G; 6 T; 0 other:

Query Match 100.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CPTGCTCTGGGGGCTCTCTG 21
1 cctgcctcctggggcctcctg 21

RESULT 2
T76106
ID T76106 standard; DNA; 21 BP.
XX
AC T76106;
XX
DT 12-SEP-1997 (first entry)
XX
DE Human triptase-I antisense oligonucleotide HUMRRVASI.
XX
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; ss.
XX
OS Synthetic.
XX
PN WO9640162-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09306.
XX
PR 07-JUN-1995; 95US-0474497.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Metzger WJ, Nyce JW;
XX
DR WPI; 1997-051871/05.
XX
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
XX
PS Claim 5; Page 26; 71pp; English.
XX
XX A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC HUMRRVASI specific for the human triptase-1. The method can be
CC used to treat airway diseases such as cystic fibrosis, asthma,
CC chronic obstructive pulmonary disease, bronchitis and other
CC airway diseases characterized by an inflammatory response. By
CC eliminating adenosine from the antisense ON, its liberation upon
CC antisense degradation is prevented, thereby preventing adenosine-
CC induced bronchoconstriction in patients with hyper-reactive airways.
SQ Sequence 21 BP: 0 A; 8 C; 7 G; 6 T; 0 other:

Query Match 100.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CPTGCTCTGGGGGCTCTCTG 21
1 cctgcctcctggggcctcctg 21

RESULT 3
X53911
ID X53911 standard; DNA; 21 BP.
XX
AC X53911;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human triptase-I antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;
KW Impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.

XX
OS Synthetic.
XX
PN WO9913886-A1.
XX
PD 25-MAR-1999.
XX
PF 17-SEP-1998; 98WO-US19419.
XX
PR 09-JUN-1998; 98US-0093972.
XX
PR 17-SEP-1997; 97US-0059160.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 1999-229400/19.
XX
PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
XX
PS Disclosure: Page 45; 120pp; English.

XX The specification describes antisense oligonucleotides (X52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences X55272-74. These multiple target
CC oligonucleotides (specifically X55180-271) can be used for the antisense
CC treatment of diseases and conditions. Typical diseases and conditions
CC are those associated with impaired respiration and inflammation,
CC including lung diseases, pulmonary vasoconstriction, inflammation,
CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC metastases, as well as all types of cancers which may metastasize or have

CC metastasized to the lungs, including breast and prostate cancer.
 XX Sequence 21 BP; 0 A; 8 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGCTCTGCGGCGCCCTCG 21
 |||
 Db 1 ctgctctcctggggccctccg 21

RESULT 4
 X53908
 ID X53908 standard; DNA; 21 BP.

AC X53908;

DT 05-JUL-1999 (first entry)

DE Human beta tryptase antisense oligonucleotide fragment.

KW Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.

XX Synthetic.

OS WO913886-A1.

PN 25-MAR-1999.

PF 17-SEP-1998; 98WO-US19419.

PR 09-JUN-1998; 98US-0093972.

PR 17-SEP-1997; 97US-0059160.

PA (UYEC-) UNIV EAST CAROLINA.

PI NYce JW;

PT WPI; 1999-229400/19.

DR New antisense oligonucleotides used in treatment of, e.g. pulmonary
 XX vasoconstriction
 XX

PS Disclosure; Page 45; 120pp; English.

CC The specification describes antisense oligonucleotides (X52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,

CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have
 CC metastasized to the lungs, including breast and prostate cancer.
 XX

SQ Sequence 21 BP; 0 A; 8 C; 7 G; 6 T; 0 other;

Query Match 100.0%; Score 21; DB 20; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGCTCTGCGGCGCCCTCG 21
 |||
 Db 1 ctgctctcctggggccctccg 21

RESULT 5
 F19473
 ID F19473 standard; DNA; 21 BP.

AC F19473;

DT 14-MAR-2001 (first entry)

DE Human beta tryptase polynucleotide fragment #1040.

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX Homo sapiens.

PN WO200062736-A2.

PD 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US08020.

PR 06-APR-1999; 99US-0127958.

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PI NYce JW;

PT WPI; 2000-679539/66.

DR Low adenosine (A) content antisense oligonucleotides which do not
 XX trigger adenosine receptors during metabolism, useful e.g. for treating
 XX cancers and respiratory obstructions -
 XX

PS Claim 14; Page 141; 1592pp; English.

CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and


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XX NYce JW;
PI
XX
XX WPI; 2000-205971/18.
DR
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
XX Claim 18; Page 395; 1343pp; English.
PS
XX
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytosstatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONS reduces side effects. The A-containing ONS break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 185, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33922) are specifically claimed ONS from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
CC
XX Sequence 21 BP; 0 A; 8 C; 7 G; 6 T; 0 other:
SO
Query Match 100.0%; Score 21; DB 21; Length 21;
Best local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTGCTCTGGGGGCTCTCG 21
1 cttgctctgggggctctcctg 21
DB
RESULT 8
A33354
ID A33354 standard; DNA; 21 BP.
XX
XX A33354;
AC
XX
XX 28-JUL-2000 (first entry)
DT
XX
XX Low adenosine antisense oligonucleotide SEQ ID NO:1043.
DE
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
OS
XX Homo sapiens.
XX
XX WO200009525-A2.
XX

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PD 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17712.
PF
XX
XX 03-AUG-1998; 98US-0095212.
PR
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX
XX NYce JW;
PI
XX
XX WPI; 2000-205971/18.
PS
XX
XX Claim 18; Page 395; 1343pp; English.
CC
XX
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytosstatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONS reduces side effects. The A-containing ONS break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 185, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33922) are specifically claimed ONS from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
CC
XX Sequence 21 BP; 0 A; 8 C; 7 G; 6 T; 0 other:
SO
Query Match 100.0%; Score 21; DB 21; Length 21;
Best local Similarity 100.0%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTGCTCTGGGGGCTCTCG 21
1 cttgctctgggggctctcctg 21
DB
RESULT 9
X54581
ID X54581 standard; DNA; 123 BP.
XX
XX X54581;
AC
XX
XX 05-JUL-1999 (first entry)
DT
XX
XX Human beta tryptase antisense oligonucleotide fragment.
DE
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impaired respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX

```

KM chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KM colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KM hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KM prostate cancer; ss.
 OS Synthetic.
 XX
 XX WO9913886-A1.
 PN
 XX
 XX 25-MAR-1999.
 PD
 XX
 XX 17-SEP-1998; 98WO-US19419.
 PF
 XX
 XX 09-JUN-1998; 98US-0093972.
 PR
 XX 17-SEP-1997; 97US-0059160.
 PA
 XX (UYEC-) UNIV EAST CAROLINA.
 PI
 XX Nyce JW;
 DR
 XX WPI: 1999-229400/19.
 PT
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 XX
 XX Disclosure: Page 45; 120pp; English.
 PS
 XX The specification describes antisense oligonucleotides (X52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the junction between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have
 CC metastasized to the lungs, including breast and prostate cancer.
 CC
 XX Sequence 123 BP; 0 A; 43 C; 49 G; 19 T; 12 other;
 SQ
 Query Match 100.0%; Score 21; DB 20; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGCTCTGGGGGCGCTCTG 21
 Db 1 cttgctcctgggggcctcctg 21
 RESULT 10
 F20150
 ID F20150 standard; DNA: 123 BP.
 XX
 AC F20150;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human beta tryptase polynucleotide fragment #1717.
 XX
 KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;

KM immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200062736-A2.
 PN
 XX
 XX 26-OCT-2000.
 PD
 XX
 XX 24-MAR-2000; 2000WO-US08020.
 PF
 XX
 XX 06-APR-1999; 99US-0127958.
 PR
 XX
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX (NYCE/) NYCE J W.
 PI
 XX Nyce JW;
 DR
 XX WPI: 2000-679539/66.
 PT
 XX
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Claim 14; Page 141; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 CC
 XX Sequence 123 BP; 0 A; 43 C; 49 G; 19 T; 12 other;
 SQ
 Query Match 100.0%; Score 21; DB 21; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGCTCTGGGGGCGCTCTG 21
 Db 1 cttgctcctgggggcctcctg 21

RESULT 11
 A34028 ID A34028 standard; DNA; 123 BP.
 XX
 AC A34028;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:1717.
 XX
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytosolic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 KW
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PI
 PY Nyce JW;
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 PS
 XX Disclosure; Page 478; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytosolic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A32313 to A35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
 CC to A33992) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 CC
 XX Sequence 123 BP; 0 A; 43 C; 49 G; 19 T; 12 other;

Query Match 100.0%; Score 21; DB 21; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGCTCCTGGGGGCTCCMG 21
 ||||||||||||||||||||
 Db 1 ctgcctccctg99g9cctccg 21
 RESULT 12
 X54585 ID X54585 standard; DNA; 132 BP.
 XX
 AC X54585;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human tryptase-I antisense oligonucleotide fragment.
 XX
 KW Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impaired respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 KW prostate cancer; ss.
 KW
 OS Synthetic.
 XX
 PN WO9913886-A1.
 XX
 PD 25-MAR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19419.
 XX
 PR 09-JUN-1998; 98US-0093972.
 PR 17-SEP-1997; 97US-0059160.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PI
 PY Nyce JW;
 DR WPI; 1999-229400/19.
 XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 PS
 XX Disclosure; Page 45; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (X52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impaired respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have
 CC metastasized to the lungs, including breast and prostate cancer.
 CC
 XX Sequence 132 BP; 0 A; 48 C; 48 G; 21 T; 15 other;

Query Match 100.0%; Score 21; DB 20; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGCGGGGCTCTCG 21
 |||
 Db 1 ctgtcctcctg99g9cctcctg 21

RESULT 13
 F20154
 ID F20154 standard; DNA; 132 BP.
 XX F20154;
 AC
 XX
 XX 14-MAR-2001 (first entry)
 DT
 XX
 XX Human trypsinase-I polynucleotide fragment #1721.
 DE
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KM immunosuppressive; antisthmatic; analgesic; hypotensive; cytosolic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 KM
 XX Homo sapiens.
 OS
 XX WO200062736-A2.
 PN
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US08020.
 PF
 XX 06-APR-1999; 99US-0127958.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 PI WPI: 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 XX Claim 14; Page 141; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antisthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with the lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors and vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction

CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.

SQ Sequence 132 BP; 0 A; 48 C; 48 G; 21 T; 15 other;

Query Match 100.0%; Score 21; DB 21; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGCGGGGCTCTCG 21
 |||
 Db 1 ctgtcctcctg99g9cctcctg 21

RESULT 14
 A34032
 ID A34032 standard; DNA; 132 BP.
 AC
 XX A34032;
 AC
 XX 28-JUL-2000 (first entry)
 DT
 XX
 XX Human adenosine receptor related polynucleotide seq ID NO:1721.
 DE
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KM phosphorothioate; impaired respiration; inflammation; allergy;
 KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KM antiallergic; antisthmatic; cytosolic; analgesic; impaired airway;
 KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 KM
 XX Homo sapiens.
 OS
 XX WO200009525-A2.
 PN
 XX 24-FEB-2000.
 PD
 XX 03-AUG-1999; 99WO-US17712.
 PF
 XX 03-AUG-1998; 98US-0095212.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA
 XX
 XX Nyce JW;
 PI WPI: 2000-205971/18.
 DR
 XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 XX Disclosure: Page 479; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antisthmatic, cytosolic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating

CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONS reduces side effects. The A-containing ONS break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A32313 to A35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
 CC to A33992) are specifically claimed ONS from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 XX
 SQ Sequence 132 BP; 0 A; 48 C; 48 G; 21 T; 15 other;

Query Match 100.0%; Score 21; DB 21; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGTGGGGCCCTCCTG 21
 ||||||||||||||||||
 DB 1 ctgtcctcctgtgggctcctg 21

RESULT 15
 240172/c
 ID 240172 standard; DNA; 735 BP.
 XX

AC 240172;

DT 18-FEB-2000 (first entry)

DE Human beta-tryptase coding sequence.

XX
 XX
 KM Beta-tryptase; human; DNA expression construct; protein production;
 KM combinatorial library screening; X ray crystallography; antigen;
 KM antibody generation; ss.
 XX
 OS Homo sapiens.
 XX

PN WO9960139-A1.

XX 25-NOV-1999.

PF 29-OCT-1998; 98WO-US22994.

XX 15-MAY-1998; 98US-0079970.

XX (PROM-) PROMEGA CORP.

PA Maffitt MA, Niles AL, Haak-Frendscho M;

XX WPI: 2000-053300/04.

DR P-PSDB; Y35010.

XX
 PT New DNA expression construct for production of enzymatically active
 PT recombinant human beta-tryptase -
 XX

PS Claim 4; Page 40-41; 50pp; English.

XX
 CC This sequence encodes the human beta-tryptase. The invention relates to a
 CC DNA expression construct comprising (5' to 3') a promoter linked to a
 CC signal sequence which is linked to a sequence encoding human
 CC beta-tryptase. The DNA construct is useful for transforming host cells to
 CC express, post translationally process and secrete enzymatically active
 CC human tryptase. The method is useful for the production of large amounts
 CC of tryptase with defined specifications. The transformant is useful for

CC pharmacological studies, combinatorial library screens and X ray
 CC crystallographic studies. The tryptase produced allows for the
 CC development of tryptase agonists and/or antagonists, is useful as an
 CC antigen to generate antihuman tryptase antibodies in various animals,
 CC can be used in screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists etc. and to assay for the presence of tryptase in
 CC biological or other solutions. Tryptase inhibitors, antagonists, agonists
 CC etc. may be useful as therapeutics. The tryptase does not require any
 CC post-expression or post-purification modifications or manipulations to
 CC initiate tryptase activity and it has enzymatic activity which compares
 CC favourably with cadaveric tryptase. The availability of enzymatically
 CC active tryptase facilitates the large scale screening of combinatorial
 CC libraries for specific tryptase inhibitors as potential therapeutics and
 CC advances the understanding of the biological significance of tryptase in
 CC mast cell mediated diseases. The tryptase can be used to detect low
 CC levels of tryptase.
 XX

SQ Sequence 735 BP; 141 A; 245 C; 229 G; 120 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ||||||||||||||||||
 DB 33 CTTGCTCTGTGGGGCCCTCCTG 13

Search completed: April 20, 2001, 00:12:52
 Job time: 10014 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:24:52 ; Search time 7150.85 Seconds
(without alignments)
0.429 Million cell updates/sec

Title: US-09-016-464-15
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4	18	85.7	263	147	BF356271	BF356271 RC4-HT088
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6	17.8	84.8	481	2	AA087428	AA087428 mn96q09.r
7	17.8	84.8	514	170	BF890958	BF890958 PM3-MT011
8	17.8	84.8	517	216	AZ084692	AZ084692 RPCI-23-3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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RESULT 1
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DEFINITION yf28e04.r1 Soares fetal liver spleen INFUS Homo sapiens CDNA clone
IMAGE:128190 5' similar to gb:s55551 BETA-TYRPTASE PRECURSOR (HUMAN
); mRNA sequence.
ACCESSION R09803
VERSION R09803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 351)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108.
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1273
High quality sequence stops: 115 Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: M13RPI
High quality sequence stop: 115.
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BASE COUNT

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61 a 110 c 106 g 68 t 6 others

```

Query Match

```

Best Local Similarity 100.0%; Score 21; DB 155; Length 351;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 CTTCGCTCTGGGGCCTCCTG 21
|||||
Db 120 CTTCGCTCTGGGGCCTCCTG 100

```

```

RESULT 2
LOCUS BF724180/c 512 bp mRNA EST 05-JAN-2001
DEFINITION bx01h02.y2 Human Iris cDNA (Un-normalized, unamplified): Bx Homo
sapiens cDNA clone bx01h02 5', mRNA sequence.
ACCESSION BF724180
VERSION BF724180
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 512)
AUTHORS Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
JOURNAL NEI/NIH: EST analysis and bioinformatics for ocular genomics
JOURNAL Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gja@nei.nih.gov
Plate: 01 row: h column: 02
Seq primer: M13RPI reverse primer (ABI).

```

FEATURES

```

source
1..512
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="bx01h02"
/clone_1ib="Human Iris cDNA (Un-normalized, unamplified):
Bx"
/tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMD10B"
/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem Iris
tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pCMVSPORT6 vector
was constructed at Life Technologies, essentially
following the protocols of the SuperScript Plasmid System
full details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor [5'-pGACTAGTCTAGATGACGAGCGCGCC(T)15-3'
]. Not I/blunt end inserts were cloned into the Not I/EcoR
v sites in the vector. EST analysis was performed on the
unamplified library at the NIH Intramural Sequencing

```

```

BASE COUNT      83 a      176 c      167 g      84 t      2 others
ORIGIN

Query Match      100.0%; Score 21; DB 168; Length 512;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCGCTCTG 21
|||||
Db 130 CTTGCTCTGGGGGCGCTCTG 110

RESULT 3
AA463316      431 bp      mRNA      EST      10-JUN-1997
LOCUS      zx71e05.r1 Soares,local_fetus_Nb2HF8_9w Homo sapiens cDNA clone
DEFINITION      IMAGE:796928 5', mRNA sequence.
ACCESSION      AA463316
VERSION      AA463316.1 GI:2188200
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 431)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Getzel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Stepien,M., Tan,F., Theisling,B., White,Y., Wyllie,
T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from AmerSham.
FEATURES
source
1..431
/organism="Homo sapiens"
/db_xref="GeneBank:6041597"
/db_xref="taxon:9606"
/clone_1fb="IMAGE:796928"
/clone_1fb="Soares,local_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACATCTGAGTGGAGCGGCGCTTAAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      91 a      133 c      130 g      77 t
ORIGIN

Query Match      87.6%; Score 18.4; DB 7; Length 431;
Best Local Similarity 95.0%; Pred. No. 5.5e+02;
Matches 19: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGCTCTCTGGGGCGCTCTG 21
|||||
Db 329 TTGCTCTCTGGGGCGCTCTG 348

```

```

RESULT 4
BF356271/c      263 bp      mRNA      EST      22-NOV-2000
LOCUS      RC4-HT0888-250800-011-e08_1 HT0888 Homo sapiens cDNA, mRNA
DEFINITION      sequence.
ACCESSION      BF356271
VERSION      BF356271.1 GI:11315345
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 263)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC4t2-RC4-HT0888-
250800-011-e08_1et3-2000-08-25et4=1)
Seq primer: puc 18 forward
High quality sequence stop: 176.
FEATURES
source
1..263
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1fb="HT0888"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      65 a      91 c      75 g      32 t
ORIGIN

Query Match      85.7%; Score 18; DB 147; Length 263;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGCTCTCTGGGGCGCTCTG 19
|||||
Db 184 TTGCTCTCTGGGGCGCTCTG 167

RESULT 5
AZ079087/c      400 bp      DNA      GSS      31-MAR-2000
LOCUS      RPCT-23-400C11.T1B RPCT-23 Mus musculus genomic clone
DEFINITION      RPCT-23-400C11, DNA sequence.
ACCESSION      AZ079087
VERSION      AZ079087.1 GI:7371986
KEYWORDS      GSS.
SOURCE      house mouse.

```

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 400)

AUTHORS Zhao, S., Nieman, W., Feldblyum, T., Malek, J., Shatsman, S., Akınret, B., Levins, M., Megam, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C. M.

TITLE Mouse BAC End Sequences from Library RPCI-23

JOURNAL Unpublished (1999)

COMMENT Other GSSs: RPCI-23-400C11.TVB

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@edj.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (inforesgen.com). BAC end page: http://www.tigr.org/cdb/bac-ends/mouse/bac_end_intro.html

Plate: 400 row: C column: 11

Seq primer: Sp6

Class: BAC ends.

FEATURES

source Location/Qualifiers

1. 400

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-400C11"

/clone_lib="RPCI-23"

/sex="Female"

/lab_host="DH10B"

/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1: EcoRI; Site: 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 86 a 136 c 110 g 68 t

ORIGIN

Query Match 84.8%; Score 17.8; DB 215; Length 400;

Best Local Similarity 90.5%; Pred. No. 9.9e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGCTCCTGGGGGCGCTCG 21

1 | | | | | | | | | | | | | | | |

Db 283 CTTGCTCCTGGTGGCTCTCG 263

RESULT 6

LOCUS AA087428 481 bp mRNA EST 15-FEB-1997

DEFINITION mn96g09.r1 Strata gene mouse lung 937302 Mus musculus CDNA clone

IMAGE:551968 5', mRNA sequence.

ACCESSION AA087428

VERSION AA087428.1 GI:1630669

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 481)

AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HHMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through INL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:332760

Seq primer: -28m3 rev1 ET from Amersham

High quality sequence stop: 394.

FEATURES

source Location/Qualifiers

1. 481

/organism="Mus musculus"

/strain="C57BL/6 x CBA"

/db_xref="taxon:10090"

/clone="IMAGE:551968"

/clone_lib="Stratagene mouse lung 937302"

/sex="female"

/tissue_type="lung"

/dev_stage="6-8 month old"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: lung; Vector: pBluescript SK-; Site: 1: EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. 6-8 month old female lung and 1.5 year old male lung were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GATTTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGT 3'."

BASE COUNT 67 a 163 c 126 g 124 t 1 others

ORIGIN

Query Match 84.8%; Score 17.8; DB 2; Length 481;

Best Local Similarity 90.5%; Pred. No. 9.9e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGCTCCTGGGGGCGCTCG 21

1 | | | | | | | | | | | | | | | |

Db 439 CTTGCTCCTGGTGGCTCTCG 459

RESULT 7

LOCUS BF890958 514 bp mRNA EST 18-JAN-2001

DEFINITION PM3-MT0110-151000-004-c09 MT0110 Homo sapiens CDNA, mRNA sequence.

ACCESSION BF890958

VERSION BF890958.1 GI:12282417

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 514)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

OY 1 CTTGCTCTCTGGGGGCTCTCTG 21
||||| ||||||| |||||||
Db 237 CTTGCCCTCTGGGGTCTCTG 257

RESULT 10
BF891052 526 bp mRNA EST 18-JAN-2001
LOCUS PM3-MT0110-181000-003-f02 MT0110 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF891052
ACCESSION BF891052.1 GI:12282511
VERSION BF891052.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 526)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&cl2=PM3-MT0110-
181000-003-f02&cl3=2000-10-18&cl4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 526.
Location/Qualifiers
1..526
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MT0110"
/dev_stage="Adult"
/note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORSTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 105 a 158 c 116 g 147 t

ORIGIN

Query Match 84.8%; Score 17.8; DB 170; Length 526;
Best Local Similarity 90.5%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTTGCTCTCTGGGGGCTCTG 21
||||| ||||||| |||||||
Db 264 CTTGCAGCTGGGGCTCTCTG 284

RESULT 11
BE380256 626 bp mRNA EST 21-JUL-2000
LOCUS 601270206F1 NCI_CGAP_Mam1 Mus musculus cDNA IMAGE:359736 5',
DEFINITION

ACCESSION mRNA sequence.
BE380256
VERSION BE380256.1 GI:9325530
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 626)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM8782 row: k column: 01
High quality sequence stop: 533.
Location/Qualifiers
1..626
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="IMAGE:359736"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 89 a 219 c 162 g 156 t

ORIGIN

Query Match 84.8%; Score 17.8; DB 166; Length 626;
Best Local Similarity 90.5%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CTTGCTCTCTGGGGGCTCTG 21
||||| ||||||| |||||||
Db 410 CTTGCTCTCTGGGGGCTCTG 430

RESULT 12
BF782735 669 bp mRNA EST 12-JAN-2001
LOCUS 602107582F1 NCI_CGAP_Ki414 Mus musculus cDNA clone IMAGE:4235853
DEFINITION 5', mRNA sequence.
ACCESSION BF782735
VERSION BF782735.1 GI:12087771
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 669)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 856)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9853 row: a column: 24

High quality sequence stop: 651.

FEATURES

source

Location/Qualifiers

1..856

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4239647"

/lab_host="NCI_CGAP_Kid14"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library. |"

BASE COUNT

144 a

278 c

213 g

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

221 t

Query Match

84.8%; Score 17.8; DB 169; Length 856;

Best Local Similarity 90.5%; Pred. No. 1e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGCTCCTGGGGCCCTCG 21

Db 271 CTTGCTCCTGGGGCCCTCG 291

Search completed: April 19, 2001, 23:24:52
Job time: 8169 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:38 ; Search time 280.46 Seconds
(without alignments)
13.074 Million cell updates/sec

Title: US-09-016-464-15

Perfect score: 21
Sequence: 1 CTGCTCTGCGGCGCTCTG 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_MA:*

1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	100.0	1081	2	US-09-016-366A-22 Sequence 22, Appl
C 2	21	100.0	1081	2	US-08-978-404B-17 Sequence 17, Appl
C 3	21	100.0	1128	2	US-09-016-366A-20 Sequence 20, Appl
C 4	21	100.0	1128	2	US-08-978-404B-15 Sequence 15, Appl
C 5	21	100.0	1137	2	US-09-016-366A-18 Sequence 18, Appl
C 6	21	100.0	1137	2	US-08-978-404B-13 Sequence 13, Appl
C 7	21	100.0	1154	2	US-09-016-366A-16 Sequence 16, Appl
C 8	21	100.0	1154	2	US-08-978-404B-11 Sequence 11, Appl
C 9	21	100.0	2218	4	US-08-845-998-5 Sequence 5, Appl
C 10	21	100.0	2218	4	US-09-206-537-5 Sequence 5, Appl
C 11	21	100.0	2259	2	US-08-845-998-3 Sequence 3, Appl
C 12	21	100.0	2259	4	US-09-206-537-3 Sequence 3, Appl
C 13	17.4	82.9	7785	2	US-08-276-967-1 Sequence 1, Appl
C 14	16.4	78.1	176373	4	US-09-128-155-17 Sequence 17, Appl
C 15	16.2	77.1	1279	4	US-08-985-950-5 Sequence 5, Appl
C 16	16.2	77.1	1728	4	US-08-985-950-7 Sequence 7, Appl
C 17	16.2	77.1	1863	2	US-08-455-073A-3 Sequence 3, Appl
C 18	16.2	77.1	2730	3	US-08-936-135-17 Sequence 17, Appl
C 19	16.2	77.1	2781	3	US-08-936-135-19 Sequence 19, Appl
C 20	15.8	75.2	849	3	US-08-807-300-2 Sequence 2, Appl
C 21	15.8	75.2	1308	1	US-08-494-577-1 Sequence 1, Appl
C 22	15.8	75.2	1308	1	US-08-795-868-1 Sequence 1, Appl
C 23	15.8	75.2	2614	2	US-08-795-868-15 Sequence 15, Appl
C 24	15.8	75.2	38506	4	US-09-320-878-19 Sequence 19, Appl
C 25	15.8	75.2	176373	4	US-09-128-155-17 Sequence 17, Appl
C 26	15.2	72.4	87	1	US-08-433-126A-166 Sequence 166, App
C 27	15.2	72.4	87	1	US-08-433-124A-166 Sequence 166, App

28	15.2	72.4	87	4	US-08-976-413A-166 Sequence 166, App
29	15.2	72.4	87	5	PCR-US96-06059-166 Sequence 166, App
C 30	15.2	72.4	1457	1	US-08-233-389C-2 Sequence 2, Appl
C 31	15.2	72.4	1457	2	US-08-801-863-2 Sequence 2, Appl
C 32	15.2	72.4	1457	2	US-08-486-596A-2 Sequence 2, Appl
C 33	15.2	72.4	1457	2	US-09-004-713-2 Sequence 2, Appl
C 34	15.2	72.4	1894	3	US-07-728-220C-1 Sequence 1, Appl
C 35	15.2	72.4	2542	4	US-08-941-445A-6 Sequence 6, Appl
C 36	15.2	72.4	2658	2	US-08-592-383-3 Sequence 3, Appl
37	15.2	72.4	2928	2	US-08-095-728B-3 Sequence 3, Appl
38	15.2	72.4	2928	5	PCR-US92-02320A-3 Sequence 3, Appl
39	15.2	72.4	2940	2	US-08-592-383-1 Sequence 1, Appl
40	15.2	72.4	2940	6	5171671-1 Patent No. 5171671
41	15.2	72.4	3036	1	US-08-306-691B-52 Sequence 52, Appl
42	15.2	72.4	3036	2	US-08-095-728B-1 Sequence 1, Appl
43	15.2	72.4	3036	5	PCR-US92-02320A-1 Sequence 1, Appl
44	15.2	72.4	3511	3	US-08-892-747-13 Sequence 13, Appl
C 45	15.2	72.4	4131	3	US-08-353-784-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-016-366A-22/c
Sequence 22, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEINASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
STRANDEDNESS: single
MOLECULE TYPE: cDNA
US-09-016-366A-22
Query Match 100.0%, Score 21: DB 2: Length 1081:
Best Local Similarity 100.0%, Pred. No. 0.68:
Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-15

Query Match 100.0%; Score 21; DB 2; Length 1128;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCTGGGGGCTCTG 21
|||||
Db 121 CTGCTCTGGGGGCTCTG 101

RESULT 5
US-09-016-366A-18/c
Sequence 18, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-016-366A-18

Query Match 100.0%; Score 21; DB 2; Length 1137;
Best Local Similarity 100.0%; Pred. No. 0.68;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCTCTGGGGGCTCTG 21
|||||
Db 119 CTGCTCTGGGGGCTCTG 99

RESULT 6
US-08-978-404B-13/c
Sequence 13, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-13

Query Match 100.0%; Score 21; DB 2; Length 1137;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCTGGGGGCTCTG 21
|||||
Db 119 CTGCTCTGGGGGCTCTG 99

RESULT 7
US-09-016-366A-16/c
Sequence 16, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-016-366A-16

Query Match 100.0%; Score 21; DB 2; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCTG 21
|||||
DB 140 CTTGCTCTGGGGGCTCTCTG 120

RESULT 8
US-08-978-404B-11/C
Sequence 11, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-11

NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-11

Query Match 100.0%; Score 21; DB 2; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCTG 21
|||||
DB 140 CTTGCTCTGGGGGCTCTCTG 120

RESULT 9
US-08-845-998-5/C
Sequence 5, Application US/08845998
Patent No. 5879892
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulle, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2218 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: NVB352/3
FEATURE:
NAME/KEY: CDS

LOCATION: 8..577
US-08-845-998-5

Query Match 100.0%; Score 21; DB 2; Length 2218;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGGGCTCCTG 21
Db 130 CTTGCTCTGCGGGGCTCCTG 110

RESULT 10
US-09-206-537-5/C
Sequence 5, Application US/09206537
Patent No. 6130052
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,537
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2218 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: NVB352/3
FEATURE:
NAME/KEY: CDS
LOCATION: 8..577
US-09-206-537-5

Query Match 100.0%; Score 21; DB 4; Length 2218;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGGGCTCCTG 21

Db 130 CTTGCTCTGCGGGGCTCCTG 110

RESULT 11
US-08-845-998-3/C
Sequence 3, Application US/08845998
Patent No. 5879892
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 8..577
US-08-845-998-3

Query Match 100.0%; Score 21; DB 2; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGCGGGGCTCCTG 21
Db 130 CTTGCTCTGCGGGGCTCCTG 110

RESULT 12
US-09-206-537-3/C
Sequence 3, Application US/09206537
Patent No. 6130052
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry

TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 8..577
US-09-206-537-3

Query Match 100.0%; Score 21; DB 4; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGCCTCTG 21
|||||
Db 130 CTTGCTCTGGGGCCTCTG 110

RESULT 13
US-08-276-967-1
Sequence 1, Application US/08276967
Patent No. 5851817
GENERAL INFORMATION:
APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
TITLE OF INVENTION: Sperm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:418\KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7785 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-276-967-1

Query Match 82.9%; Score 17.4; DB 2; Length 7785;
Best Local Similarity 94.7%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGGCTCTGGGGCCTCTG 21
|||
Db 4337 TGGCCTCTGGGGCCTCTG 4355

RESULT 14
US-09-128-155-17
Sequence 17, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 78.1%; Score 16.4; DB 4; Length 176373;
Best Local Similarity 94.4%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCTCTGGGGCCTCTG 21
|||||
Db 156949 gtcctcggggcctcctg 156966

RESULT 15
US-08-985-950-5/c
Sequence 5, Application US/08985950
Patent No. 6140076


```

GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1279 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 155..1015
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1247
OTHER INFORMATION: /note="nucleotide 1247 designated
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 218..1015
US-08-985-950-5

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Query Match	77.1%	Score 16.2	DB 4	Length 1279
Best Local Similarity	85.7%	Pred. No. 71		
Matches	18	Conservative	0	Mismatches 3; Indels 0; Gaps 0.
OY	1	CTTGCTCTGGGGCCCTCCTG	21	
db	754	CTTGCTCTGGGGCCCTCCTG	734	

Search completed: April 20, 2001, 00:03:42
Job time: 9679 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 03:21:19 ; Search time 1165 Seconds

(without alignments)
9.793 Million cell updates/sec

Title: US-09-016-464-15

Perfect score: 21

Sequence: 1 CTGCTCTGGGGCCCTCTG 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1316883 seqs, 2603265903 residues 26337766

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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42: /cgn2_6/ptodata/2/pna/US0812_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	US-08-474-497-14	Sequence 14, Appl
2	21	100.0	21	US-08-474-497-15	Sequence 15, Appl
3	21	100.0	21	US-09-016-464-14	Sequence 14, Appl
4	21	100.0	21	US-09-016-464-15	Sequence 15, Appl
5	21	100.0	21	US-09-509-152A-104	Sequence 1040, Ap
6	21	100.0	21	US-09-509-152A-104	Sequence 1043, Ap
7	21	100.0	21	US-09-509-152A-104	Sequence 1043, Ap
8	21	100.0	132	US-09-509-152A-171	Sequence 1717, Ap
9	21	100.0	132	US-09-509-152A-171	Sequence 1721, Ap
10	21	100.0	219	US-09-652-814-6418	Sequence 6418, Ap
11	21	100.0	253	US-09-535-896-32649	Sequence 32649, A
12	21	100.0	268	US-09-721-589-4001	Sequence 4001, Ap
13	21	100.0	310	US-60-213-800-537	Sequence 537, Ap
14	21	100.0	362	US-09-652-814-4508	Sequence 4508, Ap
15	21	100.0	383	US-09-235-076-6378	Sequence 6378, Ap
16	21	100.0	383	US-09-248-797-22402	Sequence 22402, A
17	21	100.0	383	US-09-332-782-6378	Sequence 6378, Ap
18	21	100.0	402	US-09-528-409-61113	Sequence 61113, A
19	21	100.0	415	US-09-293-972-32519	Sequence 32519, A
20	21	100.0	424	US-60-213-172-344	Sequence 344, Ap
21	21	100.0	424	US-60-213-172-344	Sequence 344, Ap
22	21	100.0	430	US-09-332-782-5548	Sequence 5548, Ap
23	21	100.0	430	US-09-515-694-5548	Sequence 5548, Ap
24	21	100.0	436	US-09-640-161-6734	Sequence 6734, Ap
25	21	100.0	439	US-60-213-800-59	Sequence 99, Appl
26	21	100.0	441	US-09-652-127-295	Sequence 295, Appl
27	21	100.0	454	US-09-528-409-70936	Sequence 70936, A
28	21	100.0	462	US-09-528-409-69188	Sequence 69188, A
29	21	100.0	462	US-09-516-092-113	Sequence 113, Appl
30	21	100.0	469	US-09-652-814-3761	Sequence 3761, Appl
31	21	100.0	480	US-09-248-797-21458	Sequence 21458, A
32	21	100.0	480	US-09-346-956-7982	Sequence 7982, Ap
33	21	100.0	485	US-09-528-409-71480	Sequence 71480, A
34	21	100.0	486	US-09-721-589-2368	Sequence 2368, Ap
35	21	100.0	487	US-09-234-611-19715	Sequence 19715, A
36	21	100.0	487	US-09-277-227-10408	Sequence 10408, A
37	21	100.0	487	US-09-640-161-2506	Sequence 2506, Ap
38	21	100.0	497	US-09-535-896-32605	Sequence 32605, A
39	21	100.0	560	US-09-577-410-192	Sequence 192, Appl
40	21	100.0	578	US-09-726-176-701	Sequence 701, Appl
41	21	100.0	595	US-09-736-119-663	Sequence 263, Appl
42	21	100.0	599	US-60-196-715-1	Sequence 1, Appl
43	21	100.0	599	US-60-196-718-49	Sequence 49, Appl
44	21	100.0	599	US-60-196-718-1809	Sequence 1809, Ap
45	21	100.0	600	US-60-196-718-1810	Sequence 1810, Ap
			600	US-60-196-718-1876	Sequence 1876, Ap

ALIGNMENTS

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RESULT 1
US-08-474-497-14
; Sequence 14, Application US/08474497
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,497
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-497-14

Query Match          100.0%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCGTGGGGCCTCTG 21
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DB 1 CTTGCTCTGGGGCCTCTG 21

RESULT 2
US-08-474-497-15
; Sequence 15, Application US/08474497
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
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SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,497
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-474-497-15

Query Match          100.0%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCTCTGGGGCCTCTG 21
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DB 1 CTTGCTCTGGGGCCTCTG 21

RESULT 3
US-09-016-464-14
; Sequence 14, Application US/09016464
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,464
; FILING DATE: 30-Jan-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,497
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-016-464-14

Query Match 100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCCTGGGGGCTCTG 21
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DB 1 CTTGCTCCTGGGGGCTCTG 21

RESULT 4
US-09-016-464-15

Sequence 15, Application US/09016464
GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: Method of Treatment of Lung Diseases
Using Antisense Oligonucleotides

NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Kenneth D. Sibley
STREET: Post Office Drawer 34009
CITY: Charlotte

STATE: NC
COUNTRY: USA

ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,464

FILING DATE: 30-Jan-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/474,497

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sibley, Kenneth D.

REGISTRATION NUMBER: 31,665

REFERENCE/DOCKET NUMBER: 5218-32

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 881-3140

TELEFAX: (919) 881-3175

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-016-464-15

Query Match 100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
DB 1 CTTGCTCCTGGGGGCTCTG 21

RESULT 5
US-09-509-152A-1040

Sequence 1040, Application US/09509152A
GENERAL INFORMATION:

APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS

NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESSES:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE

CITY: CRANBURY
STATE: NJ
COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/509,152A

FILING DATE: 17-Mar-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/059,160

FILING DATE: 1997-09-17

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-00991

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

INFORMATION FOR SEQ ID NO: 1040:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1040:

US-09-509-152A-1040

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Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTTGCTCCTGGGGGCTCTG 21

RESULT 6
US-09-509-152A-1043

Sequence 1043, Application US/09509152A
GENERAL INFORMATION:

APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS

NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESSES:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE

CITY: CRANBURY
STATE: NJ
COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/509,152A

FILING DATE: 17-Mar-2000

CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1043:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1043:
US-09-509-152A-1043

Query Match 100.0%; Score 21; DB 19; Length 21;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTG 21
|||||

DB 1 CTTGCTCTGGGGGCTCTG 21

RESULT 7
US-09-509-152A-1717
Sequence 1717, Application US/09509152A
GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1717:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1717:

US-09-509-152A-1717

Query Match 100.0%; Score 21; DB 19; Length 123;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTG 21
|||||

DB 1 CTTGCTCTGGGGGCTCTG 21

RESULT 8
US-09-509-152A-1721
Sequence 1721, Application US/09509152A
GENERAL INFORMATION:
APPLICANT: NYCE, JONATHAN W.
TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
FORMULATIONS, KITS & APPLICATIONS
NUMBER OF SEQUENCES: 2419
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 CLARKE DRIVE
CITY: CRANBURY
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/509,152A
FILING DATE: 17-Mar-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 1721:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1721:
US-09-509-152A-1721

Query Match 100.0%; Score 21; DB 19; Length 132;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTG 21
|||||

DB 1 CTTGCTCTGGGGGCTCTG 21

RESULT 9
US-09-652-814-6418/C
Sequence 6418, Application US/09652814
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
THEREFOR

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; FILE REFERENCE: 1600.1191-001
; CURRENT APPLICATION NUMBER: US/09/652,814
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,109
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 10797
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 6418
; LENGTH: 219
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-814-6418
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Query Match          100.0%; Score 21; DB 25; Length 219;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTTGCTCTGGGGGCGCTCCTG 21
    |||
Db 165 CTTGCTCTGGGGGCGCTCCTG 145
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RESULT 10
US-09-535-896-32649/C
; Sequence 32649, Application US/09535896
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullaly, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING HYDROLASES
; FILE REFERENCE: PD-1003 CIP
; CURRENT APPLICATION NUMBER: US/09/535,896
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 46268
; SOFTWARE: PERL Program
; SEQ ID NO 32649
; LENGTH: 253
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: hu01313433
; NAME/KEY: unsure
; LOCATION: 13, 33, 35, 39, 73, 118
; OTHER INFORMATION: a, t, c, g, or other
US-09-535-896-32649
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```
Query Match          100.0%; Score 21; DB 20; Length 253;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTTGCTCTGGGGGCGCTCCTG 21
    |||
Db 95 CTTGCTCTGGGGGCGCTCCTG 75
```

```
RESULT 11
US-09-721-589-4001/C
; Sequence 4001, Application US/09721589
; GENERAL INFORMATION:
; APPLICANT: Gealing, David P.
; APPLICANT: Villeva, Jean-Luc
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2045-001
; CURRENT APPLICATION NUMBER: US/09/721,589
; CURRENT FILING DATE: 2000-11-22
```

```
; PRIOR APPLICATION NUMBER: 60/167,380
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 7017
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4001
; LENGTH: 268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(268)
; OTHER INFORMATION: n = A,T,C or G
US-09-721-589-4001
```

```
Query Match          100.0%; Score 21; DB 29; Length 268;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTTGCTCTGGGGGCGCTCCTG 21
    |||
Db 141 CTTGCTCTGGGGGCGCTCCTG 121
```

```
RESULT 12
US-60-213-800-537/C
; Sequence 537, Application US/60213800
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000707
; CURRENT APPLICATION NUMBER: US/60/213,800
; CURRENT FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 657
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 537
; LENGTH: 310
; TYPE: DNA
; ORGANISM: HUMAN
US-60-213-800-537
```

```
Query Match          100.0%; Score 21; DB 53; Length 310;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTTGCTCTGGGGGCGCTCCTG 21
    |||
Db 174 CTTGCTCTGGGGGCGCTCCTG 154
```

```
RESULT 13
US-09-652-814-4508/C
; Sequence 4508, Application US/09652814
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1191-001
; CURRENT APPLICATION NUMBER: US/09/652,814
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,109
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 10797
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4508
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-814-4508
```

Query Match 100.0%; Score 21; DB 25; Length 362;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGCTCCTGGGGGCGCTCCTG 21
 |||||
 Db 351 CTGCTCCTGGGGGCGCTCCTG 331

RESULT 14
 US-09-235-076-6378/c

; Sequence 6378, Application US/09235076
 ; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 2041-756
 ; CURRENT APPLICATION NUMBER: US/09/235,076
 ; CURRENT FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 6378
 ; LENGTH: 383
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-235-076-6378

Query Match 100.0%; Score 21; DB 16; Length 383;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGCTCCTGGGGGCGCTCCTG 21
 |||||
 Db 135 CTGCTCCTGGGGGCGCTCCTG 115

RESULT 15

US-09-248-797-22402/c
 ; Sequence 22402, Application US/09248797

; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 2041-764
 ; CURRENT APPLICATION NUMBER: US/09/248,797
 ; CURRENT FILING DATE: 1999-02-12
 ; NUMBER OF SEQ ID NOS: 48909
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO: 22402
 ; LENGTH: 383
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-248-797-22402

Query Match 100.0%; Score 21; DB 16; Length 383;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGCTCCTGGGGGCGCTCCTG 21
 |||||
 Db 135 CTGCTCCTGGGGGCGCTCCTG 115

Search completed: April 20, 2001, 03:21:20
 Job time: 14167 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:15:26 ; Search time 101.94 seconds
(without alignments)
28.506 Million cell updates/sec

Title: US-09-016-464-15

Perfect score: 21
Sequence: 1 CTGCTCCTGGGGCCTCTG 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 46985 segs, 69187998 residues

Total number of hits satisfying chosen parameters: 93970

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New.*
1: /cgn2_6/ptodata/1/pna/PCF_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	21	US-09-543-679A-1040	Sequence 1040, Ap
2	21	100.0	21	US-09-543-679A-1043	Sequence 1043, Ap
3	21	100.0	123	US-09-543-679A-1717	Sequence 1717, Ap
4	21	100.0	132	US-09-543-679A-1721	Sequence 1721, Ap
5	21	100.0	1081	US-09-543-679A-2649	Sequence 2649, Ap
6	21	100.0	1137	US-09-543-679A-2646	Sequence 2646, Ap
7	21	100.0	1143	US-09-543-679A-2644	Sequence 2644, Ap
8	21	100.0	1145	US-09-543-679A-2645	Sequence 2645, Ap
9	21	100.0	1154	US-09-543-679A-2648	Sequence 2648, Ap
10	21	100.0	2197	US-09-543-679A-2647	Sequence 2647, Ap
11	21	100.0	2280	US-09-543-679A-2650	Sequence 2650, Ap
12	21	100.0	5441	US-09-543-679A-2641	Sequence 2641, Ap
13	21	100.0	6225	US-09-543-679A-2651	Sequence 2651, Ap
14	21	100.0	17133	US-09-543-679A-3003	Sequence 3003, Ap
15	21	100.0	35459	US-09-543-679A-1381	Sequence 1381, Ap
16	18.4	87.6	368	US-09-543-679A-2642	Sequence 2642, Ap
17	18	85.7	388	US-09-543-679A-1722	Sequence 1722, Ap
18	17	81.0	17	US-09-543-679A-505-20	Sequence 20, Appl
19	16.2	77.1	87137	US-08-276-1630-14804	Sequence 14804, A
20	15.8	75.2	499	US-09-543-679A-1800	Sequence 1800, Ap
21	15.4	73.3	105472	US-09-543-679A-1900	Sequence 1900, Ap
22	15.2	72.4	23	US-09-543-679A-4507	Sequence 4507, Ap
23	15.2	72.4	567	US-09-543-679A-3015	Sequence 3015, Ap
24	15.2	72.4	903	US-09-543-679A-3015	Sequence 3015, Ap
25	15.2	72.4	8124	US-09-543-679A-3015	Sequence 3015, Ap
26	15.2	72.4	9372	US-09-543-679A-3015	Sequence 3015, Ap
27	15.2	72.4	9372	US-09-543-679A-3015	Sequence 3015, Ap

28	15.2	72.4	24057	6	US-60-248-505-408	Sequence 408, App
29	15.2	72.4	24990	6	US-60-248-505-467	Sequence 467, App
30	15.2	72.4	35459	5	US-09-543-679A-3003	Sequence 3003, App
31	15.2	72.4	63957	5	US-09-543-679A-196	Sequence 196, App
32	15.2	72.4	84633	6	US-60-248-505-177	Sequence 177, App
33	15	71.4	312	4	US-08-276-1630-3491	Sequence 5491, App
34	14.8	70.5	255	4	US-08-276-1630-12158	Sequence 12158, A
35	14.8	70.5	315	5	US-09-739-449-1215	Sequence 1215, App
36	14.8	70.5	491	4	US-08-276-1630-11991	Sequence 11991, A
37	14.8	70.5	503	4	US-08-276-1630-12101	Sequence 12101, A
38	14.8	70.5	2245	5	US-09-543-679A-2971	Sequence 2971, App
39	14.8	70.5	31071	6	US-60-248-505-588	Sequence 588, App
40	14.8	70.5	32199	1	PCT-US01-01350-210	Sequence 210, App
41	14.8	70.5	38644	5	US-09-543-679A-2991	Sequence 2991, App
42	14.8	70.5	54477	6	US-60-248-505-143	Sequence 143, App
43	14.8	70.5	79470	6	US-60-248-505-175	Sequence 175, App
44	14.8	70.5	92585	6	US-60-248-505-383	Sequence 383, App
45	14.8	70.5	169998	5	US-09-676-610A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-543-679A-1040
Sequence 1040, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-06-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1040:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1040:
US-09-543-679A-1040
Query Match 100.0%; Score 21; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
;   NAME: Amzel, Viviana
;   REGISTRATION NUMBER: 30,930
;   REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 609-409-3035
;   TELEFAX: 413-254-9245
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1721:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 132 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1721:
US-09-543-679A-1721

Query Match          100.0%; Score 21; DB 5; Length 132;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCCTGGGGGCTCTCTG 21
   |||||||
Db 1 CTGCTCCTGGGGGCTCTCTG 21

RESULT 5
US-09-543-679A-2649/c
; Sequence 2649, Application US/09543679A
; GENERAL INFORMATION:
;   APPLICANT: NYCE, Jonathan W.
;   TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;     COMPOSITIONS, KIT & METHOD FOR TREATMENT
;     OF AIRWAY DISORDERS ASSOCIATED WITH
;     BRONCHOCONSTRICITION, LUNG INFLAMMATION,
;   NUMBER OF SEQUENCES: 3111
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;     STREET: 7 Clarke Drive
;     CITY: Cranbury
;     STATE: NJ
;     COUNTRY: USA
;     ZIP: 08512
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: CD-R
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: N/A
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/543,679A
;     FILING DATE: 13-Apr-2000
;     CLASSIFICATION: UNKNOWN
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/127,958
;     FILING DATE: 1998-08-03
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Amzel, Viviana
;     REGISTRATION NUMBER: 30,930
;     REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 609-409-3035
;   TELEFAX: 413-254-9245
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2649:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1081 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2649
US-09-543-679A-2649
```

```

Query Match          100.0%; Score 21; DB 5; Length 1081;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCCTGGGGGCTCTCTG 21
   |||||||
Db 100 CTGCTCCTGGGGGCTCTCTG 80

RESULT 6
US-09-543-679A-2646/c
; Sequence 2646, Application US/09543679A
; GENERAL INFORMATION:
;   APPLICANT: NYCE, Jonathan W.
;   TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
;     COMPOSITIONS, KIT & METHOD FOR TREATMENT
;     OF AIRWAY DISORDERS ASSOCIATED WITH
;     BRONCHOCONSTRICITION, LUNG INFLAMMATION,
;   NUMBER OF SEQUENCES: 3111
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;     STREET: 7 Clarke Drive
;     CITY: Cranbury
;     STATE: NJ
;     COUNTRY: USA
;     ZIP: 08512
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: CD-R
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: N/A
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/543,679A
;     FILING DATE: 13-Apr-2000
;     CLASSIFICATION: UNKNOWN
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/127,958
;     FILING DATE: 1998-08-03
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Amzel, Viviana
;     REGISTRATION NUMBER: 30,930
;     REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 609-409-3035
;   TELEFAX: 413-254-9245
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2646:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1137 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2646
US-09-543-679A-2646

Query Match          100.0%; Score 21; DB 5; Length 1137;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCCTGGGGGCTCTCTG 21
   |||||||
Db 119 CTGCTCCTGGGGGCTCTCTG 99

RESULT 7
US-09-543-679A-2644/c
; Sequence 2644, Application US/09543679A
; GENERAL INFORMATION:
;   APPLICANT: NYCE, Jonathan W.
;   TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
```

COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2644:
SEQUENCE CHARACTERISTICS:
LENGTH: 1143 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2644
US-09-543-679A-2644

Query Match 100.0%; Score 21; DB 5; Length 1143;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCTG 21
|||||

DB 128 CTTGCTCTGGGGGCTCTCTG 108

RESULT 8
US-09-543-679A-2645/C
Sequence 2645, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2645:
SEQUENCE CHARACTERISTICS:
LENGTH: 1145 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2645
US-09-543-679A-2645

Query Match 100.0%; Score 21; DB 5; Length 1145;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCTG 21
|||||

DB 130 CTTGCTCTGGGGGCTCTCTG 110

RESULT 9
US-09-543-679A-2648/C
Sequence 2648, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2648:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2648
US-09-543-679A-2648

Query Match 100.0%; Score 21; DB 5; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCCTGGGGGCTCTG 21
|||||
DB 140 CTGCTCCTGGGGGCTCTG 120

RESULT 10
US-09-543-679A-2647/C
Sequence 2647, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2647:
SEQUENCE CHARACTERISTICS:
LENGTH: 2197 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2647
US-09-543-679A-2647

Query Match 100.0%; Score 21; DB 5; Length 2197;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCCTGGGGGCTCTG 21
|||||
DB 734 CTGCTCCTGGGGGCTCTG 714

RESULT 11

US-09-543-679A-2650/C
Sequence 2650, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2650:
SEQUENCE CHARACTERISTICS:
LENGTH: 2280 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2650
US-09-543-679A-2650

Query Match 100.0%; Score 21; DB 5; Length 2280;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCCTGGGGGCTCTG 21
|||||
DB 548 CTGCTCCTGGGGGCTCTG 528

RESULT 12
US-09-543-679A-2641/C
Sequence 2641, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICITION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2641:
SEQUENCE CHARACTERISTICS:
LENGTH: 5441 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2641
US-09-543-679A-2641

Query Match 100.0%; Score 21; DB 5; Length 5441;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCTG 21
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Db 2393 CTTGCTCTGGGGGCTCTCTG 2373

RESULT 13
US-09-543-679A-2410
Sequence 2410, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2410:
SEQUENCE CHARACTERISTICS:
LENGTH: 6225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2410:
US-09-543-679A-2410

Query Match 100.0%; Score 21; DB 5; Length 6225;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCTG 21
|||||
Db 1 CTTGCTCTGGGGGCTCTCTG 21

RESULT 14
US-09-543-679A-2651/C
Sequence 2651, Application US/09543679A
GENERAL INFORMATION:
APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCONSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2651:
SEQUENCE CHARACTERISTICS:
LENGTH: 17133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2651
US-09-543-679A-2651

Query Match 100.0%; Score 21; DB 5; Length 17133;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTCTG 21

Db 15401 CTTGCTCTGGGGGCTCTG 15381

RESULT 15

US-09-543-679A-3003

; Sequence 3003, Application US/09543679A

; GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.

TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,

COMPOSITIONS, KIT & METHOD FOR TREATMENT

OF AIRWAY DISORDERS ASSOCIATED WITH

BRONCHOCONSTRICITION, LUNG INFLAMMATION,

NUMBER OF SEQUENCES: 3111

CORRESPONDENCE ADDRESSES:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 Claik Drive

CITY: Cranbury

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-R

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: N/A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/543,679A

FILING DATE: 13-Apr-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/127,958

FILING DATE: 1998-08-03

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-0067191b

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 3003:

SEQUENCE CHARACTERISTICS:

LENGTH: 35459 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3003:

US-09-543-679A-3003

Query Match 100.0%; Score 21; DB 5; Length 35459;

Best Local Similarity 100.0%; Pred. NO. 0.46;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCTCTGGGGGCTCTG 21
|||||
Db 1 CTTGCTCTGGGGGCTCTG 21

Search completed: April 20, 2001, 00:15:28
Job time: 9465 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:00:06 ; Search time 2028.86 Seconds
(without alignments)
60.703 Million cell updates/sec

Title: US-09-016-464-16

Perfect score: 20
Sequence: 1.GGTGTGGGGGCGCTGTGCC 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBankl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
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19: em_hcgo_hum:*
20: em_hcgo_inv:*
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85: gb_pr1:*
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87: gb_pr3:*
88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_ro1:*
95: gb_ro2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	20	100.0	827	9	AR014295	AR014295 Sequence
c 2	20	100.0	827	93	HUMPROS15	M61900 Human prost
c 3	20	100.0	827	93	HUMPROSYN	M61901 Human prost
c 4	19	95.0	4060	94	AB028461	AB028461 Rattus no
c 5	18.4	92.0	879	9	AX014330	AX014330 Sequence
c 6	18.4	92.0	149341	74	AC068451	AC068451 Homo sapi
c 7	18.4	92.0	186485	81	AL392183	AL392183 Homo sapi
c 8	18.4	92.0	201654	80	AL356130	AL356130 Homo sapi
c 9	17.4	87.0	1310	92	HSW800695	AL080175 Homo sapi
c 10	17.4	87.0	2100	85	AB031547	AB031547 Homo sapi
c 11	17.4	87.0	2992	93	HUMPSD01	M98537 Human prost

C	12	17.1	87.0	2587746	67	AC022389	Human cyto
C	13	17	85.0	1665	59	HS022103HG	L29246 Murine
C	14	17	85.0	31513	91	HS3906E	AL031600 Human DNA
C	15	17	85.0	171883	72	AC046159	AC046159 Homo sapi
C	16	17	85.0	230278	79	MC068299	U628299 Mouse cytom
C	17	16.8	84.0	30	10	I89979	I89979 Sequence 27
C	18	16.8	84.0	632	8	CPTSLRE4	U6356 Gallus gall
C	19	16.8	84.0	14917	5	GBR04108	AC084505 Caenorhab
C	20	16.8	84.0	20919	50	AP000309	AP000309 Homo sapi
C	21	16.8	84.0	27940	3	SC3D11	AL157916 Streptomy
C	22	16.8	84.0	34087	66	AC0019869	AC0019869 Drosophil
C	23	16.8	84.0	57688	90	AP000048	AP000048 Homo sapi
C	24	16.8	84.0	71336	69	AC024264	AC024264 Homo sapi
C	25	16.8	84.0	98873	78	AL138873	AL138873 Homo sapi
C	26	16.8	84.0	100000	90	AP000116	AP000116 Homo sapi
C	27	16.8	84.0	100000	90	AP000192	AP000192 Homo sapi
C	28	16.8	84.0	130184	60	AC0007648	AC0007648 Drosophil
C	29	16.8	84.0	133368	60	AC0007769	AC0007769 Drosophil
C	30	16.8	84.0	135966	80	AL356007	AL356007 Homo sapi
C	31	16.8	84.0	157080	80	AL358856	AL358856 Homo sapi
C	32	16.8	84.0	159423	79	AL354972	AL354972 Homo sapi
C	33	16.8	84.0	163908	86	AC007050	AC007050 Homo sapi
C	34	16.8	84.0	165608	75	AC018473	AC018473 Homo sapi
C	35	16.8	84.0	167467	74	AC069071	AC069071 Homo sapi
C	36	16.8	84.0	174945	78	AL139044	AL139044 Homo sapi
C	37	16.8	84.0	185822	75	AC073554	AC073554 Homo sapi
C	38	16.8	84.0	201585	82	AL513327	AL513327 Homo sapi
C	39	16.8	84.0	210464	90	CNS0180V	AL109758 Human chr
C	40	16.8	84.0	215899	74	AC069175	AC069175 Homo sapl
C	41	16.8	84.0	235457	4	AE003708	AE003708 Drosophil
C	42	16.8	84.0	340000	90	AP001717	AP001717 Homo sapi
C	43	16.4	82.0	888	9	A48334	A48334 Sequence 2
C	44	16.4	82.0	2500	88	AF233588	AF233588 Homo sapi
C	45	16.4	82.0	2888	9	A48323	A48323 Sequence 1

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ACCESSION      M61900
VERSION        M61900.1
KEYWORDS       GI:190443
SOURCE         prostaglandin D synthase; prostaglandin-H-2 D-isomerase.
ORGANISM       Homo sapiens
REFERENCE      Homo sapiens
AUTHORS        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE          1 (bases 1 to 827)
               Nagata,A., Suzuki,T., Igarashi,M., Eguchi,N., Toh,B.H., Urade,Y.
               and Hayashi,O.
               Human brain prostaglandin D synthase has been evolutionarily
               differentiated from lipophilic-ligand carrier proteins
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 88, 4020-4024 (1991)
MEDLINE        91219504
COMMENT        From EMBL
FEATURES       entry HSPROS15; dated 30-MAR-1991.
               Location/Qualifiers
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               /db_xref="taxon:9606"
               86..151
               86..658
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	ALIGNMENTS	
RESULT 1		
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LOCUS	827 bp	DNA
DEFINITION	Sequence 3 from patent US 5773290.	PAT
ACCESSION	AR014295	
VERSION	AR014295.1	GI:3971749
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 827)	
TITLE	Gould,M.N. and Chen,K.	
JOURNAL	Mammary gland-specific promoters	
FEATURES	Patent: US 5773290-A 3 30-JUN-1998;	
source	Location/Qualifiers	
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	/organism="unknown"	
BASE COUNT	156 a 302 c 224 g 145 t	
ORIGIN		

Query Match	100.0%;	Score 20;	DB 9;	Length 827;
Best Local Similarity	100.0%;	Pred. No. 94;		
Matches 20; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
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Db	68	GGTGTGCGGGCCCTGTGCC	49	

RESULT 2
HUMPROS15/c

LOCUS	HUMPROS15	827 bp	mRNA	PRI	24-MAY-1993
DEFINITION	Human prostaglandin D synthase gene, complete cds.				

QY	1	GGGTGGGGGGCGTGGTCC	20
Db	68	GGGTGGGGGGCGTGGTCC	49
RESULT	3		
LOCUS	HUMPROSYN/c		
DEFINITION	HUMPROSYN	827 bp	mRNA
ACCESSION			PRI
VERSION			24-MAY-1993
KEYWORDS	M61901.1	GI:190450	
SOURCE		prostaglandin D synthase; prostaglandin-H-2 D-isomerase.	
ORGANISM		Homo sapiens	
		Homo sapiens	

REFERENCE 1 (bases 1 to 827)
 AUTHORS Nagata, A., Suzuki, Y., Igarashi, M., Eguchi, N., Toh, B. H., Urade, Y. and Hayaishi, O.
 TITLE Human brain prostaglandin D synthase has been evolutionarily differentiated from lipophilic-ligand carrier proteins
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88, 4020-4024 (1991)
 MEDLINE 91219504
 COMMENT This entry (accession number M61901) is an allelic variant of accession number M61900. The sequences are identical. From EMBL entry HSPROSYN; dated 30-MAR-1991.

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 /db_xref="taxon:9606"
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 CDS 86..658
 /EC_number="5.3.99.2"
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 /protein_id="AA36497.1"
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 /translation="MATHHTLMGILVLLGLGLQAAPEAGVYVQPNFQPKFLGRMF
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CDS

86..658
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 EKFTAFCKAOGCTEDSIYFLPQTDCKMTEQ"
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polyA_signal 156 a 302 c 224 g 145 t
 BASE COUNT 156 a 302 c 224 g 145 t
 ORIGIN

Query Match 100.0%; Score 20; DB 93; Length 827;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGTGCGGGGCGCTGTGCC 20
 ||||||||||||||||||||
 Db 68 GGTGTGCGGGGCGCTGTGCC 49

RESULT 4
 LOCUS AB028461 4060 bp mRNA ROD 16-MAY-2000
 DEFINITION Rattus norvegicus mRNA for retina specific protein PAL, complete cds.
 ACCESSION AB028461
 VERSION AB028461.1 GI:7861532
 KEYWORDS retina specific protein PAL.
 SOURCE Rattus norvegicus retina cDNA to mRNA.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (sites)
 AUTHORS Gomi, F., Imai, T., Yoneda, T., Taniguchi, M., Mori, Y., Miyoshi, K., Hitomi, J., Fujikado, T., Tano, Y. and Tohyama, M.
 TITLE Molecular cloning of a novel membrane glycoprotein, pal, specifically expressed in photoreceptor cells of the retina and containing leucine-rich repeat
 JOURNAL J. Neurosci. 20 (9), 3206-3213 (2000)
 MEDLINE 20241965
 COMMENT 2 (bases 1 to 4060)
 Gomi, F.
 Direct Submission
 Submitted (04-JUN-1999) to the DDBJ/EMBL/GenBank databases. Fumi Gomi, Osaka University Medical School, Anatomy and Neuroscience; Yamadaoka 2-2, Suita, Osaka 565-0871, Japan
 (E-mail: fgomianat2.med.osaka-u.ac.jp, Tel: 81-6-6879-3221, Fax: 81-6-6879-3229)

FEATURES

source 1..4060
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 /issue_type="retina"
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 /product="retina specific protein PAL"
 /protein_id="BAA95680.1"
 /db_xref="GI:7861533"
 /translation="MLMLALAGCPHQANSPFCSCSGSLHLSGSKARTVYCSPPDL
 TLTPASIPPTCKLRLKRLTAIRVGEFFRLPLSRLEQMLWLPYALSELSTMLKGLR
 LRLRLPGNHLVTPFWALKDTPQLDLQANRLSTLPBAVHLEMLTFLDLSNNG
 LMRLEPEELDPMHLKTPYLSRRTRLVGLQDNPWCDCRLDVLVLLRCGANGLI
 FLRLRCGSPRLAGVAFSOLELRCCSPELRPPVTSIISPLGSTVLLRCGANGIPG
 PEMSWRRANGRLNCTVHOEVSQSSMTLLDLPVYSIFDSGDYVCOAKNGLSESL
 ISLIYEPQTSRETYTGITGALMRGEBAAATYNNKLYAHHVHPRVPPVALRKPSY
 PSIKELPLQNFQMDVPGFSRSESHQETQVNRSLKVGDTSHVSIVWKAPOAGNT
 TAFSVLVAFQGRDMRMTVEAGKTSVIEGLAPRTKYVACVYAGLVPTEQCVIFS
 TDEVVADAGTQRLIMVVISVAAILALPPLIYCCGALRRCHCKRAGGSAEAGAVY
 NLERGSHEDGSEELSRSSLSLSEADRLSARSLDSQVLGVGRIRINEYFC"

BASE COUNT 1072 a 932 c 993 g 1063 t
 ORIGIN

Query Match 95.0%; Score 19; DB 94; Length 4060;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GTGTGCGGGGCGCTGTGCC 20
 ||||||||||||||||||||
 Db 1559 GTGTGCGGGGCGCTGTGCC 1577

RESULT 5
 LOCUS AX014330 879 bp DNA PAT 07-SEP-2000
 DEFINITION Sequence 39 from Patent WO954353.
 ACCESSION AX014330
 VERSION AX014330.1 GI:10040684
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 879)
 AUTHORS Schmitt, A., Specht, T., Dahl, E., Hinemann, B., Rosenthal, A. and Pilarsky, C.
 TITLE Human nucleic acid sequences of normal uterus tissue
 JOURNAL Patent: WO 954353-A 39 28-OCT-1999;
 SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GBS FUER GENOMFORSCHUNG (DE); PILARSKI CHRISTIAN (DE)
 LOCATION/Qualifiers
 1..879
 /organism="Homo sapiens"

```

BASE COUNT      181 a 307 c 245 g 146 t
ORIGIN
Query Match      92.0%; Score 18.4; DB 9; Length 879;
Best Local Similarity 95.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1  GGTGTCGGGGCGCTGCTGCC 20
         ||||| ||||| ||||| |||||
DB      92  GGTGTCGGGGCGCTGCTGCC 73

RESULT 6
AC068451 149341 bp      DNA      HTG      28-MAY-2000
LOCUS     Homo sapiens chromosome 15 clone RP11-229P13 map 15, WORKING DRAFT
DEFINITION
ACCESSION AC068451
VERSION   AC068451.2 GI:8099866
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          2 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
          1 (bases 1 to 149341)
          Birren, B., Linton, L., Nusbaum, C. and Lander, E.
          Homo sapiens chromosome 15, clone RP11-229P13.
          Unpublished
          2 (bases 1 to 149341)
          Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
          Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
          Bonuslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,
          Campopiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
          Collamore, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S.,
          Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
          Galagan, J., Gardyna, S., Glende, S., Goyette, M., Graham, L.,
          Grand-Plerre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
          Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karakas, A.,
          Klein, J., Lacombe, K., Lamazares, R., Landers, T., Lehoczy, J.,
          Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,
          McCarthy, M., McEwan, P., McGuire, A., McKernan, K., McPheters, R.,
          McElrath, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
          Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
          O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
          Pisanelli, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
          Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
          Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
          Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J.,
          Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
          Young, G., Zainoun, J., Zimmer, A. and Zody, M.
          Direct Submission
          Submitted (02-MAY-2000) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
          On May 28, 2000 this sequence version replaced g1:7677931..
          All repeats were identified using RepeatMasker:
          Smit, A.F.A. & Green, P. (1996-1997)
          http://ftp.genome.washington.edu/RM/RepeatMasker.html

          ----- Genome Center
          Center: Whitehead Institute/ MIT Center for Genome Research
          Center code: WIBR
          Web site: http://www-seq.wi.mit.edu
          Contact: sequence_submissions@genome.wi.mit.edu

          ----- Project Information
          Center project name: L9144
          Center clone name: 229_P_13
          ----- Summary Statistics
          Sequencing vector: M13; M77815; 100% of reads
          Assembly program: Phrap; version 0.960731
          Consensus quality: 126855 bases at least Q40
          Consensus quality: 137852 bases at least Q30

```

```

Consensus quality: 142614 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 146041; sum-of-ctrls
Quality coverage: 3.5 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-ctrls
-----
NOTE: This is a 'working draft' sequence. It currently
consists of 34 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1 1277: contig of 1277 bp in length
* 1278 1377: gap of 100 bp
* 1378 2436: contig of 1059 bp in length
* 2437 2536: gap of 100 bp
* 2537 3728: contig of 1192 bp in length
* 3729 3828: gap of 100 bp
* 3829 5045: contig of 1217 bp in length
* 5046 5145: gap of 100 bp
* 5146 6248: contig of 1103 bp in length
* 6249 6348: gap of 100 bp
* 6349 7551: contig of 1203 bp in length
* 7552 7651: gap of 100 bp
* 7652 9259: contig of 1608 bp in length
* 9260 9359: gap of 100 bp
* 9360 10908: contig of 1549 bp in length
* 10909 11008: gap of 100 bp
* 11009 12747: contig of 1739 bp in length
* 12748 12847: gap of 100 bp
* 12848 14393: contig of 1546 bp in length
* 14394 14493: gap of 100 bp
* 14494 16915: contig of 2422 bp in length
* 16916 17015: gap of 100 bp
* 17016 18084: contig of 1069 bp in length
* 18085 18184: gap of 100 bp
* 18185 19831: contig of 1647 bp in length
* 19832 19931: gap of 100 bp
* 19932 22144: contig of 2213 bp in length
* 22145 22244: gap of 100 bp
* 22245 24490: contig of 2246 bp in length
* 24491 24590: gap of 100 bp
* 24591 27227: contig of 2637 bp in length
* 27228 27327: gap of 100 bp
* 27328 31008: contig of 3681 bp in length
* 31009 31108: gap of 100 bp
* 31109 33896: contig of 2788 bp in length
* 33897 33996: gap of 100 bp
* 33997 37521: contig of 3525 bp in length
* 37522 37621: gap of 100 bp
* 37622 43330: contig of 5709 bp in length
* 43331 43430: gap of 100 bp
* 43431 48048: contig of 4618 bp in length
* 48049 48148: gap of 100 bp
* 48149 53114: contig of 4966 bp in length
* 53115 53214: gap of 100 bp
* 53215 58650: contig of 5536 bp in length
* 58651 58950: gap of 100 bp
* 58951 63525: contig of 4575 bp in length
* 63526 63625: gap of 100 bp
* 63626 70043: contig of 6418 bp in length
* 70044 70143: gap of 100 bp
* 70144 77573: contig of 7430 bp in length
* 77574 77673: gap of 100 bp
* 77674 84119: contig of 6446 bp in length
* 84120 84219: gap of 100 bp
* 84220 92847: contig of 8628 bp in length
* 92848 92947: gap of 100 bp
* 92948 101945: contig of 8998 bp in length
* 101946 102045: gap of 100 bp
* 102046 109841: contig of 7796 bp in length

```

* 109842 109941: gap of 100 bp
* 109942 119233: contig of 9292 bp in length
* 119234 119333: gap of 100 bp
* 119334 128741: contig of 9408 bp in length
* 128742 128841: gap of 100 bp
* 128842 140974: contig of 1213 bp in length
* 140975 141074: gap of 100 bp
* 141075 149341: contig of 8267 bp in length.
Location/Qualifiers

FEATURES

source

1. 149341
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
/map="15"
/clone="RP11-229P13"
/clone_1lb="RPCL-11 Human Male BAC"
1. 1277
/note="assembly_fragment"
misc_feature
1378. 2436
/note="assembly_fragment"
misc_feature
2537. 3728
/note="assembly_fragment"
misc_feature
3829. 5045
/note="assembly_fragment"
misc_feature
5146. 6248
/note="assembly_fragment"
misc_feature
6349. 7551
/note="assembly_fragment"
misc_feature
7652. 9259
/note="assembly_fragment"
misc_feature
9360. 10908
/note="assembly_fragment"
misc_feature
11009. 12747
/note="assembly_fragment"
misc_feature
12848. 14393
/note="assembly_fragment"
misc_feature
14494. 16915
/note="assembly_fragment"
misc_feature
17016. 18084
/note="assembly_fragment"
misc_feature
clone_end:17
vector_side:right"
18185. 19831
/note="assembly_fragment"
misc_feature
19932. 22144
/note="assembly_fragment"
misc_feature
22245. 24490
/note="assembly_fragment"
misc_feature
24591. 27227
/note="assembly_fragment"
misc_feature
27328. 31008
/note="assembly_fragment"
misc_feature
31109. 33896
/note="assembly_fragment"
misc_feature
33997. 37521
/note="assembly_fragment"
misc_feature
37622. 43330
/note="assembly_fragment"
misc_feature
43431. 48048
/note="assembly_fragment"
misc_feature
48149. 53114
/note="assembly_fragment"
misc_feature
53215. 58850
/note="assembly_fragment"
misc_feature
58951. 63523
/note="assembly_fragment"
misc_feature
63626. 70043
/note="assembly_fragment"
misc_feature
70144. 77573
/note="assembly_fragment"
misc_feature

Query Match 92.0%; Score 18.4; DB 74; length 149341;
Best Local Similarity 95.0%; Pred. No. 86;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTGTGGGGCCGTGCC 20
||||| |||||||||
Db 118933 GGTGTCCGGGCTGTGCC 118952

RESULT 7

AL392183

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL392183 186485 bp DNA HTG 09-FEB-2001
Homo sapiens chromosome 6 clone RP11-284U1, *** SEQUENCING IN
PROGRESS *** 8 unordered pieces.
AL392183
AL392183.11 GI:12743819
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186485)
Direct Submission
Submitted (08-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Feb 10, 2001 this sequence version replaced gi:12718116.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: ba284u1
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 18365 bases at least Q40
Consensus quality: 184651 bases at least Q20
Insert size: 185785; sum-of-ctrls
Insert size: 192615; 2.7% error; agarose-fp
Quality coverage: 6.72x in Q20 bases; sum-of-ctrls Quality
coverage: 6.48x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 32223: contig of 32223 bp in length
* 32224 32323: gap of 100 bp
* 32324 49697: contig of 17374 bp in length
* 49698 49797: gap of 100 bp
* 49798 61924: contig of 12127 bp in length
* 61925 62024: gap of 100 bp
* 62025 67977: contig of 5593 bp in length
* 67978 68077: gap of 100 bp
* 68078 84786: contig of 16709 bp in length
* 84787 84886: gap of 100 bp
* 84887 115385: contig of 30499 bp in length
* 115386 115485: gap of 100 bp
* 115486 147208: contig of 31723 bp in length
* 147209 147308: gap of 100 bp
* 147309 186485: contig of 39177 bp in length.
Location/Qualifiers
1. 186485
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"

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misc_feature /clone="Rp11-284J1"
1..32223
/note="assembly_fragment:03400
fragment_chain:1
clone_end:SP6
vector_side:left"
misc_feature 32324..49697
/note="assembly_fragment:02110
fragment_chain:1"
misc_feature 49798..61924
/note="assembly_fragment:00544
fragment_chain:2"
misc_feature 62025..67977
/note="assembly_fragment:01580
fragment_chain:2"
misc_feature 68078..84786
/note="assembly_fragment:02282
fragment_chain:3"
misc_feature 84887..115385
/note="assembly_fragment:02240
fragment_chain:3"
misc_feature 115486..147208
/note="assembly_fragment:03283
fragment_chain:4"
misc_feature 147309..186485
/note="assembly_fragment:03903
fragment_chain:4
clone_end:T7
vector_side:right"
BASE COUNT 54211 a 40325 c 38391 g 52858 t 700 others
ORIGIN
```

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Query Match 92.0% Score 18.4; DB 81; Length 186485;
Best Local Similarity 95.0% Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGTGGCGGGGCGCTGGTGGC 20
Db 22313 GGTGTGGGGGCGCTGGGGCC 22332
```

```
RESULT 8
AL356130.201654 bp DNA HTG 25-JAN-2001
LOCUS Homo sapiens chromosome 6 clone RP11-391F23, *** SEQUENCING IN
DEFINITION
ACCESSION AL356130
VERSION AL356130.14 GI:12581003
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201654)
Thomas, D.
Direct Submission
Submitted (24-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonequests@sanger.ac.uk
On Jan 26, 2001 this sequence version replaced g1:12225414.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA391F23
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
```

```
Chemistry: Dye-primer-amerisham; 0% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 198754 bases at least Q40
Consensus quality: 199789 bases at least Q30
Consensus quality: 200600 bases at least Q20
Insert size: 201254; sum-of-contigs
Insert size: 189985; 5.3% error; agarose-fp
Quality coverage: 11.84x in Q20 bases; sum-of-contigs quality
coverage: 11.94x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 150315: contig of 150315 bp in length
* 150316 150415: gap of 100 bp
* 150416 194717: contig of 44302 bp in length
* 194718 194817: gap of 100 bp
* 194818 197268: contig of 2451 bp in length
* 197269 197368: gap of 100 bp
* 197369 199417: contig of 2049 bp in length
* 199418 199517: gap of 100 bp
* 199518 201654: contig of 2137 bp in length.
Location/Qualifiers
1..201654
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="Rp11-391F23"
/clone_lib="RPCT-11.2"
1..150315
/note="assembly_fragment:04617
fragment_chain:1
clone_end:T7
vector_side:left"
150416..194717
/note="assembly_fragment:05864
fragment_chain:1"
194818..197268
/note="assembly_fragment:00108"
197369..199417
/note="assembly_fragment:05533"
199518..201654
/note="assembly_fragment:05616"
BASE COUNT 56098 a 44074 c 43814 g 57268 t 400 others
ORIGIN
```

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Query Match 92.0% Score 18.4; DB 80; Length 201654;
Best Local Similarity 95.0% Pred. No. 79;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGTGGCGGGGCGCTGGTGGC 20
Db 23078 GGTGTGGGGGCGCTGGGGCC 23059
```

```
RESULT 9
HSMB00695 1310 bp mRNA PRI 18-FEB-2000
LOCUS Homo sapiens mRNA: CDNA DKFZP434K091 (from clone DKFZP434K091);
DEFINITION partial cds.
ACCESSION AL080175
VERSION AL080175.1 GI:5262647
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```

REFERENCE 1 (bases 1 to 1310)
AUTHORS Poustka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-1999) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp34K091) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heunerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cdna/.
FEATURES
source
Location/Qualifiers
1..1310
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp34K091"
/clone_lib="434 (synonym: htes3). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
/tissue_type="testis"
1..967
/gene="DKFZp34K091"
<1..967
/gene="DKFZp34K091"
/note="weak similarity to Bravo/Mr-CAM cell adhesion
molecule L1 homolog"
/product="hypothetical protein"
/codon_start=2
/protein_id="CAB45761.1"
/db_xref="GI:5262648"
/db_xref="SPTRMBL:Q9Y4N7"
/translation="VSSDGTSMVLGLPAVSHLDSGDYICQAKNFIQASETVISLIVT
EPPTSEHSGSGALWARTGGGEAAVYNNKLVARVPOIPKPAVLATPSPSTKEE
LTLFHFQMDALGELSDGRAGPSPEARVYKVVGDYHSVLWAKPQAKNTTAFVL
VAFQGHSMRVRVIOGKTRVITGLPKTKYVACVCGVGLPRKQCVIFSPNEVD
AENTQOLINVVVSAIVATLPTLLVCCSAIOKRCRKPNNDSPTATVTVNLEKLS
YSEDGLEELSRHSVSEADRLLSRSSVDVDFQAFGKGRINFEFC"
BASE COUNT 303 a 357 c 358 g 292 t
ORIGIN
polya_site
BASE COUNT 303 a 357 c 358 g 292 t
ORIGIN
Query Match 87.0%; Score 17.4; DB 92; Length 1310;
Best Local Similarity 94.7%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GTGTGGCGGGCGGTGCC 20
||||| |||||||||
Db 591 GTGTGCAGGCGGTGCC 609
RESULT 10
LOCUS AB031547 2100 bp mRNA PRI 16-MAY-2000
DEFINITION Homo sapiens mRNA for retina specific protein PAL, complete cds.
ACCESSION AB031547
VERSION AB031547.1 GI:7861534
KEYWORDS
SOURCE Homo sapiens adult tissue_lib:retina cDNA to mRNA.
ORGANISM Homo sapiens
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Gomi,F., Imaizumi,K., Yoneda,T., Taniguchi,M., Mori,Y., Miyoshi,K.,
Hitomi,J., Fujikado,T., Tano,Y. and Tomyama,M.
TITLE Molecular cloning of a novel membrane glycoprotein, pal,
specifically expressed in photoreceptor cells of the retina and
containing leucine-rich repeat
JOURNAL J. Neurosci. 20 (9), 3206-3213 (2000)

```

```

MEDLINE 2021965
REFERENCE 2 (bases 1 to 2100)
AUTHORS Gomi,F.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1999) to the DDBJ/EMBL/GenBank databases. Fumi
Gomi, Osaka University Medical School, Anatomy and Neuroscience;
Yamadaoka 2-2, Suita, Osaka 565-0871, Japan
(E-mail:fgomi@anat2.med.osaka-u.ac.jp, Tel:81-6-6879-3221,
Fax:81-6-6879-3229)
FEATURES
source
Location/Qualifiers
1..2100
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/dev_stage="adult"
/map="10q23"
/tissue_lib="retina"
23..1894
/gene="PAL"
23..1894
/gene="PAL"
/codon_start=1
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/protein_id="BAA93681.1"
/db_xref="GI:7861535"
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CNDPMTLPASIPPTPSRLRLEPRAIRVPEARPIGRLOMLPYNALSEIYALM
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DISSQMLRPELIVSAHLETGTFPPHRRVRLGLQDNWACDKLYDLYHLDDG
WAPNLAFTETLRGASPSRLAGVAFSLELRGQSPDLHGVASIRSLIGTALRGC
ATGVGPPEMSWRANGRLNGTGHQEVSSDGTSMVLGIIPAVSHLDSGDYICQAKNFI
GASERVISLIVTEPPTSEHSGSGPALMARTGGGEAAVYNNKLVARVPOIPKPAVL
ATGPSVPTKEELTEHFQMDALGELSDGRAGPSPEARVYKVVGDYHSVLWAKA
POAKNTAFSVLYXAFQGHSMRVRVIOGKTRVITGLPKTKYVACVCGVGLVPRKE
OCVITSTNEVVAENTQOLINVVVSAIVATLPTLLVCCSAIOKRCRKPNNDSPT
ATVTVTVNLERLGYSEDGLEELSRHSVSEADRLLSRSSVDVDFQAFGKGRINFEFC"
BASE COUNT 414 a 653 c 618 g 415 t
ORIGIN
Query Match 87.0%; Score 17.4; DB 85; Length 2100;
Best Local Similarity 94.7%; Pred. No. 8.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GTGTGGCGGGCGGTGCC 20
||||| |||||||||
Db 1518 GTGTGCAGGCGGTGCC 1536
RESULT 11
LOCUS HUMPSD01/c 2992 bp DNA PRI 31-MAR-1997
DEFINITION Human prostaglandin D2 synthase gene, promoter and exon 1.
ACCESSION M98537
VERSION M98537.1 GI:1911186
KEYWORDS prostaglandin D2 synthase.
SEGMENT 1 of 3
SOURCE human.
ORGANISM Homo sapiens
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS White,D.M., Mkol,D.D., Espinosa,R., Welner,B., Le Beau,M.M. and
Stefansson,K.
TITLE Structure and chromosomal localization of the human gene for a
brain form of prostaglandin D2 synthase
JOURNAL J. Biol. Chem. 267 (32), 23202-23208 (1992)
93054651
MEDLINE
REFERENCE 2 (bases 1 to 2878)
AUTHORS White,D.M., Takeda,T., Degroot,L.J., Stefansson,K. and
Arnason,B.G.W.
TITLE Beta-Trace gene expression is regulated by a core promoter and a
distal thyroid hormone response element

```

JOURNAL Unpublished
COMMENT On Mar 27, 1997 this sequence version replaced gl:189768.
FEATURES Location/Qualifiers
source 1..2992
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /dev_stage="adult"
 /sex="male"
 /chromosome="9"
 /map="9q34.2-q34.3"
 1..2878
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="PCAT24"
 184..198
 /note="thyroid hormone response element"
 2732..2738
 2760..2947
 /note="putative"
 /number=1
 /product="prostaglandin D2 synthase"
 2948..>2992
 /note="putative"
 /number=1
 2948..>2992
 /note="putative"
 /number=1
BASE COUNT 537 a 1006 c 939 g 510 t
ORIGIN
Query Match 87.0%; Score 17.4; DB 93; Length 2992;
Best Local Similarity 94.7%; Pred. No. 8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GGTGTCGGGGGCTGTGC 19
DB 2816 GGTGTCGGGGGCTGTGC 2798
RESULT 12
AC022389/c AC022389 258746 bp DNA HTG 10-MAY-2000
LOCUS Homo sapiens chromosome CHROM 10 clone RP11-124L5, WORKING DRAFT
DEFINITION
SEQUENCE, 56 unordered pieces.
AC022389
AC022389.3 GI:7767724
HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 258746)
AUTHORS Smith,D.R.
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 258746)
AUTHORS Smith,D.R.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
COMMENT On May 10, 2000 this sequence version replaced gl:7209016.
----- Genome Center
Center: Genome Therapeutics Corporation
Center code: GTC
Web site: http://www.genomecorp.com/
Contact: gtc-seqcenter@genomecorp.com
----- Project Information
Center project name: hg137
----- Summary Statistics
Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 990315
Consensus quality: 201841 bases at least Q40

Consensus quality: 230471 bases at least Q30
Consensus quality: 236618 bases at least Q20
Insert size: 258746; sum-of-contigs
Quality coverage: 5.4x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 56 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1122: contig of 1122 bp in length
* 1123 2241: gap of unknown length
* 2242 3534: gap of unknown length
* 3535 4881: gap of unknown length
* 4882 6044: gap of unknown length
* 6045 7094: gap of unknown length
* 7095 8494: gap of unknown length
* 8495 9739: gap of unknown length
* 9740 11083: gap of unknown length
* 11084 12228: gap of unknown length
* 12229 13277: gap of unknown length
* 13278 14747: gap of unknown length
* 14748 15820: gap of unknown length
* 15821 16833: gap of unknown length
* 16834 17928: gap of unknown length
* 17929 19058: gap of unknown length
* 19059 20120: gap of unknown length
* 20121 21194: gap of unknown length
* 21195 22241: gap of unknown length
* 22242 23690: gap of unknown length
* 23691 24996: gap of unknown length
* 24997 26212: gap of unknown length
* 26213 27593: gap of unknown length
* 27594 29270: gap of unknown length
* 29271 31254: gap of unknown length
* 31255 33134: gap of unknown length
* 33135 34676: gap of unknown length
* 34677 36624: gap of unknown length
* 36625 38260: gap of unknown length
* 38261 39573: gap of unknown length


```

* 39574 42491: contig of 2918 bp in length
* 42492 44172: contig of 1681 bp in length
* 44173 45456: contig of 1284 bp in length
* 45457 47973: gap of unknown length
* 47974 49274: gap of unknown length
* 49275 51062: contig of 1788 bp in length
* 51063 53455: gap of unknown length
* 53456 55778: gap of unknown length
* 55779 57022: gap of unknown length
* 57023 59210: gap of unknown length
* 59211 60883: gap of unknown length
* 60884 62917: gap of unknown length
* 62918 65997: gap of unknown length
* 65998 68398: gap of unknown length
* 68399 74552: gap of unknown length
* 74553 78739: gap of unknown length
* 78739 83546: gap of unknown length
* 83547 90669: gap of unknown length
* 90670 100398: gap of unknown length
* 100399 108591: gap of unknown length
* 108592 121396: gap of unknown length
* 121397 131100: gap of unknown length
* 131101 148369: gap of unknown length
* 148370 168804: gap of unknown length
* 168805 210111: gap of unknown length
* 210112 258746: contig of 48635 bp in length.

```

FEATURES

source

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1.258746
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="CHROM 10"
/clone_lib="RP11-124L5"
/clone_lib="RP11-124L5"
BASE COUNT 73754 a 58179 c 55947 g 70833 t 33 others
ORIGIN

```

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Query Match 87.0%: Score 17.4; DB 67; Length 258746;
Best Local Similarity 94.7%: Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GTGTGGGGGCTGTGTGCC 20
||||| |||||||
Db 254969 GTGTGGAGGCGCTGTGTGCC 254951

```

RESULT 13
HSSUL103HG/c

```

LOCUS HS5UL103HG 1665 bp DNA VRL 02-MAR-1995
DEFINITION Murine cytomegalovirus UL103 homologue gene, complete cds, UL102
ACCESSION L29246
VERSION L29246.1 GI:468306
KEYWORDS
SOURCE
ORGANISM Murine cytomegalovirus (strain K181) DNA.
Mouse cytomegalovirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Muromegalovirus.
REFERENCE
AUTHORS Lyons,P.A., Dallas,P.B., Carrello,C., Shellen,G.R. and Scalzo,A.A.
TITLE Mapping and transcriptional analysis of the murine cytomegalovirus
homologue of the human cytomegalovirus UL103 open reading frame
JOURNAL Virology 204 (2), 835-839 (1994)
MEDLINE 95027718
FEATURES
source
Location/Qualifiers
1..1665
/organism="Mouse cytomegalovirus 1"
/strain="K181"
/db_xref="taxon:10366"
<1..177
/feature="UL102 homologue"
/codon_start=1
/protein_id="AA62598.1"
/db_xref="GI:688449"
/translation="ETTPCTANVRPQQTIVTTTPIGLPPSSPAEVSPPRRSPQK
LETLKRNVOHLNG"
155..1108
/feature="UL103 homologue"
/codon_start=1
/protein_id="AA62599.1"
/db_xref="GI:468307"
/translation="MSSTLMVARGAMFVHNDRDYVRLMAPEIVSYSDROIMFHESG
ELIPNAQYRABSDCRSSFLGCLFTFLDEDAISERLSSITKRIRINAFRRKNTDF
TLCMLLFALESPLSRQTLHLVFTLGTFRPGTLRMCKSCIKVCTSLYFDET
DTRTRHVEPTCMLYKETOQAQATMLAEYFPGVDISSMSLVLTLDVTGDDGTG
DLAAEVLNTVCNVFVPLGTNGSGVYTRMISNDNNPKORMPDITTTDITPIPPPTTK
KNMTTATSHIALSTLNNTNTTTTTPCADIRKKSANNKK"
complement(1256..>1665)
/feature="UL104 homologue"
/codon_start=3
/protein_id="AA62600.1"
/db_xref="GI:688450"
/translation="GRMVAVVOPIDGALHDNICYNDYKKTFEVLRYLTLEKVIIVSOD
QRTNAVNNSTGEIDCVALKOETDAIYSDTGSGLDALRALRETTANVGMVE
KDTIHVLEFNDVPOQTMDFYVERISAFESMAN"

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CDS

```

155..1108
/feature="UL103 homologue"
/codon_start=1
/protein_id="AA62599.1"
/db_xref="GI:468307"
/translation="MSSTLMVARGAMFVHNDRDYVRLMAPEIVSYSDROIMFHESG
ELIPNAQYRABSDCRSSFLGCLFTFLDEDAISERLSSITKRIRINAFRRKNTDF
TLCMLLFALESPLSRQTLHLVFTLGTFRPGTLRMCKSCIKVCTSLYFDET
DTRTRHVEPTCMLYKETOQAQATMLAEYFPGVDISSMSLVLTLDVTGDDGTG
DLAAEVLNTVCNVFVPLGTNGSGVYTRMISNDNNPKORMPDITTTDITPIPPPTTK
KNMTTATSHIALSTLNNTNTTTTTPCADIRKKSANNKK"
complement(1256..>1665)
/feature="UL104 homologue"
/codon_start=3
/protein_id="AA62600.1"
/db_xref="GI:688450"
/translation="GRMVAVVOPIDGALHDNICYNDYKKTFEVLRYLTLEKVIIVSOD
QRTNAVNNSTGEIDCVALKOETDAIYSDTGSGLDALRALRETTANVGMVE
KDTIHVLEFNDVPOQTMDFYVERISAFESMAN"

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CDS

```

BASE COUNT 353 a 513 c 459 g 340 t
ORIGIN

```

```

Query Match 85.0%: Score 17; DB 59; Length 1665;
Best Local Similarity 100.0%: Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTGGGGGCGCTGTGTGCC 20
||||| ||||||| |||||||
Db 558 GTGGGGGCGCTGTGTGCC 542

```

RESULT 14

HS390E6/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

```

HS390E6 31513 bp DNA PRI 23-NOV-1999
Human DNA sequence from clone 390E6 on chromosome 16. Contains the
3' part of the CLCN7 gene for chloride channel 7, ESTs, a GSS and
four putative CpG islands, complete sequence.
AL031600
AL031600.4 GI:4826481
HTG: chloride channel 7; CLCN7; CpG Island.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiinae; Homo.

```

REFERENCE 1 (bases 1 to 31513)
 AUTHORS Donnelly,S.
 TITLE Direct Submission
 JOURNAL Submitted (12-AUG-1999) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 COMMENT On May 13, 1999 this sequence version replaced g1:4467206.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu). Where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.
 39086 is part of a clone contig from the tip of the short arm of
 chromosome 16 spanning 2mb of p13.3 (Higgs D.R., Flint J., Daniels
 R., MRC Molecular Haematology Unit, Institute of Molecular
 Medicine, Oxford (unpublished)), and is from the Los Alamos, flow
 sorted human Chromosome 16 libraries constructed by Norman Doggett
 (unpublished). The following abbreviations are used to associate
 primary accession numbers given in the feature table with their
 source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp.,
 WORMPEP. Information on the WORMPEP database can be found at
 http://www.sanger.ac.uk/projects/c_elegans/wormpep/IMPORTANT: This
 sequence is not the entire insert of clone 39086. It may be shorter
 because we only sequence overlapping sections once, or longer
 because we arrange for a small overlap between neighbouring
 submissions.
 The true left end of clone 30568 (AL031705) is at 31414 in this
 sequence.

FEATURES
 source
 Location/Qualifiers
 1..31513
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="LA16-39086"
 /clone_1fb="LA16"
 1..86
 /note="Aluub repeat: matches 59. 148 of consensus"
 87..387
 /note="Alu repeat: matches 1. 300 of consensus"
 388..347
 /note="Aluub repeat: matches 148. 293 of consensus"
 1199..1324
 /note="FLAM.C repeat: matches 1. 124 of consensus"
 1330..1629
 /note="AluSc repeat: matches 5. 308 of consensus"
 4160..4783
 /note="Cpg Island"
 /evidence=not_experimental
 4320..4425
 /note="Charles repeat: matches 2417. 2530 of consensus"
 complement(4734)
 /gene="CLCN7"
 mRNA
 complement(join(4754..6135,6424..6504,6810..6986,
 7073..7132,7773..7902,8099..8184,8384..8511,8694..8745,
 9915..10084,11041..11134,12173..12311,13252..13312,
 13829..13883,14552..14668,15149..15213,15531..15624,
 16672..16755,17112..17174,18525..18605,19836..19945,
 20234..20366,20823..20888,21021..21092,24685..24756))
 /gene="CLCN7"
 /note="match: CDNAS: Em.:267743 Em.:267744; match: ESTs:
 Em.:A1098598 Em.:R51174 Em.:A1269796 Em.:N35546 Em.:A1613247.1
 Em.:A1523975.1 Em.:R46448 Em.:A1086805 Em.:A1076529
 Em.:A1655264.1 Em.:AA539340 Em.:A1209141 Em.:A1089727
 Em.:AA937518 Em.:AA452620 Em.:A1380843.1 Em.:A1597975.1
 Em.:A1223148 Em.:AA741117 Em.:R60756 Em.:A1380856.1 Em.:N35451
 Em.:R35336 Em.:AA937240 Em.:AA576239 Em.:A1394074 Em.:A1371883

Em.:A1346775 Em.:R48082 Em.:AA431124 Em.:A1262500 Em.:R12836
 Em.:AA316825 Em.:A1285301 Em.:AA354191 Em.:A1222796
 Em.:A1401546.1 Em.:AA344952 Em.:R48089"
 /evidence=not_experimental
 /product="c39086.1 (chloride channel 7)"
 complement(4754..24756)
 /gene="CLCN7"
 /gene="CLCN7"
 complement(4758)
 /gene="CLCN7"
 complement(4761)
 /gene="CLCN7"
 complement(4773..4778)
 /gene="CLCN7"
 complement(4773..4778)
 /note="2 copies 53 mer 85% conserved"
 complement(join(6049..6135,6424..6504,6810..6986,
 7073..7132,7773..7902,8099..8184,8384..8511,8694..8745,
 9915..10084,11041..11134,12173..12311,13252..13312,
 13829..13883,14552..14668,15149..15213,15531..15624,
 16672..16755,17112..17174,18525..18605,19836..19945,
 20234..20366,20823..20888,21021..21092,24685..24756))
 /gene="CLCN7"
 /note="match: proteins: Sw.:P51798 Sw.:P51799 Wp.:CE06263
 Tr.:O60818 Sw.:O35454 Sw.:P51797 Tr.:P92943 Tr.:Q40485
 Tr.:P93567 Tr.:Q96282 Tr.:P78520 Tr.:O60820 Tr.:Q99428
 Tr.:P92942 Tr.:Q99429"
 /codon_start=1
 /evidence=not_experimental
 /product="c39086.1 (chloride channel 7)"
 /protein_id="CAB53065.1"
 /db_xref="GI:574851"
 /translation="SPRSALPRVGHMSVLELDDLPDMPDPHPPEKIPHNKLLS
 LKVESLDYDNSNOLFLEERIRNFRATRYVTKRWYCALIGITGLVACDIDYE
 NLAKIKRYIKNDKFTFKGSLSLMLATLNAFLVGVSTAFLEPVAAGGTP
 QIKCFNLGVKIPHVRLKTLVTKVGVSTVGVGLAVKEGPMHSGSVIAAGISGR
 STSLKRFKIEFEYFRDTEKRDVSGAAGVSAFGAPGVLSLEGSFMMQFL
 TWRIFFASMTSTFTLNFLVSTIGHMMDSGLINFGFSEKMAVTIHEIPVIAI
 GVGVGVGLGVFNALNWLMTMPRIYRIHRCLOVTAVALVAATVAVALVLYSSDCC
 PLOGGSMYSYPIOLPCADGEVNSMAAPFNPERSVSLFHPDGSYNPLTGLTFLYV
 FLACWYTGVLVSACVFIPLSLITGAKMRLGISLSTLTGAIAIMADPKYALMGAAG
 LGGIVATMLSLTIVIMMEATSNVTYGFPTMLVIMTKIVGDVFIEGLYPMHLOLOSVP
 LHMEAPVTSHTLAREVMSPTVCTLRREKGVIVDLSADSNINCPVVEHADDTQ
 PARLOGLIRLSOLIVLKHKVFVERSNGLVORLRLDRFADYRFPDQSIHYSD
 BEECMTDLSEFNPSPYVYPOEASLPVFKLFRALGLHLLVVDNRNVGVLTWKDL
 AARYLGRGIEELSLAQI"
 6868..7354
 /note="Cpg Island"
 /evidence=not_experimental
 9164..9296
 /note="L1me2 repeat: matches 6026. 6163 of consensus"
 9747..9808
 /note="2 copies 31 mer 98% conserved"
 10628..10913
 /note="Alu repeat: matches 9. 298 of consensus"
 11281..11360
 /note="2 copies 40 mer 93% conserved"
 12418..12730
 /note="AluSc repeat: matches 1. 308 of consensus"
 15976..16272
 /note="AluSc repeat: matches 1. 298 of consensus"
 16747..17046
 /note="6 copies 50 mer 98% conserved"
 18682..19479
 /note="Random repeat. Each repeat element 35bp, typical
 sequence: AGGGAAGGAGAGCAGCAGCAGCTTGCGGCCCC Restriction
 digest data (BAMHI) suggest there are around 6 copies of
 the repeat missing from this assembly."
 18742..19476
 /note="21 copies 35 mer 92% conserved"
 20300..20840
 /note="Cpg Island"
 /evidence=not_experimental
 20586..20810
 misc_feature

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repeat_region /note="match: GSS: Em:AQ490624"
21140..21224
/note="LIM4 repeat: matches 3611..3698 of consensus"
repeat_region 21225..21525
/note="Alus repeat: matches 5..305 of consensus"
repeat_region 21526..21598
/note="LIM4 repeat: matches 3697..3769 of consensus"
repeat_region 21665..21783
/note="FLAM_C repeat: matches 1..85 of consensus"
repeat_region 21784..22049
/note="Alus repeat: matches 46..312 of consensus"
repeat_region 22050..22100
/note="FLAM_C repeat: matches 85..143 of consensus"
repeat_region 22113..22296
/note="LIM4 repeat: matches 4771..4953 of consensus"
repeat_region 22297..22565
/note="Alus repeat: matches 1..301 of consensus"
repeat_region 22566..22762
/note="LIM4 repeat: matches 4953..5153 of consensus"
repeat_region 22773..22904
/note="FLAM_A repeat: matches 6..124 of consensus"
repeat_region 22905..23190
/note="Alus repeat: matches 1..288 of consensus"
repeat_region 23191..23207
/note="FLAM_A repeat: matches 124..141 of consensus"
repeat_region 23208..23486
/note="Alus repeat: matches 1..283 of consensus"
repeat_region 23498..23667
/note="LIM4 repeat: matches 5154..5328 of consensus"
misc_feature 23830..24276
/note="CpG island"
evidence=not_experimental
repeat_region 26089..26371
/note="Alus repeat: matches 1..311 of consensus"
repeat_region 27221..27535
/note="Alus repeat: matches 1..312 of consensus"
repeat_region 28181..28322
/note="LIM4 repeat: matches 7588..7739 of consensus"
repeat_region 28327..28653
/note="Alus repeat: matches 1..312 of consensus"
repeat_region 28654..28821
/note="LIM4 repeat: matches 5124..5282 of consensus"
repeat_region 28822..29129

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Query Match 85.0%; Score 17; DB 91; Length 31513;
Best Local Similarity 100.0%; Pred. No. 5,6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTGCGGGGCTGTGTC 20
Db 20788 GTGCGGGGCTGTGTC 20772

RESULT 15
AC046159/c AC046159 177883 bp DNA HTG 13-JAN-2001
DEFINITION Homo sapiens chromosome 16 clone RP11-270H24, WORKING DRAFT
ACCESSION AC046159
VERSION AC046159.2 GI:12203338
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 177883)
AUTHORS DOE Joint Genome Institute.
JOURNAL Sequencing of Human Chromosome 16
REFERENCE 2 (bases 1 to 177883)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (13-Apr-2000) Production Sequencing Facility, DOE Joint

COMMENT

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jan 13, 2001 this sequence version replaced gi:7547087.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 0
Center clone name: RPCI-11_270H24

Summary Statistics
Consensus quality: 121640 bases at least Q40
Consensus quality: 136890 bases at least Q30
Consensus quality: 145189 bases at least Q20
Estimated insert size: 191000; agarose-ff estimation
Estimated insert size: 174883; sum-of-contrigs estimation
Quality coverage: 3.52 in Q20 bases; agarose-ff estimation
Quality coverage: 3.85 in Q20 bases; sum-of-contrigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contrigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contrigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

1 1075: contrig of 1075 bp in length
1076 1175: gap of unknown length
1176 2368: contrig of 1193 bp in length
2369 2468: gap of unknown length
2469 3533: contrig of 1065 bp in length
3534 3633: gap of unknown length
3634 4710: contrig of 1077 bp in length
4711 4810: gap of unknown length
4811 5937: contrig of 1127 bp in length
5938 6038: gap of unknown length
6038 7194: contrig of 1157 bp in length
7195 7294: gap of unknown length
7295 8423: contrig of 1129 bp in length
8424 8524: gap of unknown length
8524 9684: contrig of 1160 bp in length
9684 11055: gap of unknown length
11056 11155: gap of unknown length
11156 12515: contrig of 1360 bp in length
12516 12615: gap of unknown length
12616 13689: contrig of 1074 bp in length
13690 15030: gap of unknown length
15031 15130: contrig of 1241 bp in length
15131 16134: gap of unknown length
16135 16234: gap of unknown length
16235 17237: contrig of 1002 bp in length
17238 17337: gap of unknown length
17338 18598: contrig of 1262 bp in length
18599 21218: gap of unknown length
21219 21318: contrig of 2520 bp in length
21319 25408: contrig of 4090 bp in length
25409 25509: gap of unknown length
25510 28682: contrig of 3174 bp in length
28683 32340: gap of unknown length
32341 32440: contrig of 3558 bp in length
32441 39478: gap of unknown length
39479 39578: contrig of 7038 bp in length
39579 45273: gap of unknown length
45274 45374: contrig of 5695 bp in length
45375 52448: gap of unknown length
52449 52548: contrig of 7075 bp in length
52549 61794: gap of unknown length
61795 61894: contrig of 9246 bp in length
61895 61894: gap of unknown length

```

```

* 61895 71299: contig of 9405 bp in length
* 71300 71399: gap of unknown length
* 71400 79399: contig of 8000 bp in length
* 79400 79499: gap of unknown length
* 79500 91287: contig of 11788 bp in length
* 91288 91387: gap of unknown length
* 91388 102397: contig of 11010 bp in length
* 102398 102497: gap of unknown length
* 102498 113593: contig of 11096 bp in length
* 113594 113693: gap of unknown length
* 113694 124177: contig of 10484 bp in length
* 124178 124277: gap of unknown length
* 124278 135521: contig of 11244 bp in length
* 135522 135621: gap of unknown length
* 135622 177883: contig of 42262 bp in length.

```

FEATURES

```

source
1.177883
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-270H24"
/clone_lib="RPC1 human BAC library 11"
BASE COUNT 39687 a 46077 c 48553 g 38297 t 5269 others
ORIGIN

```

```

Query Match 85.0%: Score 17; DB 72; Length 177883;
Best Local Similarity 100.0%: Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTGCGGGGCGCTGTGCC 20
|||||
Db 71622 GTGCGGGGCGCTGTGCC 71606

```

Search completed: April 20, 2001, 00:00:22
Job time: 9499 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:12:52 ; Search time 547.68 Seconds
(without alignments) 21.318 Million cell updates/sec

Title: US-09-016-464-16

Perfect score: 20
Sequence: 1 GGTGTGGCGGGCGCTGTGCC 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N.Geneseq_0401.*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT.*
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21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	18 T76109	Human prostaglandin D synthase
2	20	100.0	20	20 X53914	Human prostaglandin synthase
3	20	100.0	20	21 F19479	Human prostaglandin synthase
4	20	100.0	20	21 A33357	Human prostaglandin synthase
5	20	100.0	180	20 X54589	Human prostaglandin synthase
6	20	100.0	180	21 F20158	Human prostaglandin synthase
7	20	100.0	180	21 A34036	Human prostaglandin synthase
8	20	100.0	827	21 F21403	Human prostaglandin synthase
9	20	100.0	827	21 A35281	Human prostaglandin synthase
10	20	100.0	6225	20 X55273	Human prostaglandin synthase
11	20	100.0	6225	21 F20843	Human prostaglandin synthase

12	20	100.0	6225	21 A34721	Human prostaglandin synthase
13	20	100.0	35384	21 F21436	Human prostaglandin synthase
14	20	100.0	114955	20 X53491	Human prostaglandin synthase
15	18.4	92.0	307	21 C57699	Human prostaglandin synthase
16	18.4	92.0	879	20 Z41362	Human prostaglandin synthase
17	16.4	82.0	888	17 T59269	Human prostaglandin synthase
18	16.4	82.0	2888	17 T59268	Human prostaglandin synthase
19	15.8	79.0	36	9 N82502	Human prostaglandin synthase
20	15.8	79.0	840	21 Z88147	Human prostaglandin synthase
21	15.8	79.0	945	21 Z88148	Human prostaglandin synthase
22	15.8	79.0	1174	21 Z88151	Human prostaglandin synthase
23	15.8	79.0	1446	20 Z23804	Human prostaglandin synthase
24	15.8	79.0	1934	21 Z28073	Human prostaglandin synthase
25	15.8	79.0	1958	21 Z28105	Human prostaglandin synthase
26	15.8	79.0	4094	21 Z51205	Human prostaglandin synthase
27	15.8	79.0	4248	21 A28450	Human prostaglandin synthase
28	15.8	79.0	32768	20 X20515	Human prostaglandin synthase
29	15.4	77.0	1242	21 C7765	Human prostaglandin synthase
30	15.4	77.0	1269	19 V32042	Human prostaglandin synthase
31	15.4	77.0	1269	20 Z25279	Human prostaglandin synthase
32	15.4	77.0	1269	21 Z60241	Human prostaglandin synthase
33	15.4	77.0	1467	13 C20261	Human prostaglandin synthase
34	15.4	77.0	2687	21 Z20700	Human prostaglandin synthase
35	15.4	77.0	15079	16 Q91580	Human prostaglandin synthase
36	15.2	76.0	315	21 C06617	Human prostaglandin synthase
37	15.2	76.0	449	20 Z07227	Human prostaglandin synthase
38	15.2	76.0	449	21 C79117	Human prostaglandin synthase
39	15.2	76.0	568	21 A61799	Human prostaglandin synthase
40	15.2	76.0	723	21 A61701	Human prostaglandin synthase
41	15.2	76.0	803	20 X04317	Human prostaglandin synthase
42	15.2	76.0	890	21 C08973	Human prostaglandin synthase
43	15.2	76.0	952	21 A61699	Human prostaglandin synthase
44	15.2	76.0	1004	21 A61702	Human prostaglandin synthase
45	15.2	76.0	1083	21 A61700	Human prostaglandin synthase

ALIGNMENTS

RESULT	1
ID	T76109 standard; DNA; 20 BP.
XX	T76109;
AC	12-SEP-1997 (first entry)
DT	XX
DE	Human prostaglandin D synthase antisense oligonucleotide HUMPROSYNAS1.
XX	XX
KW	Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW	chronic obstructive pulmonary disease; bronchitis; ss.
OS	Synthetic.
XX	XX
PN	W09640162-A1.
XX	XX
PD	19-DEC-1996.
XX	XX
PF	06-JUN-1996; 96WO-US09306.
PR	07-JUN-1995; 95US-0474497.
XX	XX
PA	(UYEC-) UNIV EAST CAROLINA.
XX	XX
PI	Metzger WJ, Nyce JW;
XX	XX
DR	WPI; 1997-051871/05.
XX	XX
PT	Treatment of airway diseases such as asthma - by topically applying
PT	adenosine-free antisense oligo:nucleotide to airway epithelium of
PT	subject
PS	Claim 5; Page 26; 71pp; English.

CC The specification describes antisense oligonucleotides (X532869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 3'-end and the 3'-end and the junction between coding and non-coding
CC 5'-end, the 3'-end and the junction between coding and non-coding

DE Human prostaglandin D synthase polynucleotide fragment #1046.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cystostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW surfactant distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW respiratory hyperinflation; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

DATE 2000/00/00.
XX
XX

PT trigger adenosine receptors during metabolism, useful e.g. for treating

aa Claim 14; Page 141; 1592pp; English.
PS

CC The present invention describes low adenosine (A) content antisense

oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiallergic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. F18434 to F21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Sequence 20 BP; 0 A; 5 C; 11 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 GGTCGCGGGCCTGTGCC 20
|||||
Db 1 ggtctgcgggacctgtgtcc 20

RESULT 4
A33357
ID A33357 standard; DNA: 20 BP.
XX
AC A33357;
XX

28-JUL-2000 (first entry)

Low adenosine antisense oligonucleotide SEQ ID NO:1046.

Human; adenosine receptor; low adenosine antisense oligonucleotide;
phosphodiesterase; impaired respiration; inflammation; allergy;
allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
antiallergic; antiallergic; cytosolic; analgesic; impaired airway;
lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
respiratory distress syndrome; pain; cystic fibrosis; emphysema;
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99WO-US17712.

03-AUG-1998; 98US-0095212.

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;
PI

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, PT bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers

Claim 18; Page 396; 1343p; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiallergic, cytosolic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. A3313 to A35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323 to A33922) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

Sequence 20 BP; 0 A; 5 C; 11 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.6; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

OY 1 GGTCGCGGGCCTGTGCC 20
|||||
Db 1 ggtctgcgggacctgtgtcc 20

RESULT 5
X54589
ID X54589 standard; DNA: 180 BP.
XX
AC X54589;
XX

05-JUL-1999 (first entry)

Prostaglandin D synthase antisense oligonucleotide fragment.

Antisense oligonucleotide; multiple target; antisense treatment;
impaired respiration; inflammation; lung disease;
pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
respiratory distress syndrome; pain; cystic fibrosis;
pulmonary hypertension; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukaemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; pancreatic cancer;
hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
prostate cancer; ss.

Synthetic.

WO913886-A1.

OS
XX
XX
PN
XX

PD 25-MAR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19419.
 XX
 PR 09-JUN-1998; 98US-0093972.
 XX
 PR 17-SEP-1997; 97US-0059160.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI NYCE JW:
 XX
 PI WPI: 1999-229400/19.
 XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
 PT vasoconstriction
 XX
 PS Disclosure: Page 45; 120pp; English.
 XX
 CC The specification describes antisense oligonucleotides (X52869-X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of RNAs corresponding to target genes, gene
 CC initiation codons, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
 CC regions and all segments of RNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences X55272-74. These multiple target
 CC oligonucleotides (specifically X55180-271) can be used for the antisense
 CC treatment of diseases and conditions. Typical diseases and conditions
 CC are those associated with impaired respiration and inflammation,
 CC including lung diseases, pulmonary vasoconstriction, inflammation,
 CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
 CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
 CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
 CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
 CC metastases, as well as all types of cancers which may metastasize or have
 CC metastasized to the lungs, including breast and prostate cancer.
 CC
 XX Sequence 180 BP; 0 A; 62 C; 63 G; 42 T; 13 other;
 SQ
 Query Match 100.0%; Score 20; DB 20; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGTCGGGGCGCTGTGCC 20
 Db 1 ggtgcgagggcgctgtgcc 20
 RESULT 6
 F20158
 ID F20158 standard; DNA: 180 BP.
 XX
 AC F20158:
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human prostaglandin D synthase polynucleotide fragment #1725.
 XX
 KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KM human; airway disorder; bronchoconstriction; lung inflammation;
 KM surfactant depletion; bronchodilator; antiinflammatory;
 KM immunosuppressive; antisthmatic; analgesic; hypotensive; cyostatic;
 KM respiratory obstruction; pulmonary obstruction; impeded respiration;
 KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KM cancer; ss.
 KW
 XX Homo sapiens.
 OS

XX
 XX WO200062736-A2.
 XX
 PN 26-OCT-2000.
 XX
 PD 24-MAR-2000; 2000WO-US08020.
 XX
 PF 06-APR-1999; 99US-0127958.
 XX
 PR (UYEC-) UNIV EAST CAROLINA.
 XX
 PA (NYCE/) NYCE J W.
 XX
 PI NYCE JW:
 XX
 PI WPI: 2000-679539/66.
 XX
 DR Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Claim 14; Page 141; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antisthmatic, hypotensive and cyostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulin and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 CC
 XX Sequence 180 BP; 0 A; 62 C; 63 G; 42 T; 13 other;
 SQ
 Query Match 100.0%; Score 20; DB 21; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGTCGGGGCGCTGTGCC 20
 Db 1 ggtgcgagggcgctgtgcc 20
 RESULT 7
 A34036
 ID A34036 standard; DNA: 180 BP.
 XX
 AC A34036:
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human adenosine receptor related polynucleotide SEQ ID NO:1725.
 XX

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Disclosure: Page 479; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A3233 to A35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32333
 CC to A33922) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 CC
 XX
 SQ Sequence 180 BP; 0 A; 62 C; 63 G; 42 T; 13 other;

Query Match 100.0%; Score 20; DB 21; Length 180;
 Best Local Similarity 100.0%; Pred. NO. 5.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGTGCGGGCGCTGCTGCC 20
 ||||||||||||||||||||
 Db 1 ggtgtgcgggcgctgtgtgcc 20

RESULT 8
 F21403/c

ID F21403 standard; DNA; 827 BP.
 XX
 AC F21403;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human low adenosine antisense oligonucleotide related sequence #2970.
 KW
 KW low adenosine antisense oligonucleotide; phosphothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impaired respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US08020.
 XX
 PR 06-APR-1999; 99US-0127958.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure: Page 1388; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impaired respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 827 BP; 156 A; 302 C; 224 G; 145 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 827;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTGTGCGGGCCTGTGCC 20
|||||
DB 68 GGTGTGCGGGCCTGTGCC 49

RESULT 9
A35281/C
ID A35281 standard; DNA: 827 BP.
AC A35281;
XX
XX 28-JUL-2000 (first entry)
XX
XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:155.
XX
XX Human: adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antiasthmatic; cytosolic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
XX Homo sapiens.
XX
XX WO200009525-A2.
XX
XX 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US1712.
XX
XX 03-AUG-1998; 98US-0095212.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI, 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX cancers -
XX
XX Disclosure: Page 1303; 1343pp; English.

CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytosolic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences

CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX
XX SQ Sequence 827 BP; 156 A; 302 C; 224 G; 145 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 827;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTGTGCGGGCCTGTGCC 20
|||||
DB 68 GGTGTGCGGGCCTGTGCC 49

RESULT 10
X55273
ID X55273 standard; DNA: 6225 BP.
XX
XX X55273;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human enzyme-related antisense polynucleotide.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
XX impaired respiration; inflammation; lung disease;
XX pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX acute asthma; allergy; asthma; impaired respiration;
XX respiratory distress syndrome; pain; cystic fibrosis;
XX pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
XX colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX prostate cancer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO9913886-A1.
XX
XX 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US19419.
XX
XX 09-JUN-1998; 98US-0093972.
XX
XX 17-SEP-1997; 97US-0059160.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI, 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX vasoconstriction
XX
XX Disclosure: Page 24-25; 120pp; English.

CC The specification describes antisense oligonucleotides (X52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the juxta-section between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences X55272-74. These multiple target
CC oligonucleotides (specifically X55180-271) can be used for the antisense
CC treatment of diseases and conditions. Typical diseases and conditions
CC are those associated with impaired respiration and inflammation,

CC Including lung diseases, pulmonary vasoconstriction, inflammation,
CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,
CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary
CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic
CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
CC metastases, as well as all types of cancers which may metastasize or have
CC metastasized to the lungs, including breast and prostate cancer.
XX
SQ Sequence 6225 BP; 13 A; 2111 C; 2185 G; 1580 T; 336 other;

Query Match 100.0%; Score 20; DB 20; Length 6225;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTGCGGGGCGCTGTGCC 20
|||||
DB 133 ggtgtgcggggcctgtgcc 152

RESULT 11
F20843
ID F20843 standard; DNA: 6225 BP.
XX
AC F20843;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human multiple target antisense (MTA) oligonucleotide #2410.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiallergic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PA (NYCE/) NYCE J W.
XX
PI NYCE JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX
Claim 14; Page 636-637; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with

CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adenosine molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasocactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the
CC present invention.
XX
SQ Sequence 6225 BP; 13 A; 2111 C; 2186 G; 1580 T; 335 other;

Query Match 100.0%; Score 20; DB 21; Length 6225;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTGCGGGGCGCTGTGCC 20
|||||
DB 133 ggtgtgcggggcctgtgcc 152

RESULT 12
A34721
ID A34721 standard; DNA: 6225 BP.
XX
AC A34721;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2410.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiallergic; cytostatic; analgesic; impaired airway;
KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PA NYCE JW;
XX
PI NYCE JW;
XX
DR WPI; 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers -
 XX
 PS Disclosure: Page 568-569; 1343pp: English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antispasmodic, cytosstatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A32313 to A35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
 CC to A33922) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 XX
 SQ Sequence 6225 BP; 13 A; 2111 C; 2186 G; 1580 T; 335 other;
 XX
 Query Match 100.0%; Score 20; DB 21; Length 6225;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GGTGTGGGGGCGCTGGTGC 20
 Db 133 ggtgtgggggctgtgtgc 152
 XX
 RESULT 13
 F21436
 ID F21436 standard; DNA: 35384 BP.
 XX
 AC F21436;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human enzyme-related antisense polynucleotide #303.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antispasmodic; analgesic; hypotensive; cytosstatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PM WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000MO-US08020.
 XX
 PR 06-APR-1999; 9905-0127958.
 XX

PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 DR WPI: 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not
 PT trigger adenosine receptors during metabolism, useful e.g. for treating
 PT cancers and respiratory obstructions -
 XX
 PS Disclosure: Page 47-55; 1592pp: English.
 XX
 XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antispasmodic, hypotensive and cytosstatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
 CC and/or surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
 CC and antisense oligonucleotides used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 35384 BP; 7013 A; 10128 C; 10025 G; 7883 T; 335 other;
 XX
 Query Match 100.0%; Score 20; DB 21; Length 35384;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GGTGTGGGGGCGCTGGTGC 20
 Db 130 ggtgtgggggctgtgtgc 149
 XX
 RESULT 14
 X53491
 ID X53491 standard; DNA: 114955 BP.
 XX
 AC X53491;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human adenosine A1 receptor antisense oligonucleotide fragment.
 XX
 KW Antisense oligonucleotide; multiple target; antisense treatment;
 KW impaired respiration; inflammation; lung disease;
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
 KW acute asthma; allergy; asthma; impeded respiration;
 KW respiratory distress syndrome; pain; cystic fibrosis;
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
 KW

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OM nucleic - nucleic search, using sw model

Run on: April 19, 2001, 23:24:52 ; Search time 7150.85 seconds
(without alignments)
0.409 Million cell updates/sec

Title: US-09-016-464-16
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	18.4	92.0	151	AA299730	AA299730 EST12313
2	18.4	92.0	165	R30667	R30667 CBS-136 Sub
3	18.4	92.0	182	BF726597	BF726597 by09a12.y
4	18.4	92.0	193	AA299984	AA299984 EST12607
5	18.4	92.0	196	AA317069	AA317069 EST19112
6	18.4	92.0	223	C05567	C05567 C05567 Huma
7	18.4	92.0	235	AA335523	AA335523 EST19932
8	18.4	92.0	241	D56554	D56554 HUM421H03B
9	18.4	92.0	245	AA324295	AA324295 EST27090
10	18.4	92.0	246	AA317227	AA317227 EST19178
11	18.4	92.0	249	T39489	T39489 ya06e10.r2
12	18.4	92.0	254	AA299915	AA299915 EST12588
13	18.4	92.0	257	H18585	H18585 yns1a12.r1
14	18.4	92.0	258	AA336051	AA336051 EST40732
15	18.4	92.0	261	AA338917	AA338917 EST43938
16	18.4	92.0	263	AA335848	AA335848 EST10467
17	18.4	92.0	270	AA338881	AA338881 EST43892
18	18.4	92.0	277	C04118	C04118 C04118 Huma

C 19	18.4	92.0	282	121	AM900966
C 20	18.4	92.0	293	175	CO2831
C 21	18.4	92.0	295	5	AA300087
C 22	18.4	92.0	299	5	AA335999
C 23	18.4	92.0	318	175	CO5313
C 24	18.4	92.0	324	5	AA339101
C 25	18.4	92.0	324	143	BF092074
C 26	18.4	92.0	325	5	AA326323
C 27	18.4	92.0	330	175	CO5306
C 28	18.4	92.0	339	5	AA299498
C 29	18.4	92.0	343	152	D58609
C 30	18.4	92.0	351	168	BF724646
C 31	18.4	92.0	351	175	CO5354
C 32	18.4	92.0	359	31	AV693696
C 33	18.4	92.0	368	152	D56252
C 34	18.4	92.0	374	175	CO5405
C 35	18.4	92.0	375	5	AA326215
C 36	18.4	92.0	377	162	BE047690
C 37	18.4	92.0	378	5	AA335558
C 38	18.4	92.0	388	175	CO4471
C 39	18.4	92.0	431	152	H21147
C 40	18.4	92.0	440	5	AA317276
C 41	18.4	92.0	442	158	W44853
C 42	18.4	92.0	442	175	CO5072
C 43	18.4	92.0	455	168	BF724306
C 44	18.4	92.0	457	20	A1460330
C 45	18.4	92.0	458	168	BF724478

ALIGNMENTS

RESULT 1
LOCUS AA299730/c
DEFINITION EST12313 Uterus tumor I Homo sapiens CDNA 5' end similar to
prostaglandin D synthase, mRNA sequence.
ACCESSION AA299730
VERSION AA299730.1 GI:1952082
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 151)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,
C.J., Lee,N.H., Kirness,E.F., Weinstein,K.G., Gocayne,J.D., White,
O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Flege,L.D., Fitzgerald,
J.L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodok,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanguas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uteback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimhe,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.M.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,
M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other ESTs: TH0169388
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423

Email: arkerlav@ligr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

source
1..151
/organism="Homo sapiens"
/db_xref="ATCC (inhost):193156"
/db_xref="taxon:9606"
/clone_lib="Uterus tumor I"
/dev_stage="adult"
/note="Organ: uterus; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

BASE COUNT

25 a 56 c 43 g 23 t 4 others

ORIGIN

Query Match 92.0%; Score 18.4; DB 5; Length 151;
Best local Similarity 95.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTCGGGGGCTGGTCC 20
|||||
Db 47 GGTCGGGGGCTGGTCC 28

RESULT 2

R30667/c
LOCUS R30667
DEFINITION CBS-136 Subtractive cDNA library ocular ciliary body Homo sapiens
CDNA clone CBS-136 5' end similar to Prostaglandin D2 synthase
(accession # M61901), mRNA sequence.
ACCESSION R30667
VERSION R30667.1 GI:785982
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 165)
AUTHORS Escaribano,J., Ortego,J. and Coca-Prados,M.
TITLE Isolation and characterization of cell-specific cDNA clones from a
subtractive library of the ocular ciliary body of a single normal
human donor: Transcription and synthesis of plasma proteins
J. Biochem. (Tokyo) 118 (5), 921-931 (1995)

JOURNAL

MEDLINE 96318503
COMMENT Contact: Coca-Prados, M.
Department of Ophthalmology and Visual Science
Yale University Medical School
330 Cedar Street, New Haven, CT 06520-8061
Tel: 2037852742
Fax: 2037856123
Email: miguel_coca-prados@quickmail.yale.edu
Seq primer: T3.

FEATURES

source
1..165
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Subtractive cDNA library ocular ciliary body"
/note="Vector: pBluescript II SK; Site_1: EcoRI; Site_2:
XhoI; A subtractive cDNA library was developed by
hybridizing antisense, single-stranded phagemid DNA (ssDNA
) (as pBluescript SK-) from the ocular ciliary body cDNA
library (target) of a 34-year-old female donor in
lambda-uni-ZAP XR with biotinylated sense RNA of an ocular
cell line cDNA library (driver) in the same vector."

BASE COUNT

30 a 60 c 47 g 24 t 4 others

ORIGIN

Query Match

92.0%; Score 18.4; DB 155; Length 165;

Best Local Similarity 95.0%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCCGGGGCTGTGTGCC 20
||||| |||||||
DB 35 GGTGTCCGGGGCTGTGTGCC 16

RESULT 3
LOCUS BF726597 182 bp mRNA EST 05-JAN-2001
DEFINITION by09a12.y1 Human Lens cDNA (Un-normalized, unamplified): By Homo sapiens cDNA clone by09a12 5', mRNA sequence.
ACCESSION BF726597
VERSION BF726597.1 GI:12042508
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 182)
Mistow, G.J., Bernstein, S., Behal, A. and Smith, D.
TITLE NEBANK: EST analysis and bioinformatics for ocular genomics
JOURNAL Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
COMMENT Contact: Mistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gremehel@nei.nih.gov
Plate: 09 row: a column: 12
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
source
1..182
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="by09a12"
/clone_11b="Human Lens cDNA (Un-normalized, unamplified): By"
/tissue_type="lens"
/dev_stage="Adult"
/lab_host="EMDH10b"
/note="Organ: Eye; Vector: PCMVSPORT6; Two human lenses from different adults (both approximately 40 years old) together yielded 20ug of total RNA and 150ng mRNA by cDNA library synthesis. A directionally cloned cDNA library in the PCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor (5'-pGACTAGTCTAGATCGGAGCGGCGCC(T)15-3'). Not I/Dlunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

BASE COUNT 31 a 67 c 55 g 29 t
ORIGIN

Query Match 92.0%; Score 18.4; DB 168; Length 182;
Best Local Similarity 95.0%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCCGGGGCTGTGTGCC 20
||||| |||||||
DB 44 GGTGTCCGGGGCTGTGTGCC 25

RESULT 4
LOCUS AA299984 193 bp mRNA EST 18-APR-1997

DEFINITION EST12607 Uterus tumor I Homo sapiens cDNA 5' end similar to prostaglandin D synthase, mRNA sequence.
ACCESSION AA299984
VERSION AA299984.1 GI:1952335
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 193)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Pulder, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weissbrock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Val, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Matmaros, S.M., Merrick, J.M., Moreno-Palanges, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, R., Small, R.V., Spriggs, T.A., Ulterback, T.R., Weidman, J.F., Li, Y., Bedarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A., He, M.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)
MEDLINE 96026280
COMMENT Other ESTs: TH0169388
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/ldb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES
source
1..193
/organism="Homo sapiens"
/db_xref="ATCC (Inhost):192964"
/db_xref="taxon:9606"
/clone_11b="uterus tumor I"
/dev_stage="Adult"
/note="Organ: uterus; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 32 a 67 c 61 g 31 t 2 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 5; Length 193;
Best Local Similarity 95.0%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCCGGGGCTGTGTGCC 20
||||| |||||||
DB 40 GGTGTCCGGGGCTGTGTGCC 21

RESULT 5
LOCUS AA317069 196 bp mRNA EST 19-APR-1997
DEFINITION EST19112 Retina II Homo sapiens cDNA 5' end similar to prostaglandin D synthase, mRNA sequence.
ACCESSION AA317069
VERSION AA317069.1 GI:1969548
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 196)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.D., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brannon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanguas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other_ESTs: THC169388
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
Location/Qualifiers
1..196
/organism="Homo sapiens"
/db_xref="ATCC (inhost):117670"
/db_xref="taxon:9606"
/clone_lib="Retina II"
/sex="mixed"
/dev_stage="adult"
/note="Organ: retina; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 32 a 68 c 61 g 32 t 3 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 5; Length 196;
Best Local Similarity 95.0%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTGGGGGCGCTGGTCC 20
||||| |||||||||
Db 40 GGTGTCCGGGGCGCTGGTCC 21

RESULT 6
LOCUS C05567/c 223 bp mRNA EST 30-JUL-1996
DEFINITION C05567 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NH4431, mRNA sequence.
ACCESSION C05567
VERSION C05567.1 GI:1468818
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 223)
AUTHORS Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and Nakamura,Y.
TITLE Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3060 clones by partial sequencing
JOURNAL Genomics 35 (1), 231-235 (1996)
MEDLINE 96299762
COMMENT Contact: Yusuke Nakamura
Institute of Medical Science
University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
Email: yusuke@ims.u-tokyo.ac.jp.

FEATURES
source 1..223
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="3NH4431"
/clone_lib="Human heart cDNA (Ynakamura)"
/dev_stage="adult"
/note="Organ: heart; normalized directionally cloned cDNA from adult heart"

BASE COUNT 33 a 79 c 67 g 39 t 5 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 175; Length 223;
Best Local Similarity 95.0%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTGGGGGCGCTGGTCC 20
||||| |||||||||
Db 40 GGTGTCCGGGGCGCTGGTCC 21

RESULT 7
LOCUS AA335523/c 235 bp mRNA EST 21-APR-1997
DEFINITION EST39932 Epilidymus Homo sapiens cDNA 5' end similar to similar to prostaglandin D synthase, mRNA sequence.
ACCESSION AA335523
VERSION AA335523.1 GI:1987766
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 235)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.D., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brannon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanguas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other_ESTs: THC166416
Contact: Kerlavage, AR
Bioinformatics

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423

Email: arkerlavet@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hg1.html>)
Seq primer: M13 Reverse

FEATURES
source
1..235
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="ATCC (lnhost):137191"
/db_xref="taxon:9606"
/clone_1lb="Epididymus"
/sex="male"
/dev_stage="adult"
/note="Organ: epididymis; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
BASE COUNT 43 a 79 c 67 g 40 t 6 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 5; Length 235;
Best Local Similarity 95.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCCGGGGCGCTGTGCC 20
||||| ||||||| |||||||
Db 29 GGTGTCCGGGGCGCTGTGCC 10

RESULT 8
D56254/c 241 bp mRNA EST 31-AUG-1995
LOCUS HUM421H03B Clontech human fetal brain polyA+ mRNA (#6535) Homo
DEFINITION sapiens cDNA clone GEN-421H03 5', mRNA sequence.
ACCESSION D56254
VERSION D56254.1 GI:970791
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 241)
Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,
Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinozumi,H., Takaiichi,
A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H.,
Shin,S. and Nakamura,Y.

TITLE Unpublished (1995)
JOURNAL Contact: Tsutomu Fujiwara

COMMENT Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawachi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.

FEATURES
source
1..241
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GEN-421H03"
/clone_1lb="Clontech human fetal brain polyA+ mRNA (#6535)
)"
BASE COUNT 40 a 85 c 79 g 36 t 1 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 152; Length 241;
Best Local Similarity 95.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCCGGGGCGCTGTGCC 20

Db 41 GGTGTCCGGGGCGCTGTGCC 22
||||| ||||||| |||||||

RESULT 9
AA324295/c 245 bp mRNA EST 20-APR-1997
LOCUS EST27090 Cerebellum II Homo sapiens cDNA 5' end similar to
DEFINITION prostaglandin D synthase, mRNA sequence.

ACCESSION AA324295
VERSION AA324295.1 GI:1976538
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 245)
Adams,M.D., Karlavag,A.R., Fleischmann,R.D., Fulmer,R.A., Bult
C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Mai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauden,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Ulterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrer,A., Fischer,C., Hastings,G.A., He,M.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Melissner,P.S., Olsen,H., Raymond,L.,
Wel,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
96026280

OTHER ESTS: THC169388
Contact: Kerlavage, AR
Bioinformatics

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423

Email: arkerlavet@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hg1.html>)
Seq primer: M13 Reverse.

FEATURES
source
1..245
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="ATCC (lnhost):124768"
/db_xref="taxon:9606"
/clone_1lb="Cerebellum II"
/tissue_type="cerebellum"
/dev_stage="adult"
/note="Organ: brain; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
BASE COUNT 40 a 85 c 79 g 39 t 2 others
ORIGIN

Query Match 92.0%; Score 18.4; DB 5; Length 245;
Best Local Similarity 95.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCCGGGGCGCTGTGCC 20
||||| ||||||| |||||||
Db 43 GGTGTCCGGGGCGCTGTGCC 24

RESULT 10
AA317227/c
LOCUS
DEFINITION
AA317227 246 bp mRNA EST 19-APR-1997
EST19178 Retina II Homo sapiens cDNA 5' end similar to
prostaglandin D synthase, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 246)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodex,A.,
Gnethl,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utechtack,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.
TITLE
Initial assessment of human gene diversity and expression patterns
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JOURNAL
MEDLINE
Nature 377 (6547 Suppl), 3-174 (1995)
COMMENT
Other_ESTS: TNC169388
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
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1. 246
/organism="Homo sapiens"
/db_xref="ATCC (inhost):117731"
/db_xref="taxon:9606"
/clone_lib="Retina II"
/sex="mixed"
/dev_stage="adult"
/note="Organ: retina"
Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
BASE COUNT
40 a 87 c 80 g 39 t
ORIGIN
Query Match 92.0%; Score 18.4; DB 5; Length 246;
Best Local Similarity 95.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

IMAGE:60714 5' similar to similar to SP:A44455 A44455 PROSTAGLANDIN
D2 SYNTHASE -, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 249)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins
M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Martis,E., Moore
B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Treviski,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Other_ESTS: ya06e10.s1
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: M13RP1.
Location/Qualifiers
FEATURES
source
1. 249
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:60714"
/clone_lib="Stratagene placenta (#937225)"
/sex="male"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Caucasian. Average insert size: 1.2 kb. Uni-ZAP
XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'"
BASE COUNT
43 a 84 c 83 g 39 t
ORIGIN
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Best Local Similarity 95.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 11
T39489/c
LOCUS
DEFINITION
T39489 249 bp mRNA EST 27-JAN-1995
EST ya06e10.r2 Stratagene placenta (#937225) Homo sapiens cDNA clone
Query Match 92.0%; Score 18.4; DB 5; Length 246;
Best Local Similarity 95.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 12
AA299915/c
LOCUS
DEFINITION
AA299915 254 bp mRNA EST 18-APR-1997
EST12588 uterus tumor I Homo sapiens cDNA 5' end similar to
prostaglandin D synthase, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 254)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE
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JOURNAL
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MEDLINE
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COMMENT
Other_ESTs: THC169388
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
Location/Qualifiers
1..258
/organism="Homo sapiens"
/db_xref="ATCC (inhost):137917"
/db_xref="taxon:9606"
/clone_lib="Epididymus"
/sex="male"
/dev_stage="adult"
/note="Organ: epididymis; Vector: pbluescript SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT
43 a 89 c 83 g 42 t 1 others

ORIGIN

Query Match 92.0%; Score 18.4; DB 5; Length 258;
Best local Similarity 95.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGTGCGGGGCGCTGTGCC 20
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DB 43 GGTTCTCCGGGCGCTGTGCC 24

RESULT 15
AA338917/c 261 bp mRNA EST 21-APR-1997
LOCUS
DEFINITION
EST43938 Fetal brain I Homo sapiens cDNA 5' end similar to
prostaglandin D synthase, mRNA sequence.

ACCESSION
AA338917
VERSION
AA338917.1 GI:1991155

KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 261)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Val,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitchugh,W.M., Fitchman,J.L., Geoghegan,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaro,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,

Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
Location/Qualifiers
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/note="Organ: brain; Vector: pbluescript SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT
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Best local Similarity 95.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 43 GGTTCTCCGGGCGCTGTGCC 24

Search completed: April 19, 2001, 23:24:55
Job time: 8172 sec

1. The first part of the document discusses the
2. importance of maintaining accurate records
3. of all transactions and the role of the
4. auditor in ensuring the integrity of the
5. financial statements. The second part of the
6. document discusses the various methods used
7. to audit financial statements and the
8. importance of the auditor's independence.
9. The third part of the document discusses the
10. various types of audits and the role of the
11. auditor in each type of audit. The fourth
12. part of the document discusses the various
13. types of errors and the role of the auditor
14. in identifying and correcting these errors.
15. The fifth part of the document discusses the
16. various types of fraud and the role of the
17. auditor in identifying and preventing these
18. types of fraud. The sixth part of the
19. document discusses the various types of
20. controls and the role of the auditor in
21. evaluating the effectiveness of these controls.
22. The seventh part of the document discusses
23. the various types of reports and the role of
24. the auditor in preparing these reports. The
25. eighth part of the document discusses the
26. various types of standards and the role of
27. the auditor in applying these standards. The
28. ninth part of the document discusses the
29. various types of laws and the role of the
30. auditor in complying with these laws. The
31. tenth part of the document discusses the
32. various types of ethical issues and the role
33. of the auditor in addressing these issues. The
34. eleventh part of the document discusses the
35. various types of professional organizations and
36. the role of the auditor in these organizations.
37. The twelfth part of the document discusses
38. the various types of continuing education and
39. the role of the auditor in completing this
40. education. The thirteenth part of the
41. document discusses the various types of
42. career opportunities and the role of the
43. auditor in pursuing these opportunities. The
44. fourteenth part of the document discusses the
45. various types of challenges and the role of
46. the auditor in overcoming these challenges.
47. The fifteenth part of the document discusses
48. the various types of rewards and the role of
49. the auditor in receiving these rewards. The
50. sixteenth part of the document discusses the
51. various types of risks and the role of the
52. auditor in managing these risks. The
53. seventeenth part of the document discusses the
54. various types of opportunities and the role of
55. the auditor in seizing these opportunities.
56. The eighteenth part of the document
57. discusses the various types of threats and the
58. role of the auditor in mitigating these
59. threats. The nineteenth part of the
60. document discusses the various types of
61. trends and the role of the auditor in
62. adapting to these trends. The twentieth
63. part of the document discusses the various
64. types of forecasts and the role of the
65. auditor in using these forecasts. The
66. twenty-first part of the document discusses
67. the various types of scenarios and the role
68. of the auditor in developing these scenarios.
69. The twenty-second part of the document
70. discusses the various types of strategies and
71. the role of the auditor in implementing these
72. strategies. The twenty-third part of the
73. document discusses the various types of
74. tactics and the role of the auditor in
75. executing these tactics. The twenty-fourth
76. part of the document discusses the various
77. types of tools and the role of the auditor
78. in using these tools. The twenty-fifth
79. part of the document discusses the various
80. types of techniques and the role of the
81. auditor in applying these techniques. The
82. twenty-sixth part of the document discusses
83. the various types of methods and the role of
84. the auditor in following these methods. The
85. twenty-seventh part of the document
86. discusses the various types of procedures and
87. the role of the auditor in performing these
88. procedures. The twenty-eighth part of the
89. document discusses the various types of
90. processes and the role of the auditor in
91. managing these processes. The twenty-ninth
92. part of the document discusses the various
93. types of systems and the role of the auditor
94. in evaluating these systems. The thirtieth
95. part of the document discusses the various
96. types of frameworks and the role of the
97. auditor in using these frameworks. The
98. thirty-first part of the document discusses
99. the various types of models and the role of
100. the auditor in applying these models. The
101. thirty-second part of the document discusses
102. the various types of theories and the role of
103. the auditor in testing these theories. The
104. thirty-third part of the document discusses
105. the various types of hypotheses and the role
106. of the auditor in proving these hypotheses.
107. The thirty-fourth part of the document
108. discusses the various types of conclusions and
109. the role of the auditor in drawing these
110. conclusions. The thirty-fifth part of the
111. document discusses the various types of
112. recommendations and the role of the auditor
113. in making these recommendations. The
114. thirty-sixth part of the document discusses
115. the various types of findings and the role of
116. the auditor in reporting these findings. The
117. thirty-seventh part of the document discusses
118. the various types of issues and the role of
119. the auditor in addressing these issues. The
120. thirty-eighth part of the document discusses
121. the various types of questions and the role
122. of the auditor in answering these questions.
123. The thirty-ninth part of the document
124. discusses the various types of answers and the
125. role of the auditor in providing these
126. answers. The fortieth part of the document
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128. the role of the auditor in implementing these
129. solutions. The forty-first part of the
130. document discusses the various types of
131. problems and the role of the auditor in
132. solving these problems. The forty-second
133. part of the document discusses the various
134. types of challenges and the role of the
135. auditor in overcoming these challenges. The
136. forty-third part of the document discusses
137. the various types of opportunities and the
138. role of the auditor in seizing these
139. opportunities. The forty-fourth part of the
140. document discusses the various types of
141. threats and the role of the auditor in
142. mitigating these threats. The forty-fifth
143. part of the document discusses the various
144. types of trends and the role of the auditor
145. in adapting to these trends. The forty-sixth
146. part of the document discusses the various
147. types of forecasts and the role of the
148. auditor in using these forecasts. The
149. forty-seventh part of the document discusses
150. the various types of scenarios and the role
151. of the auditor in developing these scenarios.
152. The forty-eighth part of the document
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154. the role of the auditor in implementing these
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156. document discusses the various types of
157. tactics and the role of the auditor in
158. executing these tactics. The fiftieth
159. part of the document discusses the various
160. types of tools and the role of the auditor
161. in using these tools. The fifty-first part
162. of the document discusses the various types
163. of techniques and the role of the auditor
164. in applying these techniques. The fifty-
165. second part of the document discusses the
166. various types of methods and the role of the
167. auditor in following these methods. The
168. fifty-third part of the document discusses
169. the various types of procedures and the role
170. of the auditor in performing these
171. procedures. The fifty-fourth part of the
172. document discusses the various types of
173. processes and the role of the auditor in
174. managing these processes. The fifty-fifth
175. part of the document discusses the various
176. types of systems and the role of the auditor
177. in evaluating these systems. The fifty-sixth
178. part of the document discusses the various
179. types of frameworks and the role of the
180. auditor in using these frameworks. The
181. fifty-seventh part of the document discusses
182. the various types of models and the role of
183. the auditor in applying these models. The
184. fifty-eighth part of the document discusses
185. the various types of theories and the role of
186. the auditor in testing these theories. The
187. fifty-ninth part of the document discusses
188. the various types of hypotheses and the role
189. of the auditor in proving these hypotheses.
190. The sixtieth part of the document discusses
191. the various types of conclusions and the role
192. of the auditor in drawing these conclusions.
193. The sixty-first part of the document
194. discusses the various types of
195. recommendations and the role of the auditor
196. in making these recommendations. The
197. sixty-second part of the document discusses
198. the various types of findings and the role of
199. the auditor in reporting these findings. The
200. sixty-third part of the document discusses
201. the various types of issues and the role of
202. the auditor in addressing these issues. The
203. sixty-fourth part of the document discusses
204. the various types of questions and the role
205. of the auditor in answering these questions.
206. The sixty-fifth part of the document
207. discusses the various types of answers and the
208. role of the auditor in providing these
209. answers. The sixty-sixth part of the
210. document discusses the various types of
211. solutions and the role of the auditor in
212. implementing these solutions. The sixty-
213. seventh part of the document discusses the
214. various types of problems and the role of the
215. auditor in solving these problems. The
216. sixty-eighth part of the document discusses
217. the various types of challenges and the role
218. of the auditor in overcoming these
219. challenges. The sixty-ninth part of the
220. document discusses the various types of
221. opportunities and the role of the auditor in
222. seizing these opportunities. The seventy-
223. first part of the document discusses the
224. various types of threats and the role of the
225. auditor in mitigating these threats. The
226. seventy-second part of the document
227. discusses the various types of trends and the
228. role of the auditor in adapting to these
229. trends. The seventy-third part of the
230. document discusses the various types of
231. forecasts and the role of the auditor in
232. using these forecasts. The seventy-fourth
233. part of the document discusses the various
234. types of scenarios and the role of the
235. auditor in developing these scenarios. The
236. seventy-fifth part of the document
237. discusses the various types of strategies and
238. the role of the auditor in implementing these
239. strategies. The seventy-sixth part of the
240. document discusses the various types of
241. tactics and the role of the auditor in
242. executing these tactics. The seventy-seventh
243. part of the document discusses the various
244. types of tools and the role of the auditor
245. in using these tools. The seventy-eighth
246. part of the document discusses the various
247. types of techniques and the role of the
248. auditor in applying these techniques. The
249. seventy-ninth part of the document
250. discusses the various types of methods and
251. the role of the auditor in following these
252. methods. The eightieth part of the
253. document discusses the various types of
254. procedures and the role of the auditor in
255. performing these procedures. The eighty-
256. first part of the document discusses the
257. various types of processes and the role of
258. the auditor in managing these processes. The
259. eighty-second part of the document
260. discusses the various types of systems and
261. the role of the auditor in evaluating these
262. systems. The eighty-third part of the
263. document discusses the various types of
264. frameworks and the role of the auditor in
265. using these frameworks. The eighty-fourth
266. part of the document discusses the various
267. types of models and the role of the auditor
268. in applying these models. The eighty-fifth
269. part of the document discusses the various
270. types of theories and the role of the
271. auditor in testing these theories. The
272. eighty-sixth part of the document discusses
273. the various types of hypotheses and the role
274. of the auditor in proving these hypotheses.
275. The eighty-seventh part of the document
276. discusses the various types of conclusions
277. and the role of the auditor in drawing these
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 00:03:42 ; Search time 280.46 Seconds
(without alignments)
12.451 Million cell updates/sec

Title: US-09-016-464-16

Perfect score: 20

Sequence: 1 GGTGTGGGGGCTGTGCC 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/prodata/2/lna/5A.COMB.seq:*

2: /cgn2_6/prodata/2/lna/5B.COMB.seq:*

3: /cgn2_6/prodata/2/lna/6A.COMB.seq:*

4: /cgn2_6/prodata/2/lna/6B.COMB.seq:*

5: /cgn2_6/prodata/2/lna/FACTUS.COMB.seq:*

6: /cgn2_6/prodata/2/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	827	1	US-08-726-725-3
C 2	16.8	84.0	30	1	US-08-426-819A-27
C 3	16	80.0	33	1	US-08-426-819A-28
C 4	15.4	77.0	1269	1	US-08-808-641-2
C 5	15.4	77.0	1269	2	US-09-064-839-2
C 6	15.4	77.0	1269	3	US-09-351-438-2
C 7	15.4	77.0	1467	1	US-08-176-620A-3
C 8	15.4	77.0	1467	1	US-08-463-862-3
C 9	15.4	77.0	1467	2	US-08-461-985-3
C 10	15.4	77.0	1467	2	US-08-458-887-3
C 11	15.2	76.0	1190	1	US-08-310-370-1
C 12	15.2	76.0	2129	1	US-08-426-819A-34
C 13	15.2	76.0	2138	3	US-08-776-271-1
C 14	15.2	76.0	2138	4	US-09-215-035-1
C 15	15.2	76.0	4464	4	US-08-400-159-7
C 16	15.2	76.0	4483	3	US-08-611-729A-7
C 17	14.8	74.0	36	2	US-08-570-155-9
C 18	14.8	74.0	36	5	PCT-US85-02861-9
C 19	14.8	74.0	41	1	US-08-239-256-18
C 20	14.8	74.0	41	6	5177193-20
C 21	14.8	74.0	55	2	US-08-467-747-1
C 22	14.8	74.0	55	2	US-08-467-747-2
C 23	14.8	74.0	55	2	US-08-467-747-3
C 24	14.8	74.0	161	2	US-08-613-965-3
C 25	14.8	74.0	161	2	US-08-918-966-3
C 26	14.8	74.0	161	3	US-08-921-655-3
C 27	14.8	74.0	228	2	US-08-613-965-4

28	14.8	74.0	228	2	US-08-918-966-4	Sequence 4, Appl1
29	14.8	74.0	228	3	US-08-921-655-4	Sequence 4, Appl1
30	14.8	74.0	252	3	US-08-617-256-24	Sequence 24, Appl1
31	14.8	74.0	252	4	US-09-287-141-24	Sequence 24, Appl1
32	14.8	74.0	277	3	US-08-765-332-107	Sequence 107, App
33	14.8	74.0	454	6	5177193-4	Patent No. 5177193
34	14.8	74.0	1006	1	US-08-239-256-1	Sequence 1, Appl1
35	14.8	74.0	1853	1	US-08-553-110-2	Sequence 2, Appl1
36	14.8	74.0	2070	1	US-07-766-351-6	Sequence 6, Appl1
37	14.8	74.0	2070	1	US-08-059-032-6	Sequence 6, Appl1
38	14.8	74.0	2070	5	PCT-US91-07290-6	Sequence 6, Appl1
39	14.8	74.0	3467	1	US-07-745-206A-12	Sequence 12, Appl1
40	14.8	74.0	5467	2	US-08-311-363-12	Sequence 12, Appl1
41	14.8	74.0	5499	3	US-08-479-722B-1	Sequence 6, Appl1
42	14.8	74.0	5502	5	PCT-US95-02251-17	Sequence 17, Appl1
43	14.8	74.0	5904	1	US-08-309-512-1	Sequence 1, Appl1
44	14.8	74.0	5904	5	PCT-US92-08756A-1	Sequence 1, Appl1
45	14.8	74.0	7175	1	US-08-455-543A-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-726-725-3/c
; Sequence 3, Application US/08726725
; Patent No. 5773290
; GENERAL INFORMATION:
; APPLICANT: Gould, Michael N.
; TITLE OF INVENTION: MAMMARY GLAND-SPECIFIC PROMOTERS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,725
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296, 93863
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 827 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-726-725-3

Query Match 100.0%; Score 20; DB 1; Length 827;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTGTGGGGGCTGTGCC 20
|||||
Db 68 GGTGTGGGGGCTGTGCC 49

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RESULT 2
US-08-426-819A-27/c
; Sequence 27, Application US/08426819A
; Patent No. 5723318
; GENERAL INFORMATION:
; APPLICANT: Yamaguchi, No. 5723318om1
; APPLICANT: Kojima, Tetsuo
; APPLICANT: Oh-Eda, Masayoshi
; APPLICANT: Hattori, Kunihito
; TITLE OF INVENTION: Genes Coding for Megakaryocyte
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,819A
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 230-107P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic primer, 850GA"
US-08-426-819A-27

Query Match      84.0%; Score 16, 8; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGCGGGGCGCTGGTGCC 20
DB 26 GCTCTCGGGGCGCTGGTGCC 7

RESULT 3
US-08-426-819A-28
; Sequence 28, Application US/08426819A
; Patent No. 5723318
; GENERAL INFORMATION:
; APPLICANT: Yamaguchi, No. 5723318om1
; APPLICANT: Kojima, Tetsuo
; APPLICANT: Oh-Eda, Masayoshi
; APPLICANT: Hattori, Kunihito
; TITLE OF INVENTION: Genes Coding for Megakaryocyte
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
```

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COUNTRY: USA
ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,819A
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 230-107P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic primer, 850GS"
US-08-426-819A-28

Query Match      80.0%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TCGGGGCGCTGGTGCC 20
DB 2 TCGGGGCGCTGGTGCC 17

RESULT 4
US-08-808-641-2
; Sequence 2, Application US/08808641
; Patent No. 5773274
; GENERAL INFORMATION:
; APPLICANT: HONKE, Koichi
; TITLE OF INVENTION: GENE ENCODING SULFOTRANSFERASE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,641
; FILING DATE: 28-FEBRUARY-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0295P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1269 base pairs
; TYPE: nucleic acid
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-808-641-2

Query Match 77.0%; Score 15.4; DB 1; Length 1269;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTGCGGGCGCTGTGTC 20
DB 445 GTGCGGGCGCTGTGTC 461

RESULT 5
US-09-064-839-2
Sequence 2, Application US/09064839

PATENT No. 5965419
GENERAL INFORMATION:
APPLICANT: HONKE, Koichi
TITLE OF INVENTION: GENE ENCODING SULFOTRANSFERASE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,839
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,641
FILING DATE: 28-FEBRUARY-1997
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0295P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1269 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-09-064-839-2

Query Match 77.0%; Score 15.4; DB 2; Length 1269;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTGCGGGCGCTGTGTC 20
DB 445 GTGCGGGCGCTGTGTC 461

RESULT 6
US-09-351-438-2
Sequence 2, Application US/09351438
Patent No. 6020467

GENERAL INFORMATION:
APPLICANT: HONKE, Koichi
TITLE OF INVENTION: GENE ENCODING SULFOTRANSFERASE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/351,438
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,641
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0295P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1269 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-09-351-438-2

Query Match 77.0%; Score 15.4; DB 3; Length 1269;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTGCGGGCGCTGTGTC 20
DB 445 GTGCGGGCGCTGTGTC 461

RESULT 7
US-08-176-620A-3/C
Sequence 3, Application US/08176620A
Patent No. 5595904
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayiotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-176-620A-3

Query Match
Best Local Similarity 94.1%; Score 15.4; DB 1; Length 1467;
Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGTGGGGGCTGTGTC 19
DB 1456 TGTGCGGGCTGTGTC 1440

RESULT 8
US-08-463-862-3/C
Sequence 3, Application US/08463862
Patent No. 5776751
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G. et al.
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,862
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-463-862-3

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 1; Length 1467;
Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGTGGGGGCTGTGTC 19
DB 1456 TGTGCGGGCTGTGTC 1440

RESULT 9
US-08-461-985-3/C
Sequence 3, Application US/08461985
Patent No. 5872006
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayiotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,985
FILING DATE: 05-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,620
FILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-461-985-3

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 2; Length 1467;
Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TGTGCGGGCCTGTGTC 19
||||| |||||||||
DB 1456 TGTGACGGCCTGTGTC 1440

RESULT 10
US-08-458-887-3/C
; Sequence 3, Application US/08458887
; Patent No. 5914261
; GENERAL INFORMATION:
; APPLICANT: Boulton, Teri G. et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennine & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,887
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,544
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1467 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1245
; US-08-458-887-3

Query Match 77.0%; Score 15.4; DB 2; Length 1467;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TGTGCGGGCCTGTGTC 19
||||| |||||||||
DB 1456 TGTGACGGCCTGTGTC 1440

RESULT 11
US-08-310-370-1/C
; Sequence 1, Application US/08310370
; Patent No. 5672349
; GENERAL INFORMATION:
; APPLICANT: NESBURN, ANTHONY B
; APPLICANT: WECHSLER, STEVEN L
; APPLICANT: GHIAZI, HOMAYON
; TITLE OF INVENTION: PROCESS FOR THE EXPRESSION OF HERPES

; TITLE OF INVENTION: SIMPLEX VIRUS TYPE 1 GLYCOPROTEIN I AND METHODS OF USE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 611 WEST SIXTH ST.
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,370
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,999
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAKE, DEBORAH L.
; REGISTRATION NUMBER: 34,832
; REFERENCE/DOCKET NUMBER: 197/058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213/489-1600
; TELEFAX: 213/955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1190 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-310-370-1

Query Match 76.0%; Score 15.2; DB 1; Length 1190;
Best Local Similarity 85.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGTGTGCGGGCCTGTGTC 20
||||| ||| ||||| ||
DB 220 GGTGTGCGGGCCTGTGTC 201

RESULT 12
US-08-426-819A-34
; Sequence 34, Application US/08426819A
; Patent No. 5723318
; GENERAL INFORMATION:
; APPLICANT: Yamaguchi, No. 5723318om1
; APPLICANT: Kojima, Tetsuo
; APPLICANT: Oh-Eda, Masayoshi
; APPLICANT: Hattori, Kunihiko
; TITLE OF INVENTION: Genes Coding for Megakaryocyte
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P. O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 20, 2001, 03:21:20 ; Search time 1165 Seconds
(without alignments)
9.327 Million cell updates/sec

Title: US-09-016-464-16

Perfect score: 20
Sequence: 1 GGTGTGCGGCGCTGTGTC 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13168883 seqs, 2603265903 residues

Total number of hits satisfying chosen parameters: 26337766

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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39: /cgn2_6/ptodata/2/pna/US09_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US09_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US09_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US09_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US09_COMB.seq:*
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Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	8	US-08-474-497-16
2	20	100.0	20	14	US-09-016-464-16
3	20	100.0	20	19	US-09-509-152A-1046
4	20	100.0	180	19	US-09-509-152A-1725
5	20	100.0	827	14	US-09-058-707-3
6	20	100.0	6225	19	US-09-509-152A-2410
7	19	95.0	277	14	US-09-040-265A-2443
8	19	95.0	277	14	US-09-040-265A-2443
9	19	95.0	277	20	US-09-533-806-825
10	18.4	92.0	132	13	US-08-960-741-378
11	18.4	92.0	132	13	US-09-533-806-3263
12	18.4	92.0	132	35	US-06-030-888-378
13	18.4	92.0	153	20	US-09-533-806-3298
14	18.4	92.0	171	20	US-09-533-806-823
15	18.4	92.0	171	34	US-06-023-278-2937
16	18.4	92.0	179	13	US-08-960-741-846
17	18.4	92.0	179	35	US-06-030-888-98
18	18.4	92.0	191	13	US-08-960-741-298
19	18.4	92.0	191	20	US-09-533-806-811
20	18.4	92.0	191	35	US-06-030-888-298
21	18.4	92.0	208	13	US-08-960-741-1757
22	18.4	92.0	208	13	US-08-960-741-1220
23	18.4	92.0	208	13	US-06-030-888-98
24	18.4	92.0	208	13	US-08-960-741-98
25	18.4	92.0	208	13	US-08-960-741-98
26	18.4	92.0	208	13	US-08-960-741-98
27	18.4	92.0	208	13	US-08-960-741-98
28	18.4	92.0	208	13	US-08-960-741-98
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31	18.4	92.0	208	13	US-08-960-741-98
32	18.4	92.0	208	13	US-08-960-741-98
33	18.4	92.0	208	13	US-08-960-741-98
34	18.4	92.0	208	13	US-08-960-741-98
35	18.4	92.0	208	13	US-08-960-741-98
36	18.4	92.0	208	13	US-08-960-741-98
37	18.4	92.0	208	13	US-08-960-741-98
38	18.4	92.0	208	13	US-08-960-741-98
39	18.4	92.0	208	13	US-08-960-741-98
40	18.4	92.0	208	13	US-08-960-741-98
41	18.4	92.0	208	13	US-08-960-741-98
42	18.4	92.0	208	13	US-08-960-741-98
43	18.4	92.0	208	13	US-08-960-741-98
44	18.4	92.0	208	13	US-08-960-741-98
45	18.4	92.0	208	13	US-08-960-741-98

ALIGNMENTS

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RESULT 1
US-08-474-497-16
; Sequence 16, Application US/08474497
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,497
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-497-16

Query Match          100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCGGGGCCTGTCGCC 20
DB 1 GGTGTCGGGGCCTGTCGCC 20

RESULT 2
US-09-016-464-16
; Sequence 16, Application US/09016464
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: Method of Treatment of Lung Diseases
; TITLE OF INVENTION: Using Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: NC
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,464
FILING DATE: 30-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,497
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5218-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-016-464-16

Query Match          100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCGGGGCCTGTCGCC 20
DB 1 GGTGTCGGGGCCTGTCGCC 20

RESULT 3
US-09-509-152A-1046
; Sequence 1046, Application US/09509152A
; GENERAL INFORMATION:
; APPLICANT: NYCE, JONATHAN W.
; TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION
; NUMBER OF SEQUENCES: 2419
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIDENESIS PHARMACEUTICALS, INC.
; STREET: 7 CLARKE DRIVE
; CITY: CRANBURY
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/509,152A
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/059,160
; FILING DATE: 1997-09-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00091
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-408-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1046:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1046:
US-09-509-152A-1046

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCGCGGGGCGCTGGTCC 20
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Db 1 GGTCGCGGGGCGCTGGTCC 20

RESULT 4

US-09-509-152A-1725

Sequence 1725, Application US/09509152A

GENERAL INFORMATION:

APPLICANT: NYCE, JONATHAN W.

TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION

FORMULATIONS, KITS & APPLICATIONS

NUMBER OF SEQUENCES: 2419

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 CLARKE DRIVE

CITY: CRANBURY

STATE: NJ

ZIP: 08512

COUNTRY: USA

COMPUTER READABLE FORM:

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/509,152A

FILING DATE: 17-Mar-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/059,160

FILING DATE: 1997-09-17

ATTORNEY/AGENT INFORMATION:

NAME: Amzel, Viviana

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: EPI-00991

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-409-3035

TELEFAX: 413-254-9245

TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 1725:

SEQUENCE CHARACTERISTICS:

LENGTH: 180 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1725:

US-09-509-152A-1725

Query Match 100.0%; Score 20; DB 19; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCGCGGGGCGCTGGTCC 20
|||||
Db 1 GGTCGCGGGGCGCTGGTCC 20

RESULT 5
US-09-058-707-3/c

Sequence 3, Application US/09058707
GENERAL INFORMATION:
APPLICANT: Gould, Michael N.
APPLICANT: Chen, Kai-Shun
TITLE OF INVENTION: MAMMARY GLAND-SPECIFIC PROMOTERS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin

COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,707
FILING DATE:

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:

NAME: Baker, Jean C.

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 960296.95262

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 271-5709

TELEFAX: (414) 271-3552

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 827 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-058-707-3

Query Match 100.0%; Score 20; DB 14; Length 827;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCGCGGGGCGCTGGTCC 20
|||||
Db 68 GGTCGCGGGGCGCTGGTCC 49

RESULT 6

US-09-509-152A-2410

Sequence 2410, Application US/09509152A

GENERAL INFORMATION:

APPLICANT: NYCE, JONATHAN W.

TITLE OF INVENTION: MULTIPLE TARGET HYBRIDIZING COMPOSITION

FORMULATIONS, KITS & APPLICATIONS

NUMBER OF SEQUENCES: 2419

CORRESPONDENCE ADDRESS:

ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

STREET: 7 CLARKE DRIVE

CITY: CRANBURY

STATE: NJ

COUNTRY: USA

ZIP: 08512

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/509,152A

FILING DATE: 17-Mar-2000

CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/059,160
FILING DATE: 1997-09-17
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-00991
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2410:
SEQUENCE CHARACTERISTICS:
LENGTH: 6225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2410:
US-09-509-152A-2410

Query Match 100.0%; Score 20; DB 19; Length 6225;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTGCGGGGCGCTGGTGCC 20
|||||
Db 133 GGTTGCGGGGCGCTGGTGCC 152

RESULT 7
US-09-040-265-2443/C
Sequence 2443, Application US/09040265
GENERAL INFORMATION:

APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: HUMAN BRAIN PONS
NUMBER OF SEQUENCES: 3246
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,265
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,229
FILING DATE: MARCH 24, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0342 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2443:
SEQUENCE CHARACTERISTICS:

LENGTH: 277 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 3952113H1
US-09-040-265-2443

Query Match 95.0%; Score 19; DB 14; Length 277;
Best Local Similarity 95.0%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTTGCGGGGCGCTGGTGCC 20
|||||
Db 46 GGTTGCGGGGCGCTGGTGCC 27

RESULT 8

US-09-040-265A-2443/C
Sequence 2443, Application US/09040265A
GENERAL INFORMATION:

APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
TITLE OF INVENTION: HUMAN BRAIN PONS
NUMBER OF SEQUENCES: 3246
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,265A
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,229
FILING DATE: MARCH 24, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0342 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2443:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 3952113H1
US-09-040-265A-2443

Query Match 95.0%; Score 19; DB 14; Length 277;
Best Local Similarity 95.0%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTGGGGGCGCTGTGCC 20
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DB 46 GGCTGCGGGCGCTGTGCC 27

RESULT 9
US-09-533-806-825/c
; Sequence 825, Application US/09533806
; GENERAL INFORMATION:
; APPLICANT: Sellamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ISOMERASES
; FILE REFERENCE: PD-1005 CIP
; CURRENT APPLICATION NUMBER: US/09/533, 806
; CURRENT FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 07/916, 491
; PRIOR FILING DATE: 1992-07-17
; PRIOR APPLICATION NUMBER: 07/977, 780
; PRIOR FILING DATE: 1992-11-19
; PRIOR APPLICATION NUMBER: 08/100, 523
; PRIOR FILING DATE: 1993-08-03
; PRIOR APPLICATION NUMBER: 09/008, 119
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 08/196, 364
; PRIOR FILING DATE: 1994-02-14
; PRIOR APPLICATION NUMBER: 08/282, 991
; PRIOR FILING DATE: 1994-07-28
; PRIOR APPLICATION NUMBER: 08/438, 571
; PRIOR FILING DATE: 1995-05-10
; PRIOR APPLICATION NUMBER: 08/179, 873
; PRIOR FILING DATE: 1994-01-11
; PRIOR APPLICATION NUMBER: 08/504, 732
; PRIOR FILING DATE: 1995-07-20
; PRIOR APPLICATION NUMBER: 08/137, 951
; PRIOR FILING DATE: 1993-10-14
; PRIOR APPLICATION NUMBER: 08/197, 801
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/237, 491
; PRIOR FILING DATE: 1994-04-28
; PRIOR APPLICATION NUMBER: 08/296, 757
; PRIOR FILING DATE: 1994-08-26
; PRIOR APPLICATION NUMBER: 08/221, 531
; PRIOR FILING DATE: 1994-02-02
; PRIOR APPLICATION NUMBER: 08/435, 761
; PRIOR FILING DATE: 1995-05-05
; PRIOR APPLICATION NUMBER: 08/194, 317
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: 08/222, 611
; PRIOR FILING DATE: 1994-03-31
; PRIOR APPLICATION NUMBER: 08/487, 829
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/216, 595
; PRIOR FILING DATE: 1994-03-22
; PRIOR APPLICATION NUMBER: 08/499, 410
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: 08/271, 217
; PRIOR FILING DATE: 1994-06-27
; PRIOR APPLICATION NUMBER: 08/521, 383
; PRIOR FILING DATE: 1995-08-16
; PRIOR APPLICATION NUMBER: 08/274, 621
; PRIOR FILING DATE: 1994-07-08
; PRIOR APPLICATION NUMBER: 08/413, 150
; PRIOR FILING DATE: 1995-03-29
; PRIOR APPLICATION NUMBER: 08/270, 638
; PRIOR FILING DATE: 1994-07-01

; PRIOR APPLICATION NUMBER: 08/412, 033
; PRIOR FILING DATE: 1995-03-28
; PRIOR APPLICATION NUMBER: 08/276, 164
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: 08/293, 347
; PRIOR FILING DATE: 1994-08-19
; PRIOR APPLICATION NUMBER: 08/413, 793
; PRIOR FILING DATE: 1995-03-30
; PRIOR APPLICATION NUMBER: 08/303, 241
; PRIOR FILING DATE: 1994-09-07
; PRIOR APPLICATION NUMBER: 08/323, 523
; PRIOR FILING DATE: 1994-10-14
; PRIOR APPLICATION NUMBER: 08/489, 200
; PRIOR FILING DATE: 1995-06-09
; PRIOR APPLICATION NUMBER: 08/320, 011
; PRIOR FILING DATE: 1994-10-05
; PRIOR APPLICATION NUMBER: 08/440, 743
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/334, 881
; PRIOR FILING DATE: 1994-11-04
; PRIOR APPLICATION NUMBER: 08/369, 881
; PRIOR FILING DATE: 1995-01-05
; PRIOR APPLICATION NUMBER: 08/373, 361
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: 08/393, 220
; PRIOR FILING DATE: 1995-02-23
; PRIOR APPLICATION NUMBER: 08/494, 619
; PRIOR FILING DATE: 1995-06-23
; PRIOR APPLICATION NUMBER: 08/972, 819
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 08/385, 268
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: 08/964, 263
; PRIOR FILING DATE: 1997-11-04
; PRIOR APPLICATION NUMBER: 08/392, 180
; PRIOR FILING DATE: 1995-02-22
; PRIOR APPLICATION NUMBER: 08/964, 265
; PRIOR FILING DATE: 1997-11-04
; PRIOR APPLICATION NUMBER: 08/395, 244
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: 08/972, 899
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 08/451, 242
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/392, 715
; PRIOR FILING DATE: 1995-02-23
; PRIOR APPLICATION NUMBER: 08/963, 650
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 08/416, 401
; PRIOR FILING DATE: 1995-03-31
; PRIOR APPLICATION NUMBER: 08/404, 891
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: 08/406, 219
; PRIOR FILING DATE: 1995-03-16
; PRIOR APPLICATION NUMBER: 08/497, 967
; PRIOR FILING DATE: 1995-07-03
; PRIOR APPLICATION NUMBER: 08/408, 872
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: 08/413, 151
; PRIOR FILING DATE: 1995-03-29
; PRIOR APPLICATION NUMBER: 08/502, 242
; PRIOR FILING DATE: 1995-07-13
; PRIOR APPLICATION NUMBER: 08/421, 124
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/446, 910
; PRIOR FILING DATE: 1995-05-22
; PRIOR APPLICATION NUMBER: 08/429, 361
; PRIOR FILING DATE: 1995-04-26
; PRIOR APPLICATION NUMBER: 08/440, 817
; PRIOR FILING DATE: 1995-05-15
; PRIOR APPLICATION NUMBER: 60/000, 275
; PRIOR FILING DATE: 1995-06-16
; PRIOR APPLICATION NUMBER: 08/668, 236

;; PRIOR FILING DATE: 1996-06-14
;; PRIOR APPLICATION NUMBER: 60/000,744
;; PRIOR FILING DATE: 1995-06-30
;; PRIOR APPLICATION NUMBER: 08/672,741
;; PRIOR FILING DATE: 1996-06-28
;; PRIOR APPLICATION NUMBER: 60/001,754
;; PRIOR FILING DATE: 1995-08-01
;; PRIOR APPLICATION NUMBER: 60/688,870
;; PRIOR FILING DATE: 1996-07-31
;; PRIOR APPLICATION NUMBER: 60/004,416
;; PRIOR FILING DATE: 1995-09-28
;; PRIOR APPLICATION NUMBER: 60/004,657
;; PRIOR FILING DATE: 1995-10-03
;; PRIOR APPLICATION NUMBER: 08/725,587
;; PRIOR FILING DATE: 1996-10-03
;; PRIOR APPLICATION NUMBER: 60/005,175
;; PRIOR FILING DATE: 1995-10-02
;; PRIOR APPLICATION NUMBER: 08/725,863
;; PRIOR FILING DATE: 1996-10-04
;; PRIOR APPLICATION NUMBER: 60/004,810
;; PRIOR FILING DATE: 1995-10-02
;; PRIOR APPLICATION NUMBER: 08/724,751
;; PRIOR FILING DATE: 1996-10-02
;; PRIOR APPLICATION NUMBER: 60/006,111
;; PRIOR FILING DATE: 1995-10-24
;; PRIOR APPLICATION NUMBER: 08/992,868
;; PRIOR FILING DATE: 1997-12-11
;; PRIOR APPLICATION NUMBER: 60/734,050
;; PRIOR FILING DATE: 1996-10-18
;; PRIOR APPLICATION NUMBER: 60/004,490
;; PRIOR FILING DATE: 1995-09-29
;; PRIOR APPLICATION NUMBER: 08/723,972
;; PRIOR FILING DATE: 1996-09-27
;; PRIOR APPLICATION NUMBER: 60/004,672
;; PRIOR FILING DATE: 1995-10-02
;; PRIOR APPLICATION NUMBER: 08/725,029
;; PRIOR FILING DATE: 1996-10-02
;; PRIOR APPLICATION NUMBER: 60/005,526
;; PRIOR FILING DATE: 1995-09-29
;; PRIOR APPLICATION NUMBER: 08/722,922
;; PRIOR FILING DATE: 1996-09-27
;; PRIOR APPLICATION NUMBER: 60/004,809
;; PRIOR FILING DATE: 1995-10-02
;; PRIOR APPLICATION NUMBER: 08/725,693
;; PRIOR FILING DATE: 1996-09-30
;; PRIOR APPLICATION NUMBER: 60/004,674
;; PRIOR FILING DATE: 1995-10-02
;; PRIOR APPLICATION NUMBER: 08/731,034
;; PRIOR FILING DATE: 1996-10-02
;; PRIOR APPLICATION NUMBER: 60/004,676
;; PRIOR FILING DATE: 1995-10-02
;; PRIOR APPLICATION NUMBER: 08/706,766
;; PRIOR FILING DATE: 1996-09-27
;; PRIOR APPLICATION NUMBER: 60/005,023
;; PRIOR FILING DATE: 1995-10-10
;; PRIOR APPLICATION NUMBER: 08/727,870
;; PRIOR FILING DATE: 1996-10-09
;; PRIOR APPLICATION NUMBER: 60/005,197
;; PRIOR FILING DATE: 1995-10-10
;; PRIOR APPLICATION NUMBER: 08/726,759
;; PRIOR FILING DATE: 1996-10-09
;; PRIOR APPLICATION NUMBER: 60/005,008
;; PRIOR FILING DATE: 1995-10-10
;; PRIOR APPLICATION NUMBER: 08/727,737
;; PRIOR FILING DATE: 1996-10-08

Query Match 95.0%; Score 19; DB 20; Length 277;
Best Local Similarity 95.0%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCGGGGCCTGTGCC 20
DB 46 GGTGTCGGGGCCTGTGCC 27

RESULT 10
US-08-960-741-378/C
; Sequence 378, Application US/08960741
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; TITLE OF INVENTION: HUMAN TESTES
; NUMBER OF SEQUENCES: 1890
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,741
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0270P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 378:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 2006803H1
US-08-960-741-378

Query Match 92.0%; Score 18.4; DB 13; Length 132;
Best Local Similarity 95.0%; Pred. No. 7.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCGGGGCCTGTGCC 20
DB 45 GGTGTCGGGGCCTGTGCC 26

RESULT 11
US-09-533-806-3263/C
; Sequence 3263, Application US/09533806
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullaly, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ISOMERASES
; FILE REFERENCE: PD-1005 CIP

;; CURRENT APPLICATION NUMBER: US/09/533,806
;; CURRENT FILING DATE: 2000-03-24
;; PRIOR APPLICATION NUMBER: 07/916,491
;; PRIOR FILING DATE: 1992-07-17
;; PRIOR APPLICATION NUMBER: 07/977,780
;; PRIOR FILING DATE: 1992-11-19
;; PRIOR APPLICATION NUMBER: 08/100,523
;; PRIOR FILING DATE: 1993-08-03
;; PRIOR APPLICATION NUMBER: 09/008,119
;; PRIOR FILING DATE: 1998-01-16
;; PRIOR APPLICATION NUMBER: 08/196,364
;; PRIOR FILING DATE: 1994-02-14
;; PRIOR APPLICATION NUMBER: 08/282,991
;; PRIOR FILING DATE: 1994-07-28
;; PRIOR APPLICATION NUMBER: 08/438,571
;; PRIOR FILING DATE: 1995-05-10
;; PRIOR APPLICATION NUMBER: 08/179,873
;; PRIOR FILING DATE: 1994-01-11
;; PRIOR APPLICATION NUMBER: 08/504,732
;; PRIOR FILING DATE: 1995-07-20
;; PRIOR APPLICATION NUMBER: 08/137,951
;; PRIOR FILING DATE: 1993-10-14
;; PRIOR APPLICATION NUMBER: 08/197,801
;; PRIOR FILING DATE: 1994-02-17
;; PRIOR APPLICATION NUMBER: 08/237,491
;; PRIOR FILING DATE: 1994-04-28
;; PRIOR APPLICATION NUMBER: 08/296,757
;; PRIOR FILING DATE: 1994-08-26
;; PRIOR APPLICATION NUMBER: 08/221,531
;; PRIOR FILING DATE: 1994-02-02
;; PRIOR APPLICATION NUMBER: 08/435,761
;; PRIOR FILING DATE: 1995-05-05
;; PRIOR APPLICATION NUMBER: 08/194,317
;; PRIOR FILING DATE: 1994-02-04
;; PRIOR APPLICATION NUMBER: 08/222,611
;; PRIOR FILING DATE: 1994-03-31
;; PRIOR APPLICATION NUMBER: 08/487,829
;; PRIOR FILING DATE: 1995-06-07
;; PRIOR APPLICATION NUMBER: 08/216,595
;; PRIOR FILING DATE: 1994-03-22
;; PRIOR APPLICATION NUMBER: 08/499,410
;; PRIOR FILING DATE: 1995-07-07
;; PRIOR APPLICATION NUMBER: 08/271,217
;; PRIOR FILING DATE: 1994-06-27
;; PRIOR APPLICATION NUMBER: 08/521,383
;; PRIOR FILING DATE: 1995-08-16
;; PRIOR APPLICATION NUMBER: 08/274,621
;; PRIOR FILING DATE: 1994-07-08
;; PRIOR APPLICATION NUMBER: 08/413,150
;; PRIOR FILING DATE: 1995-03-29
;; PRIOR APPLICATION NUMBER: 08/270,638
;; PRIOR FILING DATE: 1994-07-01
;; PRIOR APPLICATION NUMBER: 08/412,033
;; PRIOR FILING DATE: 1995-03-28
;; PRIOR APPLICATION NUMBER: 08/276,164
;; PRIOR FILING DATE: 1994-07-15
;; PRIOR APPLICATION NUMBER: 08/293,347
;; PRIOR FILING DATE: 1994-08-19
;; PRIOR APPLICATION NUMBER: 08/413,793
;; PRIOR FILING DATE: 1995-03-30
;; PRIOR APPLICATION NUMBER: 08/303,241
;; PRIOR FILING DATE: 1994-09-07
;; PRIOR APPLICATION NUMBER: 08/323,523
;; PRIOR FILING DATE: 1994-10-14
;; PRIOR APPLICATION NUMBER: 08/489,200
;; PRIOR FILING DATE: 1995-06-09
;; PRIOR APPLICATION NUMBER: 08/320,011
;; PRIOR FILING DATE: 1994-10-05
;; PRIOR APPLICATION NUMBER: 08/440,743
;; PRIOR FILING DATE: 1995-05-12
;; PRIOR APPLICATION NUMBER: 08/334,881
;; PRIOR FILING DATE: 1994-11-04
;; PRIOR APPLICATION NUMBER: 08/369,881

;; PRIOR FILING DATE: 1995-01-05
;; PRIOR APPLICATION NUMBER: 08/373,361
;; PRIOR FILING DATE: 1995-01-17
;; PRIOR APPLICATION NUMBER: 08/393,220
;; PRIOR FILING DATE: 1995-02-23
;; PRIOR APPLICATION NUMBER: 08/494,619
;; PRIOR FILING DATE: 1995-06-23
;; PRIOR APPLICATION NUMBER: 08/972,819
;; PRIOR FILING DATE: 1997-11-18
;; PRIOR APPLICATION NUMBER: 08/385,268
;; PRIOR FILING DATE: 1995-02-07
;; PRIOR APPLICATION NUMBER: 08/964,263
;; PRIOR FILING DATE: 1997-11-04
;; PRIOR APPLICATION NUMBER: 08/392,180
;; PRIOR FILING DATE: 1995-02-22
;; PRIOR APPLICATION NUMBER: 08/964,265
;; PRIOR FILING DATE: 1997-11-04
;; PRIOR APPLICATION NUMBER: 08/395,244
;; PRIOR FILING DATE: 1995-02-27
;; PRIOR APPLICATION NUMBER: 08/972,899
;; PRIOR FILING DATE: 1997-11-18
;; PRIOR APPLICATION NUMBER: 08/451,242
;; PRIOR FILING DATE: 1995-05-25
;; PRIOR APPLICATION NUMBER: 08/392,715
;; PRIOR FILING DATE: 1995-02-23
;; PRIOR APPLICATION NUMBER: 08/963,650
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 08/416,401
;; PRIOR FILING DATE: 1995-03-31
;; PRIOR APPLICATION NUMBER: 08/404,891
;; PRIOR FILING DATE: 1995-03-15
;; PRIOR APPLICATION NUMBER: 08/406,219
;; PRIOR FILING DATE: 1995-03-16
;; PRIOR APPLICATION NUMBER: 08/497,967
;; PRIOR FILING DATE: 1995-07-03
;; PRIOR APPLICATION NUMBER: 08/408,872
;; PRIOR FILING DATE: 1995-03-21
;; PRIOR APPLICATION NUMBER: 08/413,151
;; PRIOR FILING DATE: 1995-03-29
;; PRIOR APPLICATION NUMBER: 08/502,242
;; PRIOR FILING DATE: 1995-07-13
;; PRIOR APPLICATION NUMBER: 08/421,124
;; PRIOR FILING DATE: 1995-04-12
;; PRIOR APPLICATION NUMBER: 08/446,910
;; PRIOR FILING DATE: 1995-05-22
;; PRIOR APPLICATION NUMBER: 08/429,361
;; PRIOR FILING DATE: 1995-04-26
;; PRIOR APPLICATION NUMBER: 08/440,817
;; PRIOR FILING DATE: 1995-05-15
;; PRIOR APPLICATION NUMBER: 60/000,275
;; PRIOR FILING DATE: 1995-06-16
;; PRIOR APPLICATION NUMBER: 08/668,236
;; PRIOR FILING DATE: 1996-06-14
;; PRIOR APPLICATION NUMBER: 60/000,744
;; PRIOR FILING DATE: 1995-06-30
;; PRIOR APPLICATION NUMBER: 08/672,741
;; PRIOR FILING DATE: 1996-06-28
;; PRIOR APPLICATION NUMBER: 60/001,754
;; PRIOR FILING DATE: 1995-08-01
;; PRIOR APPLICATION NUMBER: 08/688,870
;; PRIOR FILING DATE: 1996-07-31
;; PRIOR APPLICATION NUMBER: 60/004,416
;; PRIOR FILING DATE: 1995-09-28
;; PRIOR APPLICATION NUMBER: 60/004,697
;; PRIOR FILING DATE: 1995-10-03
;; PRIOR APPLICATION NUMBER: 08/725,587
;; PRIOR FILING DATE: 1996-10-03
;; PRIOR APPLICATION NUMBER: 60/005,175
;; PRIOR FILING DATE: 1995-10-02
;; PRIOR APPLICATION NUMBER: 08/725,863
;; PRIOR FILING DATE: 1996-10-04
;; PRIOR APPLICATION NUMBER: 60/004,810
;; PRIOR FILING DATE: 1995-10-02

PRIOR APPLICATION NUMBER: 08/724,751
PRIOR FILING DATE: 1996-10-02
PRIOR APPLICATION NUMBER: 60/006,111
PRIOR FILING DATE: 1995-10-24
PRIOR APPLICATION NUMBER: 08/992,868
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 08/734,050
PRIOR FILING DATE: 1996-10-18
PRIOR APPLICATION NUMBER: 60/004,490
PRIOR FILING DATE: 1995-09-29
PRIOR APPLICATION NUMBER: 08/723,972
PRIOR FILING DATE: 1996-09-27
PRIOR APPLICATION NUMBER: 60/004,672
PRIOR FILING DATE: 1995-10-02
PRIOR APPLICATION NUMBER: 08/725,029
PRIOR FILING DATE: 1996-10-02
PRIOR APPLICATION NUMBER: 60/005,526
PRIOR FILING DATE: 1995-09-29
PRIOR APPLICATION NUMBER: 08/722,922
PRIOR FILING DATE: 1996-09-27
PRIOR APPLICATION NUMBER: 60/004,809
PRIOR FILING DATE: 1995-10-02
PRIOR APPLICATION NUMBER: 08/725,693
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: 60/004,674
PRIOR FILING DATE: 1995-10-02
PRIOR APPLICATION NUMBER: 08/731,034
PRIOR FILING DATE: 1996-10-02
PRIOR APPLICATION NUMBER: 60/004,676
PRIOR FILING DATE: 1995-10-02
PRIOR APPLICATION NUMBER: 08/706,766
PRIOR FILING DATE: 1996-09-27
PRIOR APPLICATION NUMBER: 60/005,023
PRIOR FILING DATE: 1995-10-10
PRIOR APPLICATION NUMBER: 08/727,870
PRIOR FILING DATE: 1996-10-09
PRIOR APPLICATION NUMBER: 60/005,197
PRIOR FILING DATE: 1995-10-10
PRIOR APPLICATION NUMBER: 08/726,759
PRIOR FILING DATE: 1996-10-09
PRIOR APPLICATION NUMBER: 60/005,008
PRIOR FILING DATE: 1995-10-10
PRIOR APPLICATION NUMBER: 08/727,737
PRIOR FILING DATE: 1996-10-08

Query Match 92.0%; Score 18.4; DB 20; Length 132;
Best Local Similarity 95.0%; Pred. No. 7.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGTGTCGGGGCGCTGTGCC 20
||||| ||||||| |||||||
DB 45 GGTGTCGGGGCGCTGTGCC 26

RESULT 12
US-60-030-888-378/C
Sequence 378, Application US/60030888
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akertlow, Ingrid E.
APPLICANT: Deleane, Angela M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
HUMAN TESTES
NUMBER OF SEQUENCES: 1890
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/030,888
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0270P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEFAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 378:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 2006803H1
US-60-030-888-378

Query Match 92.0%; Score 18.4; DB 35; Length 132;
Best Local Similarity 95.0%; Pred. No. 7.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGTGTCGGGGCGCTGTGCC 20
||||| ||||||| |||||||
DB 45 GGTGTCGGGGCGCTGTGCC 26

RESULT 13
US-09-533-806-3298/C
Sequence 3298, Application US/09533806
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleane, Angela M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullaly, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ISOMERASES
FILE REFERENCE: PD-1005 CIP
CURRENT APPLICATION NUMBER: US/09/533,806
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 07/916,491
PRIOR FILING DATE: 1992-07-17
PRIOR APPLICATION NUMBER: 07/977,780
PRIOR FILING DATE: 1992-11-19
PRIOR APPLICATION NUMBER: 08/100,523
PRIOR FILING DATE: 1993-08-03
PRIOR APPLICATION NUMBER: 09/008,119
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 08/196,364
PRIOR FILING DATE: 1994-02-14
PRIOR APPLICATION NUMBER: 08/282,991
PRIOR FILING DATE: 1994-07-28
PRIOR APPLICATION NUMBER: 08/438,571
PRIOR FILING DATE: 1995-05-10
PRIOR APPLICATION NUMBER: 08/179,873
PRIOR FILING DATE: 1994-01-11
PRIOR APPLICATION NUMBER: 08/504,732
PRIOR FILING DATE: 1995-07-20
PRIOR APPLICATION NUMBER: 08/137,951